Table 20. Examples of carotenoid hydroxylase polypeptides.

Accession Number	GI Number	Description
AAC44852	1842246	b-carotene hydroxylase
AAC49443	1575296	beta-carotene hydroxylase [Arabidopsis thaliana]
AAD54243	5852870	carotenoid hydroxylase [Haematococcus pluvialis]
AAG10430	9971820	beta hydroxylase [Tagetes erecta]
AAG10793	9988836	beta-carotene hydroxylase [Citrus unshiu]
AAG33636	11245486	beta-carotene hydroxylase [Citrus unshiu]
AAL80006	19071768	beta carotene hydroxylase [Sandersonia aurantiaca]
AAM44971	21280903	putative beta-carotene hydroxylase [Arabidopsis thaliana]
AAM51300	21436107	putative beta-carotene hydroxylase [Arabidopsis thaliana]
AAM77007	21734857	beta-carotene hydroxylase [Vitis vinifera]
AAN85601	27228295	Beta-Carotene Hydroxylase [Pantoea stewartii]
AAO53295	28911949	carotenoid hydroxylase [Haematococcus pluvialis]
AAS48097	44887642	beta-carotene hydroxylase [Citrus sinensis]
AAS55552	45184599	putative beta-carotene hydroxylase [Brassica rapa]
AAS88426	46326968	beta-carotene hydroxylase [Glycine max]
AAT48741	49036137	beta-carotene hydroxylase [Citrus sinensis]
AAT84408	50844570	beta carotene hydroxylase [Crocus sativus]
AAV85452	56267980	beta-ring oxygenase AdKeto1 [Adonis palaestina]
AAV85453	56267982	beta-ring oxygenase AdKeto2 [Adonis palaestina]
BAA14129	216687	crtZ [Pantoea ananatis]
BAB79605	18143450	crtZ [Pantoea agglomerans pv. milletiae]
BAC77670	31790567	gamma-carotene hydroxylase [marine bacterium P99-3]
BAD07283	40809749	beta-ring hydroxylase [Citrus sinensis]
BAD07291	40809765	beta-ring hydroxylase [Citrus limon]
CAA70427	2956671	beta-carotene hydrolase [Capsicum annuum]
CAA70888	2956717	beta-carotene hydroxylase 2 [Capsicum annuum]
CAB55625	5870598	beta-carotene hydroxylase [Lycopersicon esculentum]
CAB55626	5870600	beta-carotene hydroxylase [Lycopersicon esculentum]
CAB56060	5912293	carotene hydroxylase [Paracoccus marcusii]
CAC06712	9968545	beta-carotene hydroxylase [Narcissus pseudonarcissus]
CAC95130	33145986	beta-carotene hydroxylase [Crocus sativus]
EAB30128	42926157	unknown [environmental sequence]
EAC49462	43167766	unknown [environmental sequence]
EAC86129	43241003	unknown [environmental sequence]
EAD61089	43395962	unknown [environmental sequence]
EAD76156	43443111	unknown [environmental sequence]
EAD88640	43467793	unknown [environmental sequence]
EAE27903	43546376	unknown [environmental sequence]
EAE28203	43546980	unknown [environmental sequence]
EAE78743	43647896	unknown [environmental sequence]
EAF12173	43714211	unknown [environmental sequence]
EAH29370	44130906	unknown [environmental sequence]
EAH44202	44158360	unknown [environmental sequence]
EAI00766	44256844	unknown [environmental sequence]
EAI29017	44298625	unknown [environmental sequence]
EAJ30844	44443849	unknown [environmental sequence]
EAJ72524	44504516	unknown [environmental sequence]
EAK10611	44559981	unknown [environmental sequence]
EAK53455	44620561	unknown [environmental sequence]
EAK63955	44635271	unknown [environmental sequence]

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H90469	25394049	beta carotene hydroxylase (crtZ) [imported] - Sulfolobus solfataricus
NP_745389	26989964	beta-carotene hydroxylase [Pseudomonas putida KT2440]
NP_922503	37536402	putative beta-carotene hydroxylase [Oryza sativa (japonica cultivar-group)]
P54973	1706152	Beta-carotene hydroxylase
Q44262	2498258	Beta-carotene hydroxylase
S52982	1073291	beta-carotene hydroxylase - Erwinia herbicola
XP_473611	50928167	OSJNBa0011J08.7 [Oryza sativa (japonica cultivar-group)]
YP_024309	48478603	beta carotene hydroxylase [Picrophilus torridus DSM 9790]
ZP_003055	48851297	COG3000: Sterol desaturase [Novosphingobium aromaticivorans DSM 12444]
ZP_003107	48856620	COG3000: Sterol desaturase [Cytophaga hutchinsonii]

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Table 21. Examples of astaxanthin synthase polypeptides and putative astaxanthin synthase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAM56288	21501451	Astaxanthin synthase [Xanthophyllomyces dendrorhous]
XP_571276	58268240	Cytochrome P450, putative [Cryptococcus neoformans var. neoformans JEC21]
EAL20013	50257304	hypothetical protein CNBF3400 [Cryptococcus neoformans var. neoformans B-3501A]
XP_401804	49075484	hypothetical protein UM04189.1 [Ustilago maydis 521]
XP_397817	49067054	hypothetical protein UM00202.1 [Ustilago maydis 521]
XP_399595	49070612	hypothetical protein UM01980.1 [Ustilago maydis 521]
XP_403279	49079218	hypothetical protein UM05664.1 [Ustilago maydis 521]
XP_382294	46110473	hypothetical protein FG02118.1 [Gibberella zeae PH-1]
XP_406021	49088382	hypothetical protein AN1884.2 [Aspergillus nidulans FGSC A4]
XP_381224	46108332	hypothetical protein FG01048.1 [Gibberella zeae PH-1]
XP_391479	46139577	hypothetical protein FG11303.1 [Gibberella zeae PH-1]
XP_569261	58264210	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]
EAL22841	50260180	hypothetical protein CNBB0620 [Cryptococcus neoformans var. neoformans B-3501A]
XP_359866	39940658	hypothetical protein MG04911.4 [Magnaporthe grisea 70-15]

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Table 22. Examples of carotenoid epsilon hydroxylase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
ABB52076	79155148	putative epsilon-ring carotene hydroxylase [Daucus carota subsp. sativus]
BAD94136	62319017	Cytochrom P450 -like protein [Arabidopsis thaliana]
ABD28565	87162770	E-class P450, group I [Medicago truncatula]
AAT28222	47498772	putative 97B2-like cytochrome P450 [Ginkgo biloba]
ABC68396	85001685	cytochrome P450 monooxygenase CYP97A [Glycine max]
ABC59110	84514203	cytochrome P450 monooxygenase CYP97B [Medicago truncatula]
NP_190881	42565881	LUT1 (LUTEIN DEFICIENT 1); oxygen binding [Arabidopsis thaliana]
ABB47954	78708979	cytochrome P450 monooxygenase, putative [Oryza sativa (japonica cultivar-group)]
NP_922604	37536604	putative cytochrome P450 monooxygenase [Oryza sativa (japonica cultivar-group)]

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Table 23. Examples of lycopene cyclase polypeptides, beta and epsilon subunits.

ACCESSION	GI	PROTEIN DESCRIPTION
XP_001422490	145356548	predicted protein [Ostreococcus lucimarinus CCE9901]
BAE94036	94481238	lycopene epsilon cyclase (Diospyros kaki)
AAK07431	12746307	lycopene epsilon-cyclase [Adonis palaestina]
ABB52073	79154988	putative lycopene epsilon cyclase [Daucus carota subsp. sativus]
Q38932	27735211	Lycopene epsilon cyclase, chloroplast precursor
AAB53336	1399181	lycopene epsilon cyclase
AAG10428	9971816	epsilon cyclase [Tagetes erecta]
AAK07434	12746313	lycopene epsilon-cyclase [Lactuca sativa]
AAM45382	21360359	epsilon cyclase [Tagetes erecta]
O65837	11132841	Lycopene epsilon cyclase, chloroplast precursor
AAL69394	18419661	lycopene epsilon-cyclase [Spinacia oleracea]
BAE79549	87299433	lycopene epsilon-cyclase [Chrysanthemum x morifolium]
XP_463351	50901836	putative lycopene epsilon-cyclase [Oryza sativa (japonica cultivar-group)]
AAS48096	44887640	epsilon lycopene cyclase [Citrus sinensis]
AAX92679	62638188	lycopene epsilon cyclase [Citrus maxima]
AAL92114	19569601	lycopene epsilon-cyclase [Citrus x paradisi]
AAK07433	12746311	lycopene epsilon-cyclase [Solanum tuberosum]
AAL47019	17864021	lycopene epsilon-cyclase [Citrus sinensis]
AAT46065	48686703	chloroplast lycopene epsilon-cyclase precursor [Chlamydomonas reinhardtii]
BAD07293	40809769	lycopene epsilon-cyclase [Citrus limon]
BAD07285	40809753	lycopene epsilon-cyclase [Citrus sinensis]
BAD07277	40809737	lycopene epsilon-cyclase [Citrus unshiu]
EAJ62839	44489138	unknown [environmental sequence]
BAE43547	73993068	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43550	73993074	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43557	73993088	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43558	73993090	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43553	73993080	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43545	73993064	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43556	73993086	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43552	73993078	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43560	73993094	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43554	73993082	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43551	73993076	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43519	73993012	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43535	73993044	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43541	73993056	putative lycopene beta cyclase [Cryptomeria japonica]

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BAE43542	73993058	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43517	73993008	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43534	73993042	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43537	73993048	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43533	73993040	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02774	38603277	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02766	38603261	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43540	73993054	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43514	73993002	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43544	73993062	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43538	73993050	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43528	73993030	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43546	73993066	putative lycopene beta cyclase [Taxodium distichum var. distichum]
BAE43526	73993026	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43543	73993060	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02742	38603213	putative lycopene beta cyclase [Cryptomeria japonica]
BAD02770	38603269	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43522	73993018	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43559	73993092	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43527	73993028	putative lycopene beta cyclase [Cryptomeria japonica]
BAE43548	73993070	putative lycopene beta cyclase [Taxodium distichum var. distichum]
AAF44700	14550425	lycopene beta-cyclase [Citrus sinensis]
BAE43555	73993084	putative lycopene beta cyclase [Taxodium distichum var. imbricarium]
BAE43549	73993072	putative lycopene beta cyclase [Taxodium distichum var. distichum]
AAU14144	51922063	lycopene beta-cyclase [Citrus sinensis]
AAN86060	27261727	lycopene cyclase [Citrus unshiu]
AAR89632	40756518	lycopene-beta-cyclase [Citrus maxima]
AAM21152	20530862	lycopene beta-cyclase [Citrus sinensis]
AAD38049	13959731	lycopene cyclase [Citrus x paradisi]
AAU05146	51511939	lycopene beta-cyclase [Citrus sinensis]
AAU05145	51511937	lycopene beta-cyclase [Citrus sinensis]
AAK07430	12746305	lycopene beta-cyclase [Adonis palaestina]
ABB72443	82394885	lycopene beta-cyclase [Citrus sinensis]
BAE79544	87299423	lycopene beta-cyclase [Chrysanthemum x morifolium]
BAE78471	85717882	lycopene beta cyclase [Taraxacum officinale]
Q43415	11133019	Lycopene beta cyclase, chloroplast precursor
AAF23013	6665782	lycopene epsilon-cyclase [Daucus carota]
ABB52071	79154899	putative lycopene beta cyclase [Daucus carota subsp. sativus]
AAW88382	59665024	lycopene beta-cyclase [Lycium barbarum]
AAG10429	9971818	beta cyclase [Tagetes erecta]
AAM45381	21360357	beta cyclase [Tagetes erecta]
AAM14335	20259239	putative lycopene beta cyclase [Arabidopsis thaliana]
AAO18661	27728515	lycopene beta-cyclase [Zea mays]
AAA81880	735882	lycopene cyclase
Q43503	11133022	Lycopene beta cyclase, chloroplast precursor
S66350	2129931	lycopene beta-cyclase (EC 5.5.1.-) - tomato
XP_464409	50905841	putative lycopene beta-cyclase [Oryza sativa (japonica

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		cultivar-group)]
CAD70565	45237491	lycopene cyclase [Bixa orellana]
Q43578	11133025	Lycopene beta cyclase, chloroplast precursor
AAL92175	19569782	beta-lycopene cyclase [Sandersonia aurantiaca]
AAX54906	61742130	putative chloroplast lycopene beta cyclase precursor [Chlamydomonas reinhardtii]
S66349	2129954	lycopene beta-cyclase (EC 5.5.1.-) - common tobacco
AAG21133	10644119	chromoplast-specific lycopene beta-cyclase [Lycopersicon esculentum]
CAB92977	8247354	neoxanthin synthase [Solanum tuberosum]
CAB93342	8249885	neoxanthin synthase [Lycopersicon esculentum]
Q9SEA0	11131528	Capsanthin/capsorubin synthase, chloroplast precursor
Q42435	12643508	Capsanthin/capsorubin synthase, chloroplast precursor
AAO64977	37730608	lycopene beta cyclase [Haematococcus pluvialis]
Q40424	11133011	Lycopene beta cyclase, chloroplast precursor
ABB52072	79154940	putative capsanthin-capsorubin synthase [Daucus carota subsp. sativus]
AAQ02668	33304511	lycopene cyclase [Setaria italica]
CAA54961	840729	putative chromoplastic oxydo-reductase [Capsicum annuum]
EAJ62838	44489136	unknown [environmental sequence]
YP_401079	81300871	Lycopene cyclase, beta and epsilon [Synechococcus elongatus PCC 7942]
YP_172741	56752040	lycopene cyclase [Synechococcus elongatus PCC 6301]
ZP_011...	88808972	lycopene beta cyclase [Synechococcus sp. WH 7805]
EAK50052	44615956	unknown [environmental sequence]
NP_892751	33861190	putative lycopene epsilon cyclase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_875182	33240240	Lycopene epsilon cyclase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
YP_382237	78213458	Lycopene cyclase, beta and epsilon [Synechococcus sp. CC9605]
YP_397130	78779018	Lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. MIT 9312]
NP_896821	33865262	lycopene beta cyclase [Synechococcus sp. WH 8102]
YP_397570	78779458	Lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. MIT 9312]
ZP_010...	87302144	lycopene cyclase [Synechococcus sp. WH 5701]
EAK17149	44569190	unknown [environmental sequence]
YP_291882	72382527	lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. NATL2A]
NP_875528	33240586	Lycopene beta cyclase related dehydrogenase [Prochlorococcus marinus subsp. marinus str. CCMP1375]
NP_893181	33861620	putative lycopene beta cyclase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
NP_895600	33864040	putative lycopene epsilon cyclase [Prochlorococcus marinus str. MIT 9313]
EAI47456	44325573	unknown [environmental sequence]
YP_291268	72381913	lycopene cyclase, beta and epsilon [Prochlorococcus marinus str. NATL2A]
ZP_010...	84517806	Lycopene beta cyclase related dehydrogenase [Prochlorococcus marinus str. MIT 9211]
AAF34191	6970079	lycopene epsilon cyclase [Daucus carota]

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ZP_010...	84518202	Lycopene epsilon cyclase [Prochlorococcus marinus str. MIT 9211]
YP_376736	78184301	Lycopene cyclase, beta and epsilon [Synechococcus sp. CC9902]
ZP_003...	66796756	Lycopene cyclase, beta and epsilon [Deinococcus geothermalis DSM 11300]
NP_894954	33863394	putative lycopene beta cyclase [Prochlorococcus marinus str. MIT 9313]
AAT76051	50365502	lycopene cyclase [Citrus clementina]
EAK22047	44576122	unknown [environmental sequence]
NP_294525	15805827	lycopene cyclase [Deinococcus radiodurans R1]

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Table 24. Examples of carotenoid glucosyltransferase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAA21261	148395	CrtX [Pantoea agglomerans]
AAN85597	27228291	Zeaxanthin Glucosyl Transferase [Pantoea stewartii]
BAB79601	18143446	crtX [Pantoea agglomerans pv. milletiae]
AAZ73147	72536082	zeaxanthin glucosyl transferase [Enterobacteriaceae bacterium DC413]
AAZ73128	72536060	zeaxanthin glucosyl transferase [Enterobacteriaceae bacterium DC260]
AAZ73140	72536074	zeaxanthin glucosyl transferase [Enterobacteriaceae bacterium DC416]
Q01330	231911	Zeaxanthin glucosyl transferase
ZP_006...	71674312	UDP-glycosyltransferase, MGT [Trichodesmium erythraeum IMS101]
NP_439972	16329244	zeaxanthin glucosyl transferase [Synechocystis sp. PCC 6803]
EAH29368	44130903	unknown [environmental sequence]
ZP_005...	67926135	zeaxanthin glucosyl transferase, hypothetical protein [Crocosphaera watsonii WH 8501]
YP_378763	78188425	hypothetical protein Cag_0447 [Chlorobium chlorochromatii CaD3]
ZP_005...	68549418	Glycosyl transferase, group 1 [Pelodictyon phaeoclathratiforme BU-1]
ZP_010...	85713606	glycosyl transferase, group 1 [Nitrobacter sp. Nb-311A]
YP_317171	75674750	glycosyl transferase, group 1 [Nitrobacter winogradskyi Nb-255]
ZP_006...	69929171	Glycosyl transferase, group 1 [Nitrobacter hamburgensis X14]
ZP_009...	84500589	hypothetical protein OB2597_11541 [Oceanicola batsensis HTCC2597]
ZP_009...	83953176	hypothetical protein NAS141_12746 [Sulfitobacter sp. NAS-14.1]
ZP_009...	83942121	hypothetical protein EE36_07793 [Sulfitobacter sp. EE-36]
YP_508020	89052569	glycosyl transferase, group 1 [Jannaschia sp. CCS1]
ZP_010...	85704103	hypothetical protein ROS217_13931 [Roseovarius sp. 217]
ZP_009...	83370850	probable glycosyltransferase [Rhodobacter sphaeroides ATCC 17025]
ZP_006...	69934465	Glycosyl transferase, group 1 [Paracoccus denitrificans PD1222]
ZP_009...	83949880	probable glycosyltransferase [Roseovarius nubinhibens ISM]
YP_376237	78183803	putative glycosyltransferase [Synechococcus sp. CC9902]
YP_376129	78183695	probable glycosyltransferase [Synechococcus sp. CC9902]
YP_374296	78186253	hypothetical protein Plut_0365 [Pelodictyon luteolum DSM 273]
ZP_010...	87301651	Putative glycosyltransferase [Synechococcus sp. WH 5701]
ZP_011...	88809938	Putative glycosyltransferase [Synechococcus sp. WH 7805]
BAE47471	78483937	carotenoid glucosyltransferase [Paracoccus sp. N81106]
ZP_010...	87303273	probable glycosyltransferase [Synechococcus sp. WH 5701]
YP_376127	78183693	probable glycosyltransferase [Synechococcus sp. CC9902]
YP_501334	88196509	hypothetical protein SAOUHSC_02880 [Staphylococcus aureus subsp. aureus NCTC 8325]
YP_187370	57652300	glycosyl transferase, group 2 family protein [Staphylococcus aureus subsp. aureus COL]
CAA66627	1340131u	nnamed protein product [Staphylococcus aureus]

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YP_041987	49484763	putative glycosyl transferase [Staphylococcus aureus subsp. aureus MRSA252]
YP_417885	82752144	hypothetical protein SAB2436c [Staphylococcus aureus RF122]
YP_252404	70725490	hypothetical protein SH0489 [Staphylococcus haemolyticus JCSC1435]
NP_693379	23099913	hypothetical protein OB2458 [Oceanobacillus iheyensis HTE831]
ZP_008...	82501285	conserved hypothetical protein [Caldicellulosiruptor saccharolyticus DSM 8903]
ZP_010...	87303565	hypothetical protein WH5701_09900 [Synechococcus sp. WH 5701]

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Table 25. Examples of acyl CoA:diacylglycerol acyltransferase (DGAT) polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
XP_957022	85082953	hypothetical protein [Neurospora crassa N150]
XP_386864	46124621	hypothetical protein FG06688.1 [Gibberella zeae PH-1]
XP_755172	71000982	diacylglycerol O-acyltransferase DGAT [Aspergillus fumigatus Af293]
XP_663763	67539978	hypothetical protein AN6159.2 [Aspergillus nidulans FGSC A4]
BAE65302	83775179	unnamed protein product [Aspergillus oryzae]
XP_502557	50550169	hypothetical protein [Yarrowia lipolytica]
AAS78662	56199782	diacylglycerol acyltransferase [Glycine max]
ABB84383	82582915	diacylglycerol acyltransferase [Jatropha curcas]
AAV31083	54145459	1,2-diacyl-sn-glycerol:acyl-CoA acyltransferase [Euonymus alatus]
AAG23696	10803053	diacylglycerol acyltransferase [Perilla frutescens]
AAF64065	7576941	putative diacylglycerol acyltransferase [Brassica napus]
AAS01606	41387497	acyl-CoA:diacylglycerol acyltransferase 1 [Olea europaea]
AAT73629	50299542	acyl CoA:diacylglycerol acyltransferase [Glycine max]
AAM03340	67043496	putative diacylglycerol acyltransferase [Tropaeolum majus]
XP_645633	66824557	hypothetical protein DDB0202877 [Dictyostelium discoideum]
AAF19345	6625653	diacylglycerol acylCoA acyltransferase [Nicotiana tabacum]
AAY40785	63376239	diacylglycerol acyltransferase DGAT2 [Brassica juncea]
AAW47581	57231736	diacylglycerol acyltransferase [Oryza sativa (japonica cultivar-group)]
AAR11479	38146080	diacylglycerol acyltransferase [Ricinus communis]
AAY40784	63376226	diacylglycerol acyltransferase DGAT1 [Brassica juncea]
AAP68322	31711932	At2g19450 [Arabidopsis thaliana]
AAW51456	57545061	diacylglycerol acyltransferase [Lotus corniculatus var. japonicus]
AAD45536	5579408	putative diacylglycerol acyltransferase [Brassica napus]
BAD53762	53791817	putative acyl-CoA:diacylglycerol acyltransferase [Oryza sativa (japonica cultivar-group)]
NP_956024	41054343	hypothetical protein LOC325875 [Danio rerio]
AAL49962	18642598	diacylglycerol acyltransferase 1 [Bos taurus]
XP_930884	89028385	similar to Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase) (ACAT-related gene) [Homo sapiens]
NP_777118	27819636	diacylglycerol O-acyltransferase 1 [Bos taurus]
Q9GMF1	18202926	Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase)
NP_036211	6912332	diacylglycerol O-acyltransferase 1 [Homo sapiens]
AAH06263	34782946	DGAT1 protein [Homo sapiens]
XP_780515	72006039	similar to Diacylglycerol O-acyltransferase 1 [Strongylocentrotus purpuratus]
AAD40881	5225382	putative diacylglycerol acyltransferase [Brassica napus]
XP_539214	73974769	similar to Diacylglycerol O-acyltransferase 1 (ACAT related gene product 1) isoform 1 [Canis familiaris]
AAZ22403	71063860	diacylglycerol O-acyltransferase 1 [Bubalus bubalis]
NP_999216	47522918	diacylglycerol acyltransferase [Sus scrofa]
NP_001...	50539976	hypothetical protein LOC436731 [Danio rerio]
XP_849176	73974767	similar to Diacylglycerol O-acyltransferase 1 (ACAT related gene product 1) isoform 2 [Canis familiaris]
NP_505828	71997360	H19N07.4 [Caenorhabditis elegans]

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AAF82410	9049538	diacylglycerol acyltransferase [Caenorhabditis elegans]
CAE75170	39591950	Hypothetical protein CBG23107 [Caenorhabditis briggsae]
XP_626337	66358318	diacylglycerol acyltransferase 1 [Cryptosporidium parvum Iowa II]
XP_668402	67624239	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme [Cryptosporidium hominis TU502]
AAP94208	33113253	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme [Toxoplasma gondii]
AAP94209	33113255	acyl-CoA:diacylglycerol acyltransferase 1-related enzyme [Toxoplasma gondii]
XP_579557	62652535	PREDICTED: diacylglycerol O-acyltransferase 1 [Rattus norvegicus]
BAC66171	29170489	diacylglycerol acyltransferase [Mus musculus]
Q9ERM3	18202872	Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase)
AAL78366	18698659	acyl coenzyme A:diacylglycerol acyltransferase [Drosophila melanogaster]
NP_995724	45552403	CG31991-PD, isoform D [Drosophila melanogaster]
NP_724017	24584734	CG31991-PC, isoform C [Drosophila melanogaster]
XP_858062	73974765	similar to Diacylglycerol O-acyltransferase 1 (ACAT related gene product 1) isoform 3 [Canis familiaris]
XP_728984	82915156	hypothetical protein PY01256 [Plasmodium yoelii yoelii str. 17XNL]
CAG11944	47225461	unnamed protein product [Tetraodon nigroviridis]
BAD27526	50199438	acyl-CoA:diacylglycerol acyltransferase [eukaryotic synthetic construct]
XP_317656	31226099	ENSANGP00000002281 [Anopheles gambiae str. PEST]
AAV59457	55733950	putative diacylglycerol acyltransferase [Oryza sativa (japonica cultivar-group)]
EAL33593	54644853	GA16599-PA [Drosophila pseudoobscura]
XP_678753	68073677	diacylglycerol O-acyltransferase [Plasmodium berghei strain ANKA]
XP_520014	55631434	PREDICTED: similar to Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase) [Pan troglodytes]
CAG10815	47219451	unnamed protein product [Tetraodon nigroviridis]
XP_624754	66522700	PREDICTED: similar to ENSANGP00000002281 [Apis mellifera]
CAC69884	15620769	diacylglycerol acyltransferase I [Rattus norvegicus]
XP_686181	68363630	PREDICTED: similar to Diacylglycerol O-acyltransferase 1 (Diglyceride acyltransferase) [Danio rerio]
XP_734008	70921323	diacylglycerol O-acyltransferase [Plasmodium chabaudi chabaudi]
XP_673128	68062248	hypothetical protein PB300300.00.0 [Plasmodium berghei strain ANKA]
AAS72376	45642963	acyl-CoA:cholesterol acyltransferase beta [Toxoplasma gondii]
AAS72375	45642961	acyl-CoA:cholesterol acyltransferase alpha [Toxoplasma gondii]
NP_586145	19074639	STEROL O-ACYLTRANSFERASE [Encephalitozoon cuniculi GB-M1]
XP_640280	66812202	hypothetical protein DDB0205259 [Dictyostelium discoideum]
AAY40783	63376221	diacylglycerol acyltransferase [Brassica juncea]

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XP_765774	71032265	diacylglycerol O-acyltransferase [Theileria parva strain Muguga]
Q876L2	34582301	Sterol O-acyltransferase 2 (Sterol-ester synthase 2)
XP_571260	58268208	sterol O-acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
EAL20032	50257323	hypothetical protein CNBF3580 [Cryptococcus neoformans var. neoformans B-3501A]
XP_954478	84999514	acyl transferase [Theileria annulata strain Ankara]
XP_505086	50555355	hypothetical protein [Yarrowia lipolytica]
NP_588558	19076058	hypothetical protein SPCP1E11.05c [Schizosaccharomyces pombe 972h-]
AAC49441	1389739	acyl-CoA:sterol acyltransferase
NP_014416	6324346	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; Are2p [Saccharomyces cerevisiae]
XP_750354	70991010	sterol o-acyltransferase APE2 [Aspergillus fumigatus Af293]
XP_382192	46110268	hypothetical protein FG02016.1 [Gibberella zeae PH-1]
BAE54934	83764790	unnamed protein product [Aspergillus oryzae]
XP_885914	76617939	similar to Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2) isoform 2 [Bos taurus]
XP_591251	76617937	similar to Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2) isoform 1 [Bos taurus]
BAC00846	21392392	AcylCoA:Cholesterol Acyltransferase 2 [Rattus norvegicus]
NP_649816	28571583	CG8112-PA [Drosophila melanogaster]
NP_666176	22122547	sterol O-acyltransferase 2 [Mus musculus]
O88908	18202245	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2)
XP_761502	71022545	hypothetical protein UM05355.1 [Ustilago maydis 521]
NP_714950	40254723	sterol O-acyltransferase 2 [Rattus norvegicus]
EAQ86094	88178626	hypothetical protein CHGG_07347 [Chaetomium globosum CBS 148.51]
XP_461395	50425599	hypothetical protein DEHA0F25652g [Debaryomyces hansenii CBS767]
XP_661812	67527926	hypothetical protein AN4208.2 [Aspergillus nidulans FGSC A4]
AAH96091	64654094	Sterol O-acyltransferase 2 [Homo sapiens]
O75908	18202149	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2)
AAH96090	64652990	Sterol O-acyltransferase 2 [Homo sapiens]
AAK48829	13898623	acyl coenzyme A: cholesterol acyltransferase-2 [Homo sapiens]
XP_543637	73996435	PREDICTED: similar to sterol O-acyltransferase 2 [Canis familiaris]
O77759	18202176	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (ACAT-2)
AAO32474	28564191	ARE2 [Saccharomyces castellii]
XP_323485	32405744	hypothetical protein [Neurospora crassa]
NP_982606	45184888	AAR065Cp [Eremothecium gossypii]
NP_593708	19114620	hypothetical protein SPAC13G7.06 [Schizosaccharomyces pombe 972h-]
AAO32554	28564940	ARE2 [Saccharomyces kluyveri]
EAL28962	54639560	GA20833-PA [Drosophila pseudoobscura]
XP_449806	50294790	hypothetical protein CAGL0M10571g [Candida glabrata CBS138]

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NP_033256	84619697	sterol O-acyltransferase 1 [Mus musculus]
Q61263	18202591	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
BAC34925	26342537	unnamed protein product [Mus musculus]
XP_452607	50305295	unnamed protein product [Kluyveromyces lactis]
NP_001...	77735363	hypothetical protein LOC504287 [Bos taurus]
Q60457	18202585	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
XP_320321	58393811	ENSANGP00000016512 [Anopheles gambiae str. PEST]
XP_320320	58393809	ENSANGP00000016486 [Anopheles gambiae str. PEST]
O70536	18202126	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
XP_714776	68482533	acyl-CoA cholesterol acyltransferase [Candida albicans SC5314]
P84285	56404462	Sterol O-acyltransferase 2 (Sterol-ester synthase) (ASAT)
AAH77916	50416229	Soat1-prov protein [Xenopus laevis]
XP_692855	68364838	PREDICTED: similar to Soat1-prov protein [Danio rerio]
CAI13574	55960156	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 [Homo sapiens]
AAL56227	18028942	cholesterol acyltransferase 1 [Gorilla gorilla]
AAL56228	18028944	cholesterol acyltransferase 1 [Pongo pygmaeus]
AAC37532	4878022	acyl-coenzyme A: cholesterol acyltransferase [Homo sapiens]
2201440A	1585676	acyl-CoA/cholesterol acyltransferase
Q876L3	34582302	Sterol O-acyltransferase 1 (Sterol-ester synthase 1)
BAE01048	67969393	unnamed protein product [Macaca fascicularis]
XP_514030	55588858	PREDICTED: hypothetical protein XP_514030 [Pan troglodytes]
XP_547445	73961286	similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1) [Canis familiaris]
EAQ84619	88177151	hypothetical protein CHGG_08633 [Chaetomium globosum CBS 148.51]
O77761	18202178	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1)
XP_422267	50751122	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1) [Gallus gallus]
XP_693284	68392980	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (ACAT-1) [Danio rerio]
AAT92940	51013293	YCR048W [Saccharomyces cerevisiae]
XP_956576	85080625	hypothetical protein [Neurospora crassa N150]
XP_624691	66564061	PREDICTED: similar to ENSANGP00000016486 [Apis mellifera]
CAF96514	47222847	unnamed protein product [Tetraodon nigroviridis]
XP_788209	72085563	PREDICTED: similar to sterol O-acyltransferase 1 [Strongylocentrotus purpuratus]
XP_445307	50285757	unnamed protein product [Candida glabrata]
CAE70002	39596364	Hypothetical protein CBG16409 [Caenorhabditis briggsae]
CAG07990	47225647	unnamed protein product [Tetraodon nigroviridis]
NP_510623	17549960	B0395.2 [Caenorhabditis elegans]
AAX28331	76157393	SJCHGC04421 protein [Schistosoma japonicum]
CAI96158	66347204	Diacylglycerol O-acyltransferase [Bubalus bubalis]
XP_390039	46136695	hypothetical protein FG09863.1 [Gibberella zeae PH-1]
XP_643169	66819019	hypothetical protein DDB0203882 [Dictyostelium discoideum]

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AAO53095	28850306	hypothetical protein [Dictyostelium discoideum]
AAB06959	1515472	acyl-CoA:cholesterol acyltransferase [Oryctolagus cuniculus]
NP_945619	39933343	putative alginate o-acetyltransferase AlgI [Rhodopseudomonas palustris CGA009]
ZP_008...	77691302	Membrane bound O-acyl transferase, MBOAT [Rhodopseudomonas palustris BisB5]
XP_465546	50908115	putative wax synthase [Oryza sativa (japonica cultivar-group)]

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Table 29: Examples of Prenyldiphosphate synthase polypeptides

29A: Bacteria Proteins that require a mitochondrial targeting sequence		
Accession	**GI**	**Description**
ZP_009...	83373595	Trans-hexaprenyltranstransferase [Rhodobacter sphaeroides ATCC 17029]
ZP_009...	83371280	Trans-hexaprenyltranstransferase [Rhodobacter sphaeroides ATCC 17025]
CAD24417	20429105	decaprenyl diphosphate synthase [Paracoccus zeaxanthinifaciens]
ZP_010...	85705714	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase [Roseovarius sp. 217]
ZP_010...	84515724	decaprenyl diphosphate synthase [Loktanella vestfoldensis SKA53]
YP_165582	56695234	decaprenyl diphosphate synthase [Silicibacter pomeroyi DSS-3]
ZP_010...	86139019	decaprenyl diphosphate synthase [Roseobacter sp. MED193]
ZP_009...	83941379	decaprenyl diphosphate synthase [Sulfitobacter sp. EE-36]
ZP_009...	83854856	decaprenyl diphosphate synthase [Sulfitobacter sp. NAS-14. 1]
ZP_006...	69299873	Farnesyltranstransferase [Silicibacter sp. TM1040]
ZP_010...	84683979	Geranylgeranyl pyrophosphate synthase/Polyprenyl synthetase [Rhodobacterales bacterium HTCC2654]
ZP_009...	84500217	decaprenyl diphosphate synthase [Oceanicola batsensis HTCC2597]
ZP_009...	83952381	decaprenyl diphosphate synthase [Roseovarius nubinhibens ISM]
ZP_006...	69937106	Trans-hexaprenyltranstransferase [Paracoccus denitrificans PD1222]
ZP_005...	68180845	Trans-hexaprenyltranstransferase [Jannaschia sp. CCS1]
ZP_008...	78495595	Polyprenyl synthetase [Rhodopseudomonas palustris BisB18]
AAY82368	67866738	decaprenyl diphosphate synthase [Agrobacterium tumefaciens]
NP_353656	15887975	hypothetical protein AGR_C_1125 [Agrobacterium tumefaciens str. C58]
ZP_008...	77688465	Farnesyltranstransferase [Rhodopseudomonas palustris BisB5]
NP_531334	17934544	octaprenyl-diphosphate synthase [Agrobacterium tumefaciens str. C58]
YP_484709	86748213	Farnesyltranstransferase [Rhodopseudomonas palustris HaA2]
AAP56240	37903500	decaprenyl diphosphate synthase [Agrobacterium tumefaciens]
YP_192388	58040424	Decaprenyl diphosphate synthase [Gluconobacter oxydans 621H]
29B: Subunit 1- Proteins that contain mitochondrial targeting sequence		
Accession	**GI**	**Description**
T43193	11279237	trans-pentaprenyltranstransferase homolog - fission yeast (Schizosaccharomyces pombe)
AAD28559	4732024	trans-prenyltransferase [Homo sapiens]
AAI07275	78070698	Trans-prenyltransferase [Mus musculus]
BAE48216	81157931	subunit 1 of decaprenyl diphosphate synthase [Homo sapiens]
AAH49211	29165656	PDSS1 protein [Homo sapiens]
Q33DR2	85700953	Decaprenyl-diphosphate synthase subunit 1 (Solanesyl-diphosphate synthase subunit 1) (Trans-prenyltransferase)
XP_507706	55633583	PREDICTED: similar to TPRT protein [Pan troglodytes]
XP_586717	76632198	PREDICTED: similar to trans-prenyltransferase [Bos taurus]
XP_849908	73948851	PREDICTED: similar to trans-prenyltransferase [Canis familiaris]

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29C: Subunit 2- Proteins that contain mitochondrial targeting sequence		
Accession	**GI**	**Description**
O13851	60389474	Decaprenyl-diphosphate synthase subunit 2 (Decaprenyl pyrophosphate synthetase subunit 2)
BAE48218	81157935	subunit 2 of solanesyl diphosphate synthase [Mus musculus]
BAE48217	81157933	subunit 2 of decaprenyl diphosphate synthase [Homo sapiens]

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Table 30: Examples of PHB-Polyprenyltransferase polypeptides

GI	PROTEIN DESCRIPTION
51013645	YNR041C [Saccharomyces cerevisiae]
50285815	unnamed protein product [Candida glabrata]
50311051	unnamed protein product [Kluyveromyces lactis]
45200866	AGL231Wp [Eremothecium gossypii]
50555263	hypothetical protein [Yarrowia lipolytica]
68473193	*para*-hydroxybenzoate: polyprenyl transferase [Candida albicans SC5314]
50410039	hypothetical protein DEHA0A14212g [Debaryomyces hansenii CBS767]
83769349	unnamed protein product [Aspergillus oryzae]
70994900	*para*-hydroxybenzoate-polyprenyltransferase precursor [Aspergillus fumigatus Af293]
19114131	hypothetical protein SPAC56F8. 04c [Schizosaccharomyces pombe 972h-]
39973573	hypothetical protein MG01067. 4 [Magnaporthe grisea 70-15]
85078920	protein related to *para*-hydroxybenzoate polyprenyltransferase precursor [Neurospora crassa N150]
76660839	PREDICTED: similar to *para*-hydroxybenzoate-polyprenyltransferase, mitochondrial [Bos taurus]
52138578	*para*-hydroxybenzoate-polyprenyltransferase, mitochondrial [Homo sapiens]
18088424	COQ2 protein [Homo sapiens]
47221448	unnamed protein product [Tetraodon nigroviridis]
58385249	ENSANGP00000012220 [Anopheles gambiae str. PEST]
50746583	PREDICTED: similar to hypothetical protein CL640 [Gallus gallus]
54638587	GA21912-PA [Drosophila pseudoobscura]
21355567	CG9613-PA [Drosophila melanogaster]
71005862	hypothetical protein UM01450. 1 [Ustilago maydis 521]

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Table 31. Examples of soluble transydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAD40691	5163507	soluble pyridine nucleotide transhydrogenase [Azotobacter vinelandii
2	ZP_013...	107102541	hypothetical protein PaerPA_01003605 [Pseudomonas aeruginosa PACS2]
3	ZP_012...	94416745	hypothetical protein PaerP_01001583 [Pseudomonas aeruginosa PA7]
4	O05139	11135075	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
5	YP_259077	70729340	soluble pyridine nucleotide transhydrogenase [Pseudomonas fluorescens Pf-5]
6	YP_349590	77460083	soluble pyridine nucleotide transhydrogenase [Pseudomonas fluorescens PfO-1]
7	YP_274087	71735155	soluble pyridine nucleotide transhydrogenase [Pseudomonas syringae pv. phaseolicola 1448A]
8	YP_234983	66045142	soluble pyridine nucleotide transhydrogenase [Pseudomonas syringae pv. syringae B728a]
9	YP_609219	104782721	soluble pyridine nucleotide transhydrogenase (NAD(P)(+) transhydrogenase [B-specific]) [Pseudomonas entomophila L48]
10	Q884I6	38258471	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
11	ZP_009...	82739140	soluble pyridine nucleotide transhydrogenase [Pseudomonas putida F1]
12	YP_573629	92113701	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Chromohalobacter salexigens DSM 3043]
13	ZP_008...	77951906	NAD(P) transhydrogenase [Marinobacter aquaeolei VT8]
14	YP_433907	83645472	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzyme [Hahella chejuensis KCTC 2396]
15	ZP_011...	89094310	soluble pyridine nucleotide transhydrogenase [Oceanospirillum sp. MED92]
16	ZP_013...	94499566	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzyme [Oceanobacter sp. RED65]
17	ZP_011...	88800089	soluble pyridine nucleotide transhydrogenase [Reinekea sp. MED297]
18	ZP_010...	87121312	soluble pyridine nucleotide transhydrogenase [Marinomonas sp. MED121]
19	ZP_012...	90417525	soluble pyridine nucleotide transhydrogenase [marine gamma proteobacterium HTCC2207]
20	Q7MQ83	47606104	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
21	YP_527277	90021450	regulatory protein, ArsR [Saccharophagus degradans 2-40]

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22	ZP_009...	83586194	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Escherichia coli 101-1]
23	YP_219002	62182585	soluble pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
24	YP_543498	91213512	soluble pyridine nucleotide transhydrogenase [Escherichia coli UTI89]
25	Q87KN5	33301640	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
26	YP_153038	56415963	soluble pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
27	YP_672034	110644304	soluble pyridine nucleotide transhydrogenase [Escherichia coli 536]
28	ZP_013...	106883834	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductase dimerisation region:FAD dependent oxidoreductase [Psychromonas ingrahamii 37]
29	ZP_006...	75176647	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Shigella boydii BS512]
30	Q8FB93	38258590	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
31	ZP_007...	75197835	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Escherichia coli HS]
32	ZP_007...	75513852	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Escherichia coli 53638]
33	Q8X727	21362954	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
34	YP_267100	71278420	soluble pyridine nucleotide transhydrogenase [Colwellia psychrerythraea 34H]
35	Q83MI1	39932373	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
36	ZP_007...	75238410	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Escherichia coli E110019]
37	ZP_007...	75854141	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Vibrio sp. Ex25]
38	YP_052329	50123162	soluble pyridine nucleotide transhydrogenase [Erwinia carotovora subsp. atroseptica SCRI1043]
39	ZP_008...	77973002	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Yersinia frederiksenii ATCC 33641]
40	ZP_008...	77957412	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Yersinia bercovieri ATCC 43970]
41	ZP_008...	78702791	NAD(P) transhydrogenase (B-specific) [Alkalilimnicola ehrlichei MLHE-1]

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42	YP_645986	108810219	soluble pyridine nucleotide transhydrogenase [Yersinia pestis Nepal516]
43	ZP_007...	75828016	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Vibrio cholerae O395]
44	Q7MBG9	47606102	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
45	ZP_008...	77976809	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Yersinia intermedia ATCC 29909]
46	ZP_008...	77961066	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Yersinia mollaretii ATCC 43969]
47	ZP_010...	86148649	soluble pyridine nucleotide transhydrogenase [Vibrio sp. MED222]
48	YP_205822	59713046	soluble pyridine nucleotide transhydrogenase [Vibrio fischeri ES114]
49	ZP_009...	84394322	pyridine nucleotide-disulfide oxidoreductase, class I [Vibrio splendidus 12B01]
50	ZP_011...	89074500	soluble pyridine nucleotide transhydrogenase [Photobacterium sp. SKA34]
51	YP_154714	56459433	soluble pyridine nucleotide transhydrogenase [Idiomarina loihiensis L2TR]
52	YP_046885	50085375	soluble pyridine nucleotide transhydrogenase [Acinetobacter sp. ADP1]
53	ZP_012...	90581098	soluble pyridine nucleotide transhydrogenase [Vibrio angustum S14]
54	YP_693290	110834431	NAD(P) transhydrogenase [Alcanivorax borkumensis SK2]
55	ZP_011...	88795508	soluble pyridine nucleotide transhydrogenase [Alteromonas macleodii 'Deep ecotype']
56	ZP_012...	90407259	soluble pyridine nucleotide transhydrogenase [Psychromonas sp. CNPT3]
57	E65203	7431869	probable dehydrogenase (EC 1.8.1.-) udhA - Escherichia coli (strain K-12)
58	YP_410260	82546313	putative oxidoreductase [Shigella boydii Sb227]
59	YP_312883	74314464	putative oxidoreductase [Shigella sonnei Ss046]
60	YP_131541	54310521	soluble pyridine nucleotide transhydrogenase [Photobacterium profundum SS9]
61	AAC43068	396309	ORF_f444 [Escherichia coli]
62	H86087	25284914	probable oxidoreductase udhA [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
63	ZP_012...	90414698	soluble pyridine nucleotide transhydrogenase [Photobacterium profundum 3TCK]

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64	NP_709766	56480495	soluble pyridine nucleotide transhydrogenase [Shigella flexneri 2a str. 301]
65	YP_405233	82778884	putative oxidoreductase [Shigella dysenteriae Sd197]
66	YP_691341	110807821	putative oxidoreductase [Shigella flexneri 5 str. 8401]
67	NP_667661	22124238	soluble pyridine nucleotide transhydrogenase [Yersinia pestis KIM]
68	YP_341375	77361800	soluble pyridine nucleotide transhydrogenase [Pseudoalteromonas haloplanktis TAC125]
69	YP_455837	85060135	soluble pyridine nucleotide transhydrogenase [Sodalis glossinidius str. 'morsitans']
70	ZP_012...	91771448	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductase dimerisation region:FAD dependent oxidoreductase [Psychrobacter sp. PRwf-1]
71	ZP_011...	88861405	soluble pyridine nucleotide transhydrogenase [Pseudoalteromonas tunicata D2]
72	YP_264617	71065890	soluble pyridine nucleotide transhydrogenase [Psychrobacter arcticus 273-4]
73	YP_580301	93005864	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Psychrobacter cryohalolentis K5]
74	ZP_010...	85710769	soluble pyridine nucleotide transhydrogenase [Idiomarina baltica OS145]
75	ZP_012...	91227486	soluble pyridine nucleotide transhydrogenase [Vibrio alginolyticus 12G01]
76	ZP_007...	75814072	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Vibrio cholerae V52]
77	YP_666832	110670275	soluble pyridine nucleotide transhydrogenase [Francisella tularensis subsp. tularensis FSC 198]
78	YP_169700	56707804	soluble pyridine nucleotide transhydrogenase [Francisella tularensis subsp. tularensis SCHU S4]
79	YP_513671	89256309	soluble pyridine nucleotide transhydrogenase [Francisella tularensis subsp. holarctica]
80	CAA46822	43237	udhA [Escherichia coli]
81	ZP_005...	67929855	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductase dimerisation region [Solibacter usitatus Ellin6076]
82	YP_592298	94970250	pyridine nucleotide-disulphide oxidoreductase [Acidobacteria bacterium Ellin345]
83	NP_961763	41408927	soluble pyridine nucleotide transhydrogenase [Mycobacterium avium subsp. paratuberculosis K-10]
84	P66006	54042093	Probable soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
85	ZP_007...	76783189	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related

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			enzymes [Mycobacterium tuberculosis F11]
86	YP_716291	111225497	soluble pyridine nucleotide transhydrogenase [Frankia alni ACN14a]
87	ZP_005...	68235154	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductase dimerisation domain [Frankia sp. EAN1pec]
88	ZP_012...	90205475	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductase dimerisation region [Mycobacterium vanbaalenii PYR-1]
89	YP_482962	86742562	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Frankia sp. CcI3]
90	NP_532346	17935556	soluble pyridine nucleotide transhydrogenase [Agrobacterium tumefaciens str. C58]
91	AAY87873	68165826	pyridine nucleotide-disulfide oxidoreductase class I [Vibrio cholerae]
92	AAY87863	68165806	pyridine nucleotide-disulfide oxidoreductase class I [Vibrio cholerae]
93	AAY87865	68165810	pyridine nucleotide-disulfide oxidoreductase class I [Vibrio cholerae]
94	YP_469365	86357473	probable pyridine nucleotide transhydrogenase protein [Rhizobium etli CFN 42]
95	ZP_010...	85706062	soluble pyridine nucleotide transhydrogenase [Roseovarius sp. 217]
96	ZP_014...	113873124	putative soluble pyridine nucleotide transhydrogenase [Sinorhizobium medicae WSM419]
97	NP_385835	15965482	soluble pyridine nucleotide transhydrogenase [Sinorhizobium meliloti 1021]
98	YP_169016	56698639	soluble pyridine nucleotide transhydrogenase [Silicibacter pomeroyi DSS-3]
99	ZP_009...	83951172	soluble pyridine nucleotide transhydrogenase [Roseovarius nubinhibens ISM]
100	YP_611681	99078423	pyridine nucleotide-disulphide oxidoreductase dimerisation region [Silicibacter sp. TM1040]
101	ZP_010...	86140117	soluble pyridine nucleotide transhydrogenase [Roseobacter sp. MED193]
102	BAB53939	14027670	soluble pyridine nucleotide transhydrogenase [Mesorhizobium loti MAFF303099]
103	YP_630631	108762684	NAD(P) transhydrogenase (B-specific) [Myxococcus xanthus DK 1622]
104	YP_467034	86160249	FAD-dependent pyridine nucleotide-disulphide oxidoreductase [Anaeromyxobacter dehalogenans 2CP-C]
105	YP_007724	46446359	soluble pyridine nucleotide transhydrogenase [Candidatus Protochlamydia amoebophila UWE25]
106	YP_433307	83644872	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzyme [Hahella chejuensis KCTC 2396]

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107	YP_527988	90022161	soluble pyridine nucleotide transhydrogenase [Saccharophagus degradans 2-40]
108	ZP_005...	67931474	FAD-dependent pyridine nucleotide-disulphide oxidoreductase:Pyridine nucleotide-disulphide oxidoreductase dimerisation region [Solibacter usitatus Ellin6076]
109	YP_575887	92116158	Dihydrolipoamide dehydrogenase [Nitrobacter hamburgensis X14]
110	NP_539063	17986429	dihydrolipoamide dehydrogenase [Brucella melitensis 16M]
111	NP_698895	23502768	dihydrolipoamide dehydrogenase [Brucella suis 1330]
112	YP_415258	82700684	Pyridine nucleotide-disulphide oxidoreductase, class-II:NAD binding site:Adrenodoxin reductase:Mercuric reductase:Pyridine nu... [Brucella melitensis biovar Abortus 2308]
113	ZP_011...	88945707	Dihydrolipoamide dehydrogenase [Desulfotomaculum reducens MI-1]
114	YP_675936	110635728	dihydrolipoamide dehydrogenase [Mesorhizobium sp. BNC1]
115	YP_483896	86747400	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palustris HaA2]
116	ZP_006...	71836831	Dihydrolipoamide dehydrogenase [Pelobacter propionicus DSM 2379]
117	BAB50985	14024381	ferric leghemoglobin reductase-2 precursor, dihydrolipoamide dehydrogenase [Mesorhizobium loti MAFF303099]
118	ZP_011...	88946629	Dihydrolipoamide dehydrogenase [Desulfotomaculum reducens MI-1]
119	YP_032854	49474812	dihydrolipoamide dehydrogenase [Bartonella quintana str. Toulouse]
120	YP_317044	75674623	dihydrolipoamide dehydrogenase [Nitrobacter winogradskyi Nb-255]
121	ZP_012...	90421039	2-oxoglutarate dehydrogenase, E3 component, lipoamide dehydrogenase [Aurantimonas sp. SI85-9A1]
122	NP_533297	17936507	dihydrolipoamide dehydrogenase [Agrobacterium tumefaciens str. C58]
123	AAR21288	38489206	2-oxoglutarate dehydrogenase E3 component [Bartonella henselae]
124	YP_034342	49476301	dihydrolipoamide dehydrogenase [Bartonella henselae str. Houston-1]
125	ZP_008...	78694497	Dihydrolipoamide dehydrogenase [Bradyrhizobium sp. BTAi1]
126	ZP_010...	85713709	dihydrolipoamide dehydrogenase [Nitrobacter sp. Nb-311A]
127	YP_471355	86359463	dihydrolipoamide dehydrogenase protein [Rhizobium etli CFN 42]
128	ZP_008...	77739670	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palustris BisA53]

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129	NP_387154	15966801	dihydrolipoamide dehydrogenase [Sinorhizobium meliloti 1021]
130	YP_567689	91975030	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palustris BisB5]
131	ZP_009...	83750811	COG1249: Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes [Bartonella bacilliformis KC583]
132	NP_767089	27375560	dihydrolipoamide dehydrogenase [Bradyrhizobium japonicum USDA 110]
133	ZP_014...	113873546	dihydrolipoamide dehydrogenase [Sinorhizobium medicae WSM419]
134	ZP_011...	88801370	Pyruvate/2-oxoglutarate dehydrogenase complex [Polaribacter irgensii 23-P]
135	AAN03817	22652790	dihydrolipoamide dehydrogenase [Methylobacterium extorquens]
136	NP_945538	39933262	dihydrolipoamide dehydrogenase [Rhodopseudomonas palustris CGA009]
137	ZP_010...	86142639	Dihydrolipoyl dehydrogenase [Flavobacterium sp. MED217]
138	YP_005669	46200002	dihydrolipoamide dehydrogenase [Thermus thermophilus HB27]
139	ZP_012...	90589077	Dihydrolipoamide dehydrogenase [Flavobacterium johnsoniae UW101]
140	YP_143553	55980256	2-oxoglutarate dehydrogenase E3 component (dihydrolipoamide dehydrogenase) [Thermus thermophilus HB8]
141	YP_679939	110639729	dihydrolipoyl dehydrogenanse [Cytophaga hutchinsonii ATCC 33406]
142	YP_530077	90421707	Dihydrolipoamide dehydrogenase [Rhodopseudomonas palustris BisB18]
143	YP_681916	110678909	dihydrolipoamide dehydrogenase [Roseobacter denitrificans OCh 114]
144	ZP_010...	86135035	dihydrolipoamide dehydrogenase [Tenacibaculum sp. MED152]
145	ZP_011...	89068141	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamide dehydrogenase [Oceanicola granulosus HTCC2516]
146	ZP_007...	75761004	Dihydrolipoamide dehydrogenase [Bacillus thuringiensis serovar israelensis ATCC 35646]
147	ZP_010...	84684243	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Rhodobacterales bacterium HTCC2654]
148	ZP_009...	84500199	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Oceanicola batsensis HTCC2597]
149	ZP_006...	71900956	Dihydrolipoamide dehydrogenase [Xylella fastidiosa Ann-1]
150	XP_829730	74026328	dihydrolipoyl dehydrogenase [Trypanosoma brucei TREU927]

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151	ZP_010...	86132778	dihydrolipoamide dehydrogenase [Cellulophaga sp. MED134]
152	P71317	11135239	Soluble pyridine nucleotide transhydrogenase (STH) (NAD(P)(+) transhydrogenase [B-specific])
153	ZP_012...	89891405	dihydrolipoyl dehydrogenase (pyruvate 2-oxoglutarate dehydrogenase) [Flavobacteria bacterium BBFL7]
154	ZP_009...	83950445	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Roseovarius nubinhibens ISM]
155	AAA21748	472330	dihydrolipoamide dehydrogenase
156	Q04933	416906	Dihydrolipoyl dehydrogenase (Dihydrolipoamide dehydrogenase)
157	ZP_011...	88805521	Pyruvate/2-oxoglutarate dehydrogenase complex [Robiginitalea biformata HTCC2501]
158	YP_351398	77461891	dihydrolipoamide dehydrogenase [Pseudomonas fluorescens PfO-1]
159	ZP_006...	71900678	Dihydrolipoamide dehydrogenase [Xylella fastidiosa Ann-1]
160	ZP_011...	88936095	Dihydrolipoamide dehydrogenase [Geobacter uraniumreducens Rf4]
161	YP_430607	83590598	Dihydrolipoamide dehydrogenase [Moorella thermoacetica ATCC 39073]
162	YP_165603	56695257	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamide dehydrogenase [Silicibacter pomeroyi DSS-3]
163	ZP_011...	89359154	Dihydrolipoamide dehydrogenase [Xanthobacter autotrophicus Py2]
164	YP_007150	46445785	dihydrolipoamide dehydrogenase [Candidatus Protochlamydia amoebophila UWE25]
165	YP_632394	108758911	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydrogenase [Myxococcus xanthus DK 1622]
166	ZP_010...	85704799	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Roseovarius sp. 217]
167	NP_778978	28198664	dihydrolipoamide dehydrogenase [Xylella fastidiosa Temecula1]
168	ZP_011...	88949385	Dihydrolipoamide dehydrogenase [Halorhodospira halophila SL1]
169	XP_749345	70988990	dihydrolipoamide dehydrogenase [Aspergillus fumigatus Af293]
170	YP_359567	78044229	alpha keto acid dehydrogenase complex, E3 component, lipoamide dehydrogenase [Carboxydothermus hydrogenoformans Z-2901]
171	XP_959535	85092766	hypothetical protein [Neurospora crassa OR74A]
172	ZP_009...	83856665	Dihydrolipoyl dehydrogenase [Croceibacter atlanticus HTCC2559]
173	ZP_006...	69259929	Dihydrolipoamide dehydrogenase [Magnetococcus sp. MC-1]

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174	NP_298837	15838149	dihydrolipoamide dehydrogenase [Xylella fastidiosa 9a5c]
175	YP_508779	89053328	Dihydrolipoamide dehydrogenase [Jannaschia sp. CCS1]
176	CAA72131	1854569	dihydrolipoamide dehydrogenase [Trypanosoma cruzi]
177	ZP_011...	88713490	Dihydrolipoyl dehydrogenase [Flavobacteriales bacterium HTCC2170]
178	P90597	6166121	Dihydrolipoyl dehydrogenase (Dihydrolipoamide dehydrogenase)
179	ZP_009...	83944432	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Sulfitobacter sp. EE-36]
180	ZP_009...	83953473	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Sulfitobacter sp. NAS-14.1]
181	ZP_010...	86141935	dihydrolipoamide dehydrogenase, E3 component of 2-oxoglutarate andpyruvate dehydrogenase complexes [Flavobacterium sp. MED217]
182	XP_818792	71663602	dihydrolipoyl dehydrogenase [Trypanosoma cruzi strain CL Brener]
183	XP_812294	71422952	dihydrolipoyl dehydrogenase [Trypanosoma cruzi strain CL Brener]
184	CAA72132	1854571	dihydrolipoamide dehydrogenase [Trypanosoma cruzi]
185	NP_623271	20808100	Dihydrolipoamide dehydrogenase/glutathione oxidoreductase and related enzyme [Thermoanaerobacter tengcongensis MB4]
186	YP_265659	71082940	Dihydrolipoyl dehydrogenase [Candidatus Pelagibacter ubique HTCC1062]
187	ZP_012...	91762636	Dihydrolipoyl dehydrogenase [Candidatus Pelagibacter ubique HTCC1002]
188	CAA11554	4210334	2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]
189	NP_566570	30684428	LPD2 (LIPOAMIDE DEHYDROGENASE 2); FAD binding / dihydrolipoyl dehydrogenase/ disulfide oxidoreductase/ oxidoreductase [Arabidopsis thaliana]
190	ZP_010...	84515869	2-oxoglutarate dehydrogenase, E3 component, dihydrolipoamidedehydrogenase [Loktanella vestfoldensis SKA53]
191	YP_355777	77917962	2-oxoglutarate dehydrogenase complex, E3 component, lipoamide dehydrogenase [Pelobacter carbinolicus DSM 2380]
192	AAS47708	44804791	dihydrolipoamide dehydrogenase [Leishmania major]
193	AAC26053	3309269	ferric leghemoglobin reductase-2 precursor [Glycine max]
194	XP_712334	68487571	putative mitochondrial matrix dihydrolipoamide dehydrogenase Lpd1p [Candida albicans SC5314]
195	ZP_008...	78702525	Dihydrolipoamide dehydrogenase [Alkalilimnicola ehrlichei MLHE-1]

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196	YP_002403	45658317	dihydrolipoamide dehydrogenase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]
197	ZP_008...	82736566	Dihydrolipoamide dehydrogenase [Pseudomonas putida F1]
198	CAD60736	27803033	unnamed protein product [Podospora anserina]
199	NP_747467	26992042	dihydrolipoamide dehydrogenase [Pseudomonas putida KT2440]
200	ZP_013...	106891371	Dihydrolipoamide dehydrogenase [Roseiflexus sp. RS-1]
201	EAQ92192	88184724	conserved hypothetical protein [Chaetomium globosum CBS 148.51]

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Table 32. Examples of transhydrogenase subunit alpha polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_416120	16129561	NAD(P) transhydrogenase subunit alpha [Escherichia coli K12].
2	ZP_007...	75512964	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli 53638]
3	ZP_009...	83587938	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli 101-1]
4	YP_669455	110641725	NAD(P) transhydrogenase subunit alpha [Escherichia coli 536]
5	YP_540800	91210814	NAD(P) transhydrogenase subunit alpha [Escherichia coli UTI89]
6	ZP_007...	75236686	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli F11]
7	NP_753890	26247850	NAD(P) transhydrogenase subunit alpha [Escherichia coli CFT073]
8	YP_310491	74312072	pyridine nucleotide transhydrogenase, alpha subunit [Shigella sonnei Ss046]
9	ZP_007...	75234916	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli E110019]
10	YP_403177	82776828	pyridine nucleotide transhydrogenase, alpha subunit [Shigella dysenteriae Sd197]
11	ZP_007...	75190643	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli E24377A]
12	ZP_009...	83570993	COG3288: NAD/NADP transhydrogenase alpha subunit [Shigella dysenteriae 1012]
13	ZP_007...	75257022	COG3288: NAD/NADP transhydrogenase alpha subunit [Escherichia coli E22]
14	YP_407977	82544030	pyridine nucleotide transhydrogenase, alpha subunit [Shigella boydii Sb227]
15	ZP_006...	75178502	COG3288: NAD/NADP transhydrogenase alpha subunit [Shigella boydii BS512]
16	YP_689096	110805576	pyridine nucleotide transhydrogenase, alpha subunit [Shigella flexneri 5 str. 8401]
17	NP_310336	15831563	NAD(P) transhydrogenase subunit alpha [Escherichia coli O157:H7 str. Sakai]
18	YP_216484	62180067	NAD(P) transhydrogenase subunit alpha [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
19	NP_460439	16764824	NAD(P) transhydrogenase subunit alpha [Salmonella typhimurium LT2]
20	NP_805194	29141852	NAD(P) transhydrogenase subunit alpha [Salmonella enterica subsp. enterica serovar Typhi Ty2]
21	ABF71058	102621428	NADP transhydrogenase alpha subunit [Enterobacter cloacae]
22	ZP_008...	77963333	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia mollaretii ATCC 43969]
23	ZP_008...	77958020	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia bercovieri ATCC 43970]
24	ZP_008...	77975377	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia frederiksenii ATCC 33641]
25	YP_647693	108811926	NAD(P) transhydrogenase alpha subunit [Yersinia pestis Nepal516]
26	YP_070740	51596549	NAD(P) transhydrogenase subunit alpha [Yersinia pseudotuberculosis IP 32953]
27	ZP_007...	77629299	COG3288: NAD/NADP transhydrogenase alpha subunit

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			[Yersinia pseudotuberculosis IP 31758]
28	YP_050297	50121130	NAD(P) transhydrogenase subunit alpha [Erwinia carotovora subsp. atroseptica SCRI1043]
29	ZP_008...	77979498	COG3288: NAD/NADP transhydrogenase alpha subunit [Yersinia intermedia ATCC 29909]
30	NP_929427	37526083	NAD(P) transhydrogenase subunit alpha [Photorhabdus luminescens subsp. laumondii TTO1]
31	YP_455168	85059466	pyridine nucleotide transhydrogenase alpha subunit [Sodalis glossinidius str. 'morsitans']
32	YP_206544	59713769	NAD(P) transhydrogenase subunit alpha [Vibrio fischeri ES114]
33	ZP_007...	75831475	COG3288: NAD/NADP transhydrogenase alpha subunit [Vibrio cholerae MO10]
34	ZP_010...	86147993	NAD(P) transhydrogenase subunit alpha [Vibrio sp. MED222]
35	ZP_009...	84393928	NAD(P) transhydrogenase subunit alpha [Vibrio splendidus 12B01]
36	ZP_007...	75857576	COG3288: NAD/NADP transhydrogenase alpha subunit [Vibrio sp. Ex25]
37	ZP_012...	91226112	NAD(P) transhydrogenase subunit alpha [Vibrio alginolyticus 12G01]
38	NP_936868	37676472	NAD(P) transhydrogenase subunit alpha [Vibrio vulnificus YJ016]
39	NP_800432	28900777	NAD(P) transhydrogenase subunit alpha [Vibrio parahaemolyticus RIMD 2210633]
40	NP_762287	27366760	NAD(P) transhydrogenase subunit alpha [Vibrio vulnificus CMCP6]
41	ZP_012...	90577759	NAD(P) transhydrogenase subunit alpha [Vibrio angustum S14]
42	ZP_011...	89073747	NAD(P) transhydrogenase subunit alpha [Photobacterium sp. SKA34]
43	NP_245690	15602618	NAD(P) transhydrogenase subunit alpha [Pasteurella multocida subsp. multocida str. Pm70]
44	YP_088416	52425279	NAD(P) transhydrogenase subunit alpha [Mannheimia succiniciproducens MBEL55E]
45	YP_718440	113460378	NAD(P)(+) transhydrogenase, alpha subunit (pyridine nucleotide transhydrogenase) [Haemophilus somnus 129PT]
46	ZP_001...	32030098	COG3288: NAD/NADP transhydrogenase alpha subunit [Haemophilus somnus 2336]
47	ZP_005...	68545628	NAD(P) transhydrogenase, alpha subunit [Shewanella amazonensis SB2B]
48	ZP_012...	90412639	NAD(P) transhydrogenase subunit alpha [Photobacterium profundum 3TCK]
49	ZP_007...	75429914	NAD/NADP transhydrogenase alpha subunit [Actinobacillus succinogenes 130Z]
50	YP_249235	68250123	NAD(P) transhydrogenase subunit alpha [Haemophilus influenzae 86-028NP]
51	YP_132574	54302581	NAD(P) transhydrogenase subunit alpha [Photobacterium profundum SS9]
52	NP_439513	16273272	NAD(P) transhydrogenase subunit alpha [Haemophilus influenzae Rd KW20]
53	ZP_009...	82741968	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. W3-18-1]
54	ZP_014...	113949477	NAD(P) transhydrogenase, alpha subunit [Shewanella baltica OS195]
55	YP_561942	91792291	NAD(P) transhydrogenase, alpha subunit [Shewanella

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			denitrificans OS217]
56	NP_719279	24375236	NAD(P) transhydrogenase subunit alpha [Shewanella oneidensis MR-1]
57	NP_874046	33152693	NAD(P) transhydrogenase subunit alpha [Haemophilus ducreyi 35000HP]
58	YP_735209	113971416	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. MR-4]
59	ZP_008...	78686308	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. ANA-3]
60	YP_736947	114046397	NAD(P) transhydrogenase, alpha subunit [Shewanella sp. MR-7]
61	ZP_006...	69950756	NAD(P) transhydrogenase, alpha subunit [Shewanella frigidimarina NCIMB 400]
62	ZP_007...	75818840	COG3288: NAD/NADP transhydrogenase alpha subunit [Vibrio cholerae V51]
63	ZP_013...	106883669	NAD(P) transhydrogenase, alpha subunit [Psychromonas ingrahamii 37]
64	NP_283944	15794122	NAD(P) transhydrogenase subunit alpha [Neisseria meningitidis Z2491]
65	YP_434236	83645801	NAD(P) transhydrogenase, alpha subunit [Hahella chejuensis KCTC 2396]
66	NP_274017	15676872	NAD(P) transhydrogenase subunit alpha [Neisseria meningitidis MC58]
67	YP_208522	59801810	NAD(P) transhydrogenase subunit alpha [Neisseria gonorrhoeae FA 1090]
68	ZP_012...	90408904	PntA [Psychromonas sp. CNPT3]
69	YP_268514	71281713	NAD(P) transhydrogenase subunit alpha [Colwellia psychrerythraea 34H]
70	ZP_001...	32035329	COG3288: NAD/NADP transhydrogenase alpha subunit [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
71	ZP_012...	90202099	NAD(P) transhydrogenase, alpha subunit [Mycobacterium vanbaalenii PYR-1]
72	YP_342322	77163797	NAD(P) transhydrogenase subunit alpha [Nitrosococcus oceani ATCC 19707]
73	ZP_009...	84495285	NAD(P) transhydrogenase subunit alpha [Janibacter sp. HTCC2649]
74	AAY87755	68165590	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
75	ZP_011...	89340414	NAD(P) transhydrogenase, alpha subunit [Mycobacterium flavescens PYR-GCK]
76	AAY87751	68165582	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
77	AAY87754	68165588	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
78	AAY87762	68165604	NAD(P) transhydrogenase alpha subunit [Vibrio cholerae]
79	YP_422187	83311923	NAD/NADP transhydrogenase alpha subunit [Magnetospirillum magneticum AMB-1]
80	YP_637279	108797082	NAD(P) transhydrogenase, alpha subunit [Mycobacterium sp. MCS]
81	YP_115165	53803088	NAD(P) transhydrogenase subunit alpha [Methylococcus capsulatus str. Bath]
82	NP_821578	29826944	NAD(P) transhydrogenase subunit alpha [Streptomyces avermitilis MA-4680]
83	ZP_006...	69261416	NAD(P) transhydrogenase, alpha subunit [Magnetococcus sp. MC-1]
84	NP_440856	16330128	NAD(P) transhydrogenase subunit alpha [Synechocystis sp.

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			PCC 6803]
85	ZP_002...	46202292	COG3288: NAD/NADP transhydrogenase alpha subunit [Magnetospirillum magnetotacticum MS-1]
86	YP_298860	73538493	NAD(P) transhydrogenase subunit alpha [Ralstonia eutropha JMP134]
87	ZP_004...	66966825	NAD(P) transhydrogenase, alpha subunit [Arthrobacter sp. FB24]
88	ZP_006...	71366730	NAD(P) transhydrogenase, alpha subunit [Nocardioides sp. JS614]
89	YP_524985	89902514	NAD(P) transhydrogenase, alpha subunit [Rhodoferax ferrireducens T118]
90	YP_055339	50842112	NAD(P) transhydrogenase subunit alpha [Propionibacterium acnes KPA171202]
91	NP_631664	21225885	NAD(P) transhydrogenase subunit alpha [Streptomyces coelicolor A3(2)]
92	ZP_006...	74018096	NAD(P) transhydrogenase, alpha subunit [Burkholderia ambifaria AMMD]
93	CAJ96500	113530153	NAD(P) transhydrogenase subunit alpha [Ralstonia eutropha H16]
94	YP_366916	78060341	NAD(P) transhydrogenase subunit alpha [Burkholderia sp. 383]
95	YP_574538	92114610	NAD(P) transhydrogenase, alpha subunit [Chromohalobacter salexigens DSM 3043]
96	ZP_004...	67542770	NAD(P) transhydrogenase, alpha subunit [Burkholderia vietnamiensis G4]
97	YP_702683	111019711	NAD(P) transhydrogenase alpha subunit [Rhodococcus sp. RHA1]
98	ZP_007...	75821435	COG3288: NAD/NADP transhydrogenase alpha subunit [Vibrio cholerae RC385]
99	ZP_011...	88798022	NAD(P) transhydrogenase subunit alpha [Reinekea sp. MED297]
100	ZP_009...	83371049	NAD(P) transhydrogenase, alpha subunit [Rhodobacter sphaeroides ATCC 17025]
101	ZP_006...	69933435	NAD(P) transhydrogenase, alpha subunit [Paracoccus denitrificans PD1222]
102	YP_353313	77463809	NAD(P) transhydrogenase subunit alpha [Rhodobacter sphaeroides 2.4.1]
103	ZP_009...	83373326	NAD(P) transhydrogenase, alpha subunit [Rhodobacter sphaeroides ATCC 17029]
104	ZP_010...	85704984	NAD(P) transhydrogenase subunit alpha [Roseovarius sp. 217]
105	YP_612703	99080549	NAD(P) transhydrogenase, alpha subunit [Silicibacter sp. TM1040]
106	YP_683504	110680497	NAD(P) transhydrogenase, alpha subunit [Roseobacter denitrificans OCh 114]
107	AAQ87369	36958944	NAD(P) transhydrogenase subunit alpha [Rhizobium sp. NGR234]
108	ZP_010...	86137634	NAD(P) transhydrogenase subunit alpha [Roseobacter sp. MED193]
109	XP_799127	72030333	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Strongylocentrotus purpuratus]
110	ZP_010...	84503572	NAD(P) transhydrogenase subunit alpha [Oceanicola batsensis HTCC2597]
111	ZP_010...	84516763	NAD(P) transhydrogenase subunit alpha [Loktanella vestfoldensis SKA53]

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112	NP_533164	17936374	NAD(P) transhydrogenase subunit alpha [Agrobacterium tumefaciens str. C58]
113	XP_562937	57968100	ENSANGP00000025507 [Anopheles gambiae str. PEST]
114	YP_511224	89055773	NAD(P) transhydrogenase, alpha subunit [Jannaschia sp. CCS1]
115	ZP_009...	83942708	NAD(P) transhydrogenase subunit alpha [Sulfitobacter sp. EE-36]
116	YP_168028	56697658	NAD(P) transhydrogenase subunit alpha [Silicibacter pomeroyi DSS-3]
117	EAT35199	108870974	nadp transhydrogenase [Aedes aegypti]
118	ZP_009...	83953947	NAD(P) transhydrogenase subunit alpha [Sulfitobacter sp. NAS-14.1]
119	ZP_009...	83949483	NAD(P) transhydrogenase subunit alpha [Roseovarius nubinhibens ISM]
120	XP_367628	39972475	hypothetical protein MG07539.4 [Magnaporthe grisea 70-15]
121	NP_999921	47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]
122	XP_961047	85100871	hypothetical protein (mitochondrial nicotinamide nucleotide transhydrogenase-related protein [imported] - Neurospora crassa OR74A)
123	AAH81117	51703526	MGC83563 protein [Xenopus laevis]
124	CAF99322	47223713	unnamed protein product [Tetraodon nigroviridis]
125	CAB88572	16416047	related to mitochondrial nicotinamide nucleotide transhydrogenase [Neurospora crassa]
126	AAI10544	83405154	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
127	AAI10545	83405537	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
128	NP_509028	17550456	Nicotinamide Nucleotide Transhydrogenase family member (nnt-1) [Caenorhabditis elegans]
129	2211247B	1589396	nicotinamide nucleotide transhydrogenase
130	ZP_010...	84686399	NAD(P) transhydrogenase subunit alpha [Rhodobacterales bacterium HTCC2654]
131	NP_776368	27806831	nicotinamide nucleotide transhydrogenase [Bos taurus]
132	AAA21440	163397	nicotinamide nucleotide transhydrogenase
133	P11024	128400	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
134	XP_536481	73953769	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 1 [Canis familiaris]
135	XP_970382	91083631	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Tribolium castaneum]
136	NP_001...	61557127	nicotinamide nucleotide transhydrogenase [Rattus norvegicus]
137	NP_892022	33695086	nicotinamide nucleotide transhydrogenase [Homo sapiens]
138	XP_867928	73953777	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 5 [Canis familiaris]
139	NP_036475	33695084	nicotinamide nucleotide transhydrogenase [Homo sapiens]
140	XP_424784	50761621	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Gallus gallus]
141	XP_646840	66826971	NAD(P)+ transhydrogenase (AB-specific) [Dictyostelium discoideum AX4]
142	BAC40113	26352966	unnamed protein product [Mus musculus]
143	EAS31570	90301939	conserved hypothetical protein [Coccidioides immitis RS]

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144	XP_867922	73953775	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 4 [Canis familiaris]
145	CAF99856	47230663	unnamed protein product [Tetraodon nigroviridis]
146	Q61941	51338804	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
147	2211247A	1589395	nicotinamide nucleotide transhydrogenase
148	NP_032736	31543330	nicotinamide nucleotide transhydrogenase [Mus musculus]
149	BAE35294	74198248	unnamed protein product [Mus musculus]
150	XP_748064	70985116	nicotinamide nucleotide transhydrogenase [Aspergillus fumigatus Af293]
151	XP_389182	46130902	hypothetical protein FG09006.1 [Gibberella zeae PH-1]
152	CAE68875	39598183	Hypothetical protein CBG14838 [Caenorhabditis briggsae]
153	AAK18179	13310152	nicotinamide nucleotide transhydrogenase [Acetabularia acetabulum]
154	AAG02246	11597233	NAD(P)H transhydrogenase [Acetabularia acetabulum]
155	AAC41577	6478876	pyridine nucleotidetranshydrogenase [Entamoeba histolytica]
156	XP_627136	66359916	pyridine nucleotide/ NAD(P) transhydrogenase alpha plus beta subunits, duplicated gene, [Cryptosporidium parvum Iowa II]
157	XP_666495	67602649	transhydrogenase 7B2 [Cryptosporidium hominis TU502]
158	BAE40577	74219995	unnamed protein product [Mus musculus]
159	CAH90079	55726630	hypothetical protein [Pongo pygmaeus]
160	AAA80188	571367	nicotinamide nucleotide transhydrogenase
161	EAQ86424	88178956	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
162	AAA29077	305062	transhydrogenase
163	AAA29081	158904	transhydrogenase
164	YP_724141	113478080	NAD(P)(+) transhydrogenase (AB-specific) [Trichodesmium erythraeum IMS101]
165	NP_487450	17230902	nicotinamide nucleotide transhydrogenase, subunit alpha [Nostoc sp. PCC 7120]
166	YP_323932	75909636	Alanine dehydrogenase/PNT-like [Anabaena variabilis ATCC 29413]
167	ZP_005...	67924536	NAD(P)(+) transhydrogenase (AB-specific) [Crocosphaera watsonii WH 8501]
168	ZP_013...	110607624	Alanine dehydrogenase/PNT-like [Maricaulis maris MCS10]
169	ZP_012...	91222948	NAD(P) transhydrogenase subunit alpha [Psychroflexus torquis ATCC 700755]
170	ZP_009...	82737423	NAD/NADP transhydrogenase, NAD(H)-binding DI subunit [Pseudomonas putida F1]
171	YP_000046	45655960	proton-translocating transhydrogenase, subunit alpha part 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]
172	YP_257267	70733627	NAD(P) transhydrogenase, alpha subunit part 1 [Pseudomonas fluorescens Pf-5]
173	ZP_001...	23130320	COG3288: NAD/NADP transhydrogenase alpha subunit [Nostoc punctiforme PCC 73102]
174	ZP_013...	110593183	NAD(P)(+) transhydrogenase (AB-specific) [Acidovorax sp. JS42]
175	ZP_009...	83859916	nicotinamide nucleotide transhydrogenase, subunit [Oceanicaulis alexandrii HTCC2633]

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176	YP_526430	90020603	Glycogen/starch/alpha-glucan phosphorylase [Saccharophagus degradans 2-40]
177	ZP_012...	89362826	nicotinamide nucleotide transhydrogenase, subunit alpha1 [Xanthobacter autotrophicus Py2]
178	YP_277175	71737873	NAD(P) transhydrogenase, subunit alpha part 1 [Pseudomonas syringae pv. phaseolicola 1448A]
179	YP_238081	66048240	Alanine dehydrogenase/PNT, C-terminal:Alanine dehydrogenase/PNT, N-terminal [Pseudomonas syringae pv. syringae B728a]
180	YP_675347	110635139	alanine dehydrogenase/PNT-like [Mesorhizobium sp. BNC1]
181	YP_345847	77456342	NAD(P)(+) transhydrogenase (AB-specific) [Pseudomonas fluorescens PfO-1]
182	AAQ87237	36958769	NAD(P) transhydrogenase subunit alpha [Rhizobium sp. NGR234]
183	ZP_013...	94499798	pyridine nucleotide transhydrogenase alpha subunit [Oceanobacter sp. RED65]
184	NP_881481	33593837	NAD(P) transhydrogenase, subunit alpha part 1 [Bordetella pertussis Tohama I]
185	P0C186	91207608	NAD(P) transhydrogenase subunit alpha part 1 (Pyridine nucleotide transhydrogenase subunit alpha 1) (Nicotinamide nucleotide transhydrogenase subunit alpha 1) (Proton-translocating transhydrogenase component 1) (dl)
186	1PTJB	37927621	Chain B, Crystal Structure Analysis Of The Di And Diii Complex Of Transhydrogenase With A Thio-Nicotinamide Nucleotide Analogue
187	YP_485056	86748560	NAD(P)(+) transhydrogenase (AB-specific) [Rhodopseudomonas palustris HaA2]
188	YP_620103	107021776	alanine dehydrogenase/PNT-like [Burkholderia cenocepacia AU 1054]
189	ZP_008...	77952426	pyridine nucleotide transhydrogenase alpha subunit [Marinobacter aquaeolei VT8]
190	NP_840933	30248863	Alanine dehydrogenase and pyridine nucleotide transhydrogenase [Nitrosomonas europaea ATCC 19718]
191	2FRDB	90109601	Chain B, Structure Of Transhydrogenase (Di.S138a.Nadh)2(Diii.Nadph)1 Asymmetric Complex
192	NP_888491	33600931	NAD(P) transhydrogenase, subunit alpha part 1 [Bordetella bronchiseptica RB50]
193	XP_726447	82596885	NAD(P) transhydrogenase subunit beta [Plasmodium yoelii yoelii str. 17XNL]
194	YP_551329	91790377	NAD(P)(+) transhydrogenase (AB-specific) [Polaromonas sp. JS666]
195	ZP_006...	71548985	NAD(P)(+) transhydrogenase (AB-specific) [Nitrosomonas eutropha C71]
196	YP_568553	91975894	NAD(P)(+) transhydrogenase (AB-specific) [Rhodopseudomonas palustris BisB5]
197	2FSVB	90109621	Chain B, Structure Of Transhydrogenase (Di.D135n.Nad+) 2(Diii.E155w.Nadp+)1 Asymmetric Complex
198	1NM5B	42543078	Chain B, R. Rubrum Transhydrogenase (Di.Q132n)2(Diii)1 Asymmetric Complex
199	1L7DB	27065343	Chain B, Crystal Structure Of R. Rubrum Transhydrogenase Domain I Without Bound Nad(H)

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200	ZP_012...	90418769	NAD(P) transhydrogenase, subunit alpha part 1 [Aurantimonas sp. SI85-9A1]
201	2FR8B	90109598	Chain B, Structure Of Transhydrogenase (Di.R127a.Nad+)2(Diii.Nadp+)1 Asymmetric Complex

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Table 33. Examples of transhydrogenase subunit beta polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	NP_416119	16129560	pyridine nucleotide transhydrogenase [Escherichia coli K12].
2	YP_669454	110641724	NAD(P) transhydrogenase subunit beta [Escherichia coli 536]
3	ZP_007...	75234915	COG1282: NAD/NADP transhydrogenase beta subunit [Escherichia coli E110019]
4	ZP_007...	75230949	COG1282: NAD/NADP transhydrogenase beta subunit [Escherichia coli B7A]
5	YP_407978	82544031	pyridine nucleotide transhydrogenase, beta subunit [Shigella boydii Sb227]
6	YP_150630	56413555	pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
7	YP_216485	62180068	pyridine nucleotide transhydrogenase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
8	ABF71059	102621429	NADP transhydrogenase beta subunit [Enterobacter cloacae]
9	NP_929428	37526084	pyridine nucleotide transhydrogenase [Photorhabdus luminescens subsp. laumondii TTO1]
10	YP_050298	50121131	pyridine nucleotide transhydrogenase [Erwinia carotovora subsp. atroseptica SCRI1043]
11	ZP_008...	77979497	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia intermedia ATCC 29909]
12	ZP_008...	77975378	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia frederiksenii ATCC 33641]
13	ZP_008...	77958019	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia bercovieri ATCC 43970]
14	ZP_008...	77963332	COG1282: NAD/NADP transhydrogenase beta subunit [Yersinia mollaretii ATCC 43969]
15	YP_647692	108811925	NAD(P) transhydrogenase subunit beta [Yersinia pestis Nepal516]
16	YP_455167	85059465	pyridine nucleotide transhydrogenase beta subunit [Sodalis glossinidius str. 'morsitans']
17	NP_719280	24375237	pyridine nucleotide transhydrogenase [Shewanella oneidensis MR-1]
18	YP_736946	114046396	NAD(P) transhydrogenase, beta subunit [Shewanella sp. MR-7]
19	ZP_009...	82741967	NAD(P) transhydrogenase, beta subunit [Shewanella sp. W3-18-1]
20	NP_245689	15602617	pyridine nucleotide transhydrogenase [Pasteurella multocida subsp. multocida str. Pm70]
21	ZP_005...	68541685	NAD(P) transhydrogenase, beta subunit [Shewanella baltica OS155]
22	ZP_012...	90412640	putative NAD(P) transhydrogenase, beta subunit [Photobacterium profundum 3TCK]
23	ZP_001...	53732668	COG1282: NAD/NADP transhydrogenase beta subunit [Haemophilus influenzae R2846]
24	YP_249234	68250122	pyridine nucleotide transhydrogenase [Haemophilus influenzae 86-028NP]
25	NP_439514	16273273	pyridine nucleotide transhydrogenase [Haemophilus influenzae Rd KW20]
26	ZP_005...	68545629	NAD(P) transhydrogenase, beta subunit [Shewanella

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			amazonensis SB2B]
27	YP_132575	54302582	pyridine nucleotide transhydrogenase [Photobacterium profundum SS9]
28	ZP_011...	89073748	pyridine nucleotide transhydrogenase [Photobacterium sp. SKA34]
29	NP_800431	28900776	pyridine nucleotide transhydrogenase [Vibrio parahaemolyticus RIMD 2210633]
30	ZP_012...	90577760	pyridine nucleotide transhydrogenase [Vibrio angustum S14]
31	ZP_007...	75857577	COG1282: NAD/NADP transhydrogenase beta subunit [Vibrio sp. Ex25]
32	NP_936867	37676471	pyridine nucleotide transhydrogenase [Vibrio vulnificus YJ016]
33	ZP_007...	75818461	COG1282: NAD/NADP transhydrogenase beta subunit [Vibrio cholerae V51]
34	ZP_007...	75831476	COG1282: NAD/NADP transhydrogenase beta subunit [Vibrio cholerae MO10]
35	ZP_012...	91226113	pyridine nucleotide transhydrogenase [Vibrio alginolyticus 12G01]
36	YP_206543	59713768	pyridine nucleotide transhydrogenase [Vibrio fischeri ES114]
37	YP_088415	52425278	pyridine nucleotide transhydrogenase [Mannheimia succiniciproducens MBEL55E]
38	ZP_001...	32035330	COG1282: NAD/NADP transhydrogenase beta subunit [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
39	ZP_006...	69950757	NAD(P) transhydrogenase, beta subunit [Shewanella frigidimarina NCIMB 400]
40	ZP_010...	86147992	pyridine nucleotide transhydrogenase [Vibrio sp. MED222]
41	ZP_009...	84393927	NAD(P) transhydrogenase, beta subunit [Vibrio splendidus 12B01]
42	ZP_007...	75429915	NAD/NADP transhydrogenase beta subunit [Actinobacillus succinogenes 130Z]
43	NP_274015	15676870	pyridine nucleotide transhydrogenase [Neisseria meningitidis MC58]
44	NP_283942	15794120	pyridine nucleotide transhydrogenase [Neisseria meningitidis Z2491]
45	YP_208524	59801812	pyridine nucleotide transhydrogenase [Neisseria gonorrhoeae FA 1090]
46	YP_718441	113460379	NAD(P)(+) transhydrogenase, beta subunit (pyridine nucleotide transhydrogenase) [Haemophilus somnus 129PT]
47	NP_874045	33152692	pyridine nucleotide transhydrogenase [Haemophilus ducreyi 35000HP]
48	YP_561941	91792290	NAD(P) transhydrogenase, beta subunit [Shewanella denitrificans OS217]
49	YP_434235	83645800	NAD/NADP transhydrogenase beta subunit [Hahella chejuensis KCTC 2396]
50	YP_268515	71280969	pyridine nucleotide transhydrogenase [Colwellia psychrerythraea 34H]
51	ZP_013...	106883670	NAD(P) transhydrogenase, beta subunit [Psychromonas ingrahamii 37]
52	ZP_009...	84495284	pyridine nucleotide transhydrogenase [Janibacter sp. HTCC2649]

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53	YP_637278	108797081	NAD(P) transhydrogenase, beta subunit [Mycobacterium sp. MCS]
54	ZP_012...	90408905	NAD(P) transhydrogenase subunit beta [Psychromonas sp. CNPT3]
55	ZP_011...	89340413	NAD(P) transhydrogenase, beta subunit [Mycobacterium flavescens PYR-GCK]
56	ZP_012...	90202100	NAD(P) transhydrogenase, beta subunit [Mycobacterium vanbaalenii PYR-1]
57	NP_631663	21225884	NAD(P) transhydrogenase beta subunit [Streptomyces coelicolor A3(2)]
58	NP_821577	29826943	pyridine nucleotide transhydrogenase, beta subunit [Streptomyces avermitilis MA-4680]
59	YP_702682	111019710	NAD(P) transhydrogenase beta subunit [Rhodococcus sp. RHA1]
60	YP_422186	83311922	NAD/NADP transhydrogenase beta subunit [Magnetospirillum magneticum AMB-1]
61	ZP_006...	71366731	NAD(P) transhydrogenase, beta subunit [Nocardioides sp. JS614]
62	YP_115164	53803089	NAD(P) transhydrogenase, beta subunit [Methylococcus capsulatus str. Bath]
63	YP_524984	89902513	NAD(P) transhydrogenase, beta subunit [Rhodoferax ferrireducens T118]
64	NP_440860	16330132	pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp. PCC 6803]
65	ZP_004...	66966824	NAD(P) transhydrogenase, beta subunit [Arthrobacter sp. FB24]
66	ZP_011...	88798021	pyridine nucleotide transhydrogenase [Reinekea sp. MED297]
67	YP_342321	77163796	NAD(P) transhydrogenase, beta subunit [Nitrosococcus oceani ATCC 19707]
68	ZP_006...	69261415	NAD(P) transhydrogenase, beta subunit [Magnetococcus sp. MC-1]
69	ZP_004...	67542769	NAD(P) transhydrogenase, beta subunit [Burkholderia vietnamiensis G4]
70	YP_366915	78060340	NAD(P) transhydrogenase, beta subunit [Burkholderia sp. 383]
71	ZP_006...	74018097	NAD(P) transhydrogenase, beta subunit [Burkholderia ambifaria AMMD]
72	YP_298859	73538492	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
73	YP_055340	50842113	NAD(P) transhydrogenase subunit beta [Propionibacterium acnes KPA171202]
74	ZP_009...	83949482	NAD(P)+ transhydrogenase, beta subunit [Roseovarius nubinhibens ISM]
75	CAJ96499	113530152	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
76	ZP_006...	69933434	NAD(P) transhydrogenase, beta subunit [Paracoccus denitrificans PD1222]
77	YP_168027	56697657	NAD(P)+ transhydrogenase, beta subunit [Silicibacter pomeroyi DSS-3]
78	NP_533165	17936375	NAD(P)+ transhydrogenase beta chain [Agrobacterium tumefaciens str. C58]
79	AAQ87370	36958945	NAD(P) transhydrogenase subunit beta [Rhizobium sp. NGR234]

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80	ZP_009...	83942707	NAD(P)+ transhydrogenase, beta subunit [Sulfitobacter sp. EE-36]
81	ZP_009...	83953946	NAD(P)+ transhydrogenase, beta subunit [Sulfitobacter sp. NAS-14.1]
82	ZP_007...	75813705	COG1282: NAD/NADP transhydrogenase beta subunit [Vibrio cholerae V52]
83	ZP_010...	84503573	NAD(P)+ transhydrogenase, beta subunit [Oceanicola batsensis HTCC2597]
84	ZP_010...	84686400	NAD(P)+ transhydrogenase, beta subunit [Rhodobacterales bacterium HTCC2654]
85	YP_612702	99080548	NAD(P) transhydrogenase, beta subunit [Silicibacter sp. TM1040]
86	ZP_010...	84516762	NAD(P)+ transhydrogenase, beta subunit [Loktanella vestfoldensis SKA53]
87	ZP_010...	86137633	NAD(P)+ transhydrogenase, beta subunit [Roseobacter sp. MED193]
88	YP_511223	89055772	NAD(P) transhydrogenase, beta subunit [Jannaschia sp. CCS1]
89	ZP_010...	85704983	NAD(P)+ transhydrogenase, beta subunit [Roseovarius sp. 217]
90	ZP_007...	75822802	COG1282: NAD/NADP transhydrogenase beta subunit [Vibrio cholerae RC385]
91	YP_683503	110680496	NAD(P) transhydrogenase, beta subunit [Roseobacter denitrificans OCh 114]
92	NP_949516	39937240	nicotinamide nucleotide transhydrogenase, subunit beta [Rhodopseudomonas palustris CGA009]
93	YP_418478	83269187	NAD(P) transhydrogenase, beta subunit [Brucella melitensis biovar Abortus 2308]
94	YP_485058	86748562	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris HaA2]
95	ZP_009...	83859918	nicotinamide nucleotide transhydrogenase, subunit beta [Oceanicaulis alexandrii HTCC2633]
96	ZP_008...	77740973	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris BisA53]
97	ZP_012...	89362731	NAD(P) transhydrogenase, beta subunit [Xanthobacter autotrophicus Py2]
98	ZP_008...	77814001	NAD(P) transhydrogenase, beta subunit [Shewanella putrefaciens CN-32]
99	ZP_010...	84704197	PntB, NAD(P) transhydrogenase, beta subunit [Parvularcula bermudensis HTCC2503]
100	YP_533811	90425441	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris BisB18]
101	P0C188	91207612	NAD(P) transhydrogenase subunit beta (Pyridine nucleotide transhydrogenase subunit beta) (Nicotinamide nucleotide transhydrogenase subunit beta) (Proton-translocating transhydrogenase NADP(H)-binding component) (dIII)
102	YP_568555	91975896	NAD(P) transhydrogenase, beta subunit [Rhodopseudomonas palustris BisB5]
103	ZP_012...	90418771	NAD(P) transhydrogenase, subunit beta [Aurantimonas sp. SI85-9A1]
104	YP_526432	90020605	NAD(P) transhydrogenase, beta subunit [Saccharophagus degradans 2-40]
105	ZP_008...	78699497	NAD(P)+ transhydrogenase beta chain [Bradyrhizobium sp. BTAi1]

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106	XP_424784	50761621	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Gallus gallus]
107	XP_799127	72030333	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Strongylocentrotus purpuratus]
108	ZP_010...	85716091	NAD/NADP transhydrogenase beta subunit [Nitrobacter sp. Nb-311A]
109	YP_605919	104779421	pyridine nucleotide transhydrogenase, beta subunit [Pseudomonas entomophila L48]
110	YP_457359	85373297	PntB, NAD(P) transhydrogenase, beta subunit [Erythrobacter litoralis HTCC2594]
111	XP_970382	91083631	PREDICTED: similar to nicotinamide nucleotide transhydrogenase [Tribolium castaneum]
112	BAB51677	14025075	nicotinamide nucleotide transhydrogenase, subunit beta [Mesorhizobium loti MAFF303099]
113	ZP_012...	94413536	hypothetical protein PaerP_01004711 [Pseudomonas aeruginosa PA7]
114	ZP_011...	88938736	NAD/NADP transhydrogenase beta subunit-like [Acidiphilium cryptum JF-5]
115	NP_795188	28872569	NAD(P) transhydrogenase, beta subunit [Pseudomonas syringae pv. tomato str. DC3000]
116	YP_257265	70733625	NAD(P) transhydrogenase, beta subunit [Pseudomonas fluorescens Pf-5]
117	NP_773764	27382235	NAD(P)+ transhydrogenase beta chain [Bradyrhizobium japonicum USDA 110]
118	YP_576517	92116788	NAD(P) transhydrogenase, beta subunit [Nitrobacter hamburgensis X14]
119	ZP_013...	107099186	hypothetical protein PaerPA_01000196 [Pseudomonas aeruginosa PACS2]
120	YP_557045	91781839	Putative NAD(P) transhydrogenase, beta subunit [Burkholderia xenovorans LB400]
121	ZP_009...	82737421	pyridine nucleotide transhydrogenase, beta subunit [Pseudomonas putida F1]
122	YP_345845	77456340	NAD(P) transhydrogenase, beta subunit [Pseudomonas fluorescens PfO-1]
123	NP_999921	47550793	nicotinamide nucleotide transhydrogenase [Danio rerio]
124	YP_411848	82702282	NAD(P) transhydrogenase, beta subunit [Nitrosospira multiformis ATCC 25196]
125	CAF99856	47230663	unnamed protein product [Tetraodon nigroviridis]
126	YP_675345	110635137	NAD(P) transhydrogenase, beta subunit [Mesorhizobium sp. BNC1]
127	EAT35199	108870974	nadp transhydrogenase [Aedes aegypti]
128	YP_277177	71736851	NAD(P) transhydrogenase, beta subunit [Pseudomonas syringae pv. phaseolicola 1448A]
129	YP_263852	71065125	NAD(P) transhydrogenase, beta subunit [Psychrobacter arcticus 273-4]
130	NP_840935	30248865	NAD(P) transhydrogenase beta subunit [Nitrosomonas europaea ATCC 19718]
131	XP_867922	73953775	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 4 [Canis familiaris]

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132	XP_867916	73953773	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 3 [Canis familiaris]
133	XP_536481	73953769	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 1 [Canis familiaris]
134	XP_867928	73953777	PREDICTED: similar to NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase) isoform 5 [Canis familiaris]
135	NP_001...	61557127	nicotinamide nucleotide transhydrogenase [Rattus norvegicus]
136	YP_238083	66048242	NAD(P) transhydrogenase, beta subunit [Pseudomonas syringae pv. syringae B728a]
137	BAE40577	74219995	unnamed protein product [Mus musculus]
138	BAC39226	26351179	unnamed protein product [Mus musculus]
139	ZP_013...	94494989	NAD(P) transhydrogenase, beta subunit [Sphingomonas sp. SKA58]
140	NP_032736	31543330	nicotinamide nucleotide transhydrogenase [Mus musculus]
141	BAC40113	26352966	unnamed protein product [Mus musculus]
142	ZP_004...	67155631	NAD(P) transhydrogenase, beta subunit [Azotobacter vinelandii AvOP]
143	YP_579812	93005375	NAD(P) transhydrogenase, beta subunit [Psychrobacter cryohalolentis K5]
144	YP_297031	73542511	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
145	YP_585107	94311897	NAD(P) transhydrogenase, beta subunit [Ralstonia metallidurans CH34]
146	YP_497119	87199862	NAD(P) transhydrogenase, beta subunit [Novosphingobium aromaticivorans DSM 12444]
147	AAQ87239	36958771	NAD(P) transhydrogenase subunit beta [Rhizobium sp. NGR234]
148	NP_888489	33600929	NAD(P) transhydrogenase subunit beta [Bordetella bronchiseptica RB50]
149	Q61941	51338804	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
150	NP_776368	27806831	nicotinamide nucleotide transhydrogenase [Bos taurus]
151	NP_884728	33597085	NAD(P) transhydrogenase subunit beta [Bordetella parapertussis 12822]
152	AAA21440	163397	nicotinamide nucleotide transhydrogenase
153	YP_441808	83721084	NAD(P) transhydrogenase, beta subunit [Burkholderia thailandensis E264]
154	AAI10544	83405154	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
155	NP_899769	34495554	NAD(P) transhydrogenase, beta subunit [Chromobacterium

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			violaceum ATCC 12472]
156	NP_422097	16127533	NAD(P) transhydrogenase, beta subunit [Caulobacter crescentus CB15]
157	XP_312859	58383882	ENSANGP00000016622 [Anopheles gambiae str. PEST]
158	ZP_009...	84360819	COG1282: NAD/NADP transhydrogenase beta subunit [Burkholderia dolosa AUO158]
159	ZP_014...	113935785	NAD(P) transhydrogenase, beta subunit [Caulobacter sp. K31]
160	ZP_006...	71548983	NAD(P) transhydrogenase, beta subunit [Nitrosomonas eutropha C71]
161	AAH81117	51703526	MGC83563 protein [Xenopus laevis]
162	CAH90079	55726630	hypothetical protein [Pongo pygmaeus]
163	BAE35294	74198248	unnamed protein product [Mus musculus]
164	ZP_014...	113872300	probable NAD(P) transhydrogenase subunit beta transmembrane protein [Sinorhizobium medicae WSM419]
165	AAI10545	83405537	Nicotinamide nucleotide transhydrogenase [Homo sapiens]
166	NP_036475	33695084	nicotinamide nucleotide transhydrogenase [Homo sapiens]
167	YP_727574	113869085	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
168	2211247B	1589396	nicotinamide nucleotide transhydrogenase
169	2211247A	1589395	nicotinamide nucleotide transhydrogenase
170	AAN62246	24461677	putative pyridine nucleotide transhydrogenase, beta subunit [Pseudomonas aeruginosa]
171	P11024	128400	NAD(P) transhydrogenase, mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase)
172	NP_892022	33695086	nicotinamide nucleotide transhydrogenase [Homo sapiens]
173	NP_386966	15966613	PROBABLE NAD(P) TRANSHYDROGENASE SUBUNIT BETA TRANSMEMBRANE PROTEIN [Sinorhizobium meliloti 1021]
174	YP_299910	73539543	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
175	ZP_012...	91769178	NAD(P) transhydrogenase, beta subunit [Psychrobacter sp. PRwf-1]
176	YP_293241	72383887	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
177	YP_299480	73539113	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
178	YP_293567	72384213	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
179	YP_725774	113867285	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
180	YP_620105	107021778	NAD(P) transhydrogenase, beta subunit [Burkholderia cenocepacia AU 1054]

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181	YP_725367	113866878	NAD(P) transhydrogenase subunit beta [Ralstonia eutropha H16]
182	NP_520854	17547452	PROBABLE TRANSMEMBRANE NADP TRANSHYDROGENASE (BETA SUBUNIT) OXIDOREDUCTASE PROTEIN [Ralstonia solanacearum GMI1000]
183	ZP_009...	83746755	PntB [Ralstonia solanacearum UW551]
184	ZP_013...	100235717	hypothetical protein Bpse4_03000891 [Burkholderia pseudomallei 406e]
185	YP_334763	76809085	NAD(P) transhydrogenase subunit beta [Burkholderia pseudomallei 1710b]
186	ZP_013...	100917505	hypothetical protein Bmal10_03001254 [Burkholderia mallei 10399]
187	ZP_004...	67667725	NAD(P) transhydrogenase, beta subunit [Burkholderia cenocepacia HI2424]
188	ZP_012...	91762289	NAD(p) transhydrogenase subunit beta [Candidatus Pelagibacter ubique HTCC1002]
189	YP_471093	86359201	NAD(P)(+) transhydrogenase (AB-specific), beta subunit protein [Rhizobium etli CFN 42]
190	ZP_010...	85707884	PntB, NAD(P) transhydrogenase, beta subunit [Erythrobacter sp. NAP1]
191	YP_293266	72383912	NAD(P) transhydrogenase, beta subunit [Ralstonia eutropha JMP134]
192	ZP_009...	84356795	COG1282: NAD/NADP transhydrogenase beta subunit [Burkholderia cenocepacia PC184]
193	YP_266000	71083281	NAD(p) transhydrogenase subunit beta [Candidatus Pelagibacter ubique HTCC1062]
194	CAE68875	39598183	Hypothetical protein CBG14838 [Caenorhabditis briggsae]
195	YP_368033	78065264	NAD(P) transhydrogenase, beta subunit [Burkholderia sp. 383]
196	YP_616428	103486867	NAD(P) transhydrogenase, beta subunit [Sphingopyxis alaskensis RB2256]
197	YP_246075	67458451	NAD(p) transhydrogenase subunit beta [Rickettsia felis URRWXCal2]
198	YP_537194	91204839	NAD(p) transhydrogenase subunit beta [Rickettsia bellii RML369-C]
199	XP_646840	66826971	NAD(P)+ transhydrogenase (AB-specific) [Dictyostelium discoideum AX4]
200	ZP_009...	83747817	NAD(P) transhydrogenase subunit beta [Ralstonia solanacearum UW551]
201	YP_047599	50086089	pyridine nucleotide transhydrogenase, beta subunit [Acinetobacter sp. ADP1]

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Table 34. Examples of pox2 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_505264.1	50555712	YlPOX2 [Yarrowia lipolytica].
2	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
3	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
6	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
12	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
13	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
14	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
15	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansenii CBS767]
16	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
17	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
18	AAA34362	170912	acyl-coenzyme A oxidase II precursor
19	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
20	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
21	AAA34361	170910	PXP-2 protein
22	1306283A	225549	oxidase,fatty acyl
23	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
24	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
25	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansenii CBS767]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
29	AAA34891	172217	acyl-coenzyme A oxidase
30	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
31	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-chain acyl-CoA oxidase) (AtCX1)
33	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
34	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
35	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
36	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
37	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA

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			oxidase) (AOX)
38	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
39	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
40	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
41	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
42	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
43	AAA19113	458119	acyl-CoA oxidase
44	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
45	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
46	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
47	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
48	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
49	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
50	CAD97622	31873262	hypothetical protein [Homo sapiens]
51	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
52	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
53	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
54	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
55	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
56	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
57	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
58	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
59	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
60	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
61	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
62	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
63	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
64	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
65	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
66	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
67	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
68	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
69	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
70	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes]
71	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmaniae]
72	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
73	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
74	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
75	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
76	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
77	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]

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78	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
79	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
80	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
81	AAH21339	18204156	Acox2 protein [Mus musculus]
82	BAE25794	74188249	unnamed protein product [Mus musculus]
83	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
84	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
85	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
86	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegicus]
87	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
88	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
89	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
90	BAC26167	26324826	unnamed protein product [Mus musculus]
91	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
92	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
93	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
94	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
95	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
96	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
97	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
98	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
99	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
100	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
101	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
102	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
103	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
104	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
105	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
106	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
107	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
108	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]

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109	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
110	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
111	AAH54727	68262425	Acox1 protein [Mus musculus]
112	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmitoyl [Strongylocentrotus purpuratus]
113	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
114	AAL28144	16767852	GH01266p [Drosophila melanogaster]
115	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
116	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
117	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
118	BAC35782	74197284	unnamed protein product [Mus musculus]
119	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
120	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
121	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
122	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
123	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
124	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
125	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
126	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
127	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoniae UW101]
128	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
129	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
130	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
131	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
132	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
133	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
134	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A4]
135	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
136	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
137	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
138	AAL39944	17862934	SD03592p [Drosophila melanogaster]
139	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
140	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
141	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
142	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
143	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)

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144	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
145	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
146	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
147	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
148	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
149	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
150	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
151	AAL48010	17944231	LD22081p [Drosophila melanogaster]
152	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
153	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
154	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
155	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
156	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
157	AAH44725	28703869	Acox3 protein [Mus musculus]
158	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
159	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
160	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
161	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
162	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Tribolium castaneum]
163	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
164	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
165	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
166	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
167	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
168	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
169	BAC26136	26324764	unnamed protein product [Mus musculus]
170	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
171	BAE42553	74143079	unnamed protein product [Mus musculus]
172	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
173	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
174	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
175	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
176	NP_961035	41408199	hypothetical protein MAP2101 [Mycobacterium avium subsp. paratuberculosis K-10]
177	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
178	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalenii PYR-1]
179	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]

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180	BAE60166	83770031	unnamed protein product [Aspergillus oryzae]
181	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavescens PYR-GCK]
182	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
183	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
184	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
185	AAH17053	16877606	ACOX3 protein [Homo sapiens]
186	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
187	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
188	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
189	AAL48950	17945806	RE34879p [Drosophila melanogaster]
190	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
191	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
192	AAL14003	16186117	SD05719p [Drosophila melanogaster]
193	XP_642669	66817952	hypothetical protein DDBDRAFT_0169270 [Dictyostelium discoideum AX4]
194	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]
195	NP_500943	17540842	F58F9.7 [Caenorhabditis elegans]
196	XP_664369	67541190	hypothetical protein AN6765.2 [Aspergillus nidulans FGSC A4]

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Table 35. Examples of pox1a polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504703	50554589	YIPOX1 [Yarrowia lipolytica].
2	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
3	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
4	XP_502199	50549457	YIPOX5 [Yarrowia lipolytica]
5	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
6	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
7	XP_504475	50554133	YIPOX4 [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
12	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
13	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
14	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
15	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansenii CBS767]
16	AAA34362	170912	acyl-coenzyme A oxidase II precursor
17	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansenii CBS767]
18	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
19	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
20	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
21	AAA34361	170910	PXP-2 protein
22	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
23	1306283A	225549	oxidase,fatty acyl
24	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
25	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
29	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
30	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
31	AAA34891	172217	acyl-coenzyme A oxidase
32	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-chain acyl-CoA oxidase) (AtCX1)
33	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
34	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
35	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
36	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
37	AAL01888	15553480	acyl-CoA oxidase [Glycine max]

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38	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
39	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
40	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
41	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
42	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
43	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
44	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
45	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
46	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
47	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmaniae]
48	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
49	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
50	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
51	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
52	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
53	AAA19113	458119	acyl-CoA oxidase
54	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
55	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
56	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
57	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
58	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
59	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
60	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
61	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
62	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
63	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
64	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
65	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
66	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
67	CAD97622	31873262	hypothetical protein [Homo sapiens]
68	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
69	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
70	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
71	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
72	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
73	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
74	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
75	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
76	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]

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77	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
78	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes]
79	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
80	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
81	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
82	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
83	BAC26167	26324826	unnamed protein product [Mus musculus]
84	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
85	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
86	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
87	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
88	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
89	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
90	AAH21339	18204156	Acox2 protein [Mus musculus]
91	BAE25794	74188249	unnamed protein product [Mus musculus]
92	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
93	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
94	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
95	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
96	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
97	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
98	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
99	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
100	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
101	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
102	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegicus]
103	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A4]
104	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
105	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
106	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
107	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
108	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
109	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
110	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]

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111	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
112	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
113	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmitoyl [Strongylocentrotus purpuratus]
114	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
115	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
116	AAH54727	68262425	Acox1 protein [Mus musculus]
117	BAC35782	74197284	unnamed protein product [Mus musculus]
118	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
119	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
120	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
121	AAL39944	17862934	SD03592p [Drosophila melanogaster]
122	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
123	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoniae UW101]
124	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
125	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
126	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
127	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
128	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
129	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
130	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
131	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
132	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
133	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
134	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
135	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
136	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
137	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
138	AAH44725	28703869	Acox3 protein [Mus musculus]
139	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
140	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
141	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
142	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]

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143	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
144	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
145	AAL28144	16767852	GH01266p [Drosophila melanogaster]
146	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
147	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
148	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
149	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
150	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
151	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
152	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
153	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
154	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Tribolium castaneum]
155	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
156	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
157	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
158	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
159	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
160	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
161	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
162	BAE42553	74143079	unnamed protein product [Mus musculus]
163	BAC26136	26324764	unnamed protein product [Mus musculus]
164	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
165	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
166	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
167	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
168	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
169	AAL48010	17944231	LD22081p [Drosophila melanogaster]
170	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
171	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
172	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
173	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
174	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
175	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
176	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
177	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor

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178	XP_395486	66564429	PREDICTED: similar to CG9527-PA [Apis mellifera]
179	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
180	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalenii PYR-1]
181	AAL48950	17945806	RE34879p [Drosophila melanogaster]
182	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
183	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase, N-terminal [Nocardioides sp. JS614]
184	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
185	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
186	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
187	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
188	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
189	XP_642669	66817952	hypothetical protein DDBDRAFT_0169270 [Dictyostelium discoideum AX4]
190	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]
191	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavescens PYR-GCK]
192	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linens BL2]
193	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
194	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
195	AAL14003	16186117	SD05719p [Drosophila melanogaster]
196	AAH17053	16877606	ACOX3 protein [Homo sapiens]
197	EAL32912	54644170	GA21857-PA [Drosophila pseudoobscura]

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Table 36. Examples of pox4 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504475.1	50554133	YlPOX4 [Yarrowia lipolytica]
2	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
3	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
6	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
12	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
13	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
14	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
15	AAA34362	170912	acyl-coenzyme A oxidase II precursor
16	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
17	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
18	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
19	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansenii CBS767]
20	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
21	1306283A	225549	oxidase,fatty acyl
22	AAA34361	170910	PXP-2 protein
23	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansenii CBS767]
24	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
25	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
29	AAA34891	172217	acyl-coenzyme A oxidase
30	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
31	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-chain acyl-CoA oxidase) (AtCX1)
33	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
34	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
35	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
36	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
37	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
38	AAH63727	39795632	MGC68531 protein [Xenopus laevis]

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39	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
40	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
41	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
42	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
43	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
44	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
45	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
46	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
47	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
48	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
49	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
50	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmaniae]
51	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
52	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
53	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
54	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
55	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
56	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
57	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
58	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
59	AAA19113	458119	acyl-CoA oxidase
60	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
61	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
62	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
63	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
64	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
65	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
66	CAD97622	31873262	hypothetical protein [Homo sapiens]
67	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
68	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
69	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
70	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
71	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
72	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
73	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
74	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
75	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
76	BAE25794	74188249	unnamed protein product [Mus musculus]
77	AAH21339	18204156	Acox2 protein [Mus musculus]
78	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate

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79	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
80	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
81	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
82	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
83	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes]
84	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
85	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
86	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmitoyl [Strongylocentrotus purpuratus]
87	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegicus]
88	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
89	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
90	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
91	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
92	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
93	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
94	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
95	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
96	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
97	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
98	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
99	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
100	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
101	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
102	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
103	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
104	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
105	BAC26167	26324826	unnamed protein product [Mus musculus]
106	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
107	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
108	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
109	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
110	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
111	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]

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112	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
113	AAL28144	16767852	GH01266p [Drosophila melanogaster]
114	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
115	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
116	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
117	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
118	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
119	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
120	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
121	AAL39944	17862934	SD03592p [Drosophila melanogaster]
122	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
123	AAH54727	68262425	Acox1 protein [Mus musculus]
124	BAC35782	74197284	unnamed protein product [Mus musculus]
125	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
126	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
127	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
128	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
129	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
130	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
131	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
132	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A4]
133	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
134	AAL48010	17944231	LD22081p [Drosophila melanogaster]
135	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoniae UW101]
136	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
137	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
138	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
139	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
140	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
141	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
142	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
143	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
144	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
145	YP_445820	83816544	acyl-coenzyme A oxidase l, putative [Salinibacter ruber DSM 13855]
146	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
147	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]

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148	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
149	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
150	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
151	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
152	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
153	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
154	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
155	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
156	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
157	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
158	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Tribolium castaneum]
159	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
160	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
161	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
162	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
163	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
164	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
165	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
166	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
167	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
168	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
169	NP_961035	41408199	hypothetical protein MAP2101 [Mycobacterium avium subsp. paratuberculosis K-10]
170	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
171	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
172	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
173	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
174	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalenii PYR-1]
175	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
176	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
177	CAA68661	2674	44 kD translation product [Candida tropicalis]
178	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
179	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
180	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]

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181	BAE60166	83770031	unnamed protein product [Aspergillus oryzae]
182	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavescens PYR-GCK]
183	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
184	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase, N-terminal [Nocardioides sp. JS614]
185	AAL14003	16186117	SD05719p [Drosophila melanogaster]
186	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
187	AAH44725	28703869	Acox3 protein [Mus musculus]
188	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
189	EAL33335	54644594	GA14550-PA [Drosophila pseudoobscura]
190	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
191	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
192	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
193	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
194	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
195	ZP_006...	69287897	Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region [Kineococcus radiotolerans SRS30216]
196	BAE47462	78483008	acyl-CoA oxidase [Arthrobacter ureafaciens]

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Table 37. Examples of pox1 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica].
2	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
3	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
4	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
5	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
6	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
7	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	AAA34362	170912	acyl-coenzyme A oxidase II precursor
11	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
12	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
13	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
14	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
15	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
16	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
17	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
18	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
19	AAA34361	170910	PXP-2 protein
20	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
21	1306283A	225549	oxidase,fatty acyl
22	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
23	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansenii CBS767]
24	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
25	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansenii CBS767]
26	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
27	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
29	AAA34891	172217	acyl-coenzyme A oxidase
30	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)

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31	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
33	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
34	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-chain acyl-CoA oxidase) (AtCX1)
35	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
36	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
37	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
38	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
39	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
40	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
41	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
42	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
43	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
44	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
45	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
46	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
47	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
48	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
49	BAE25794	74188249	unnamed protein product [Mus musculus]
50	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
51	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
52	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
53	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
54	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
55	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
56	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
57	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
58	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
59	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmaniae]
60	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
61	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
62	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)

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63	AAH21339	18204156	Acox2 protein [Mus musculus]
64	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
65	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
66	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
67	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
68	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
69	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
70	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
71	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
72	CAD97622	31873262	hypothetical protein [Homo sapiens]
73	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
74	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
75	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
76	AAA19113	458119	acyl-CoA oxidase
77	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
78	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
79	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
80	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
81	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes]
82	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
83	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
84	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
85	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegicus]
86	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
87	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
88	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
89	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]

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90	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
91	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
92	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
93	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
94	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
95	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
96	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
97	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
98	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmitoyl [Strongylocentrotus purpuratus]
99	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
100	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
101	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
102	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
103	BAC26167	26324826	unnamed protein product [Mus musculus]
104	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
105	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
106	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
107	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A4]
108	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
109	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
110	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
111	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
112	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
113	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
114	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
115	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
116	AAH54727	68262425	Acox1 protein [Mus musculus]
117	BAC35782	74197284	unnamed protein product [Mus musculus]

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118	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
119	AAL39944	17862934	SD03592p [Drosophila melanogaster]
120	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
121	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoniae UW101]
122	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
123	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
124	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
125	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
126	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
127	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
128	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
129	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
130	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
131	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
132	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
133	AAH44725	28703869	Acox3 protein [Mus musculus]
134	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Tribolium castaneum]
135	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
136	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
137	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
138	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
139	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
140	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
141	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
142	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
143	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
144	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
145	BAE42553	74143079	unnamed protein product [Mus musculus]
146	AAL28144	16767852	GH01266p [Drosophila melanogaster]
147	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
148	BAC26136	26324764	unnamed protein product [Mus musculus]
149	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]

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150	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
151	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
152	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
153	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
154	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
155	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
156	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
157	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
158	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
159	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
160	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
161	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
162	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
163	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
164	AAH17053	16877606	ACOX3 protein [Homo sapiens]
165	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
166	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
167	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
168	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
169	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
170	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
171	XP_317513	58390136	ENSANGP00000010039 [Anopheles gambiae str. PEST]
172	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalenii PYR-1]
173	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
174	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
175	XP_395486	66564429	PREDICTED: similar to CG9527-PA [Apis mellifera]
176	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
177	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
178	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linens BL2]
179	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]

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180	NP_500943	17540842	F58F9.7 [Caenorhabditis elegans]
181	EAT39346	108875121	acyl-CoA oxidase [Aedes aegypti]
182	CAA96917	1945301	POX1 [Saccharomyces cerevisiae]
183	NP_609027	45550141	CG9527-PA [Drosophila melanogaster]
184	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
185	AAL48010	17944231	LD22081p [Drosophila melanogaster]
186	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
187	CAE61577	39584202	Hypothetical protein CBG05491 [Caenorhabditis briggsae]
188	AAL48950	17945806	RE34879p [Drosophila melanogaster]
189	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
190	AAL14003	16186117	SD05719p [Drosophila melanogaster]
191	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
192	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavescens PYR-GCK]
193	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
194	ZP_011...	88803915	acyl-coenzyme A oxidase I, putative [Robiginitalea biformata HTCC2501]
195	EAL32912	54644170	GA21857-PA [Drosophila pseudoobscura]
196	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
197	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]

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Table 38. Examples of pox3 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503244	50551539	YlPOX3 [Yarrowia lipolytica]
2	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica]
3	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
4	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
5	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
6	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
9	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
10	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
11	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
12	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
13	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
14	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
15	AAA34362	170912	acyl-coenzyme A oxidase II precursor
16	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
17	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
18	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
19	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
20	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansenii CBS767]
21	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
22	AAA34361	170910	PXP-2 protein
23	1306283A	225549	oxidase,fatty acyl
24	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
25	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansenii CBS767]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
29	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
30	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
31	AAA34891	172217	acyl-coenzyme A oxidase
32	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
33	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
34	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-chain acyl-CoA oxidase) (AtCX1)
35	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
36	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
37	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
38	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
39	AAL01888	15553480	acyl-CoA oxidase [Glycine max]

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40	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
41	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
42	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
43	BAE25794	74188249	unnamed protein product [Mus musculus]
44	AAL01887	15553478	acyl-CoA oxidase [Glycine max]
45	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
46	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
47	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmaniae]
48	AAH21339	18204156	Acox2 protein [Mus musculus]
49	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
50	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
51	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
52	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
53	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
54	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
55	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
56	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
57	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
58	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegicus]
59	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
60	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
61	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
62	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
63	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
64	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
65	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
66	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
67	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
68	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
69	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
70	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
71	CAD97622	31873262	hypothetical protein [Homo sapiens]
72	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
73	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
74	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
75	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
76	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
77	AAA18595	495475	peroxisomal fatty acyl-coA oxidase

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78	AAA19113	458119	acyl-CoA oxidase
79	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
80	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
81	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
82	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
83	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
84	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
85	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]
86	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
87	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
88	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
89	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
90	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
91	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
92	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
93	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
94	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
95	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
96	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
97	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes]
98	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
99	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
100	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
101	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
102	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
103	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
104	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
105	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
106	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
107	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
108	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
109	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
110	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]

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111	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
112	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
113	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
114	BAC26167	26324826	unnamed protein product [Mus musculus]
115	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
116	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
117	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
118	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
119	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
120	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
121	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
122	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
123	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A4]
124	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmitoyl [Strongylocentrotus purpuratus]
125	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
126	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
127	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
128	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
129	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
130	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
131	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
132	AAL39944	17862934	SD03592p [Drosophila melanogaster]
133	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
134	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
135	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
136	AAL48010	17944231	LD22081p [Drosophila melanogaster]
137	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
138	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
139	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
140	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
141	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
142	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
143	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
144	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
145	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
146	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]

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147	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Tribolium castaneum]
148	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
149	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
150	BAC35782	74197284	unnamed protein product [Mus musculus]
151	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
152	AAH44725	28703869	Acox3 protein [Mus musculus]
153	AAH54727	68262425	Acox1 protein [Mus musculus]
154	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
155	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoniae UW101]
156	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]
157	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
158	AAL28144	16767852	GH01266p [Drosophila melanogaster]
159	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
160	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
161	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
162	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
163	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
164	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
165	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
166	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
167	BAC26136	26324764	unnamed protein product [Mus musculus]
168	BAE42553	74143079	unnamed protein product [Mus musculus]
169	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
170	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
171	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
172	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
173	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
174	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
175	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
176	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
177	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalenii PYR-1]
178	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
179	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
180	ZP_011...	89339305	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium flavescens PYR-GCK]

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181	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
182	BAE60166	83770031	unnamed protein product [Aspergillus oryzae]
183	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]
184	NP_961035	41408199	hypothetical protein MAP2101 [Mycobacterium avium subsp. paratuberculosis K-10]
185	YP_640598	108800401	acyl-CoA dehydrogenase-like protein [Mycobacterium sp. MCS]
186	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
187	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
188	BAE47462	78483008	acyl-CoA oxidase [Arthrobacter ureafaciens]
189	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linens BL2]
190	AAH17053	16877606	ACOX3 protein [Homo sapiens]
191	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
192	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase, N-terminal [Nocardioides sp. JS614]
193	ZP_009...	84496319	hypothetical protein JNB_02330 [Janibacter sp. HTCC2649]
194	ZP_004...	66967405	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal [Arthrobacter sp. FB24]
195	ZP_011...	88803915	acyl-coenzyme A oxidase I, putative [Robiginitalea biformata HTCC2501]
196	CAA68661	2674	44 kD translation product [Candida tropicalis]

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Table 39. Examples of pox5 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_502199	50549457	YlPOX5 [Yarrowia lipolytica].
2	O74936	59799074	Acyl-coenzyme A oxidase 3 (Acyl-CoA oxidase 3)
3	O74934	59799072	Acyl-coenzyme A oxidase 1 (Acyl-CoA oxidase 1)
4	XP_504703	50554589	YlPOX1 [Yarrowia lipolytica]
5	O74935	59799073	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2)
6	XP_504475	50554133	YlPOX4 [Yarrowia lipolytica]
7	XP_503632	50552444	hypothetical protein [Yarrowia lipolytica]
8	XP_760471	71020481	hypothetical protein UM04324.1 [Ustilago maydis 521]
9	XP_571768	58269224	Acyl-coenzyme A oxidase I [Cryptococcus neoformans var. neoformans JEC21]
10	BAA83482	5763520	acyl-CoA oxidase [Candida tropicalis]
11	BAA83483	5763522	acyl-CoA oxidase [Candida tropicalis]
12	OXCKPM	66060	acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
13	P08790	17373073	Acyl-coenzyme A oxidase 5 (Acyl-CoA oxidase 5) (PXP-5)
14	AAA34362	170912	acyl-coenzyme A oxidase II precursor
15	OXCKX5	66061	acyl-CoA oxidase (EC 1.3.3.6) POX5, peroxisomal - yeast (Candida tropicalis)
16	XP_717995	68475844	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
17	Q9Y7B1	60391213	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
18	XP_721610	68468582	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
19	AAA34361	170910	PXP-2 protein
20	XP_721613	68468588	putative fatty-acyl coenzyme A oxidase [Candida albicans SC5314]
21	P06598	17373023	Acyl-coenzyme A oxidase 4 (Acyl-CoA oxidase 4) (PXP-4) (Peroxisomal fatty acyl-CoA oxidase)
22	Q6BRD5	59799027	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
23	1306283A	225549	oxidase,fatty acyl
24	XP_457726	50417804	hypothetical protein DEHA0C01155g [Debaryomyces hansenii CBS767]
25	XP_459232	50421365	hypothetical protein DEHA0D18667g [Debaryomyces hansenii CBS767]
26	Q00468	2498206	Acyl-coenzyme A oxidase 2 (Acyl-CoA oxidase 2) (AOX 2)
27	Q756A9	60391210	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
28	Q6FY63	59799032	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
29	NP_011310	6321233	Fatty-acyl coenzyme A oxidase, involved in the fatty acid beta-oxidation pathway; localized to the peroxisomal matrix; Pox1p [Saccharomyces cerevisiae]
30	AAA34891	172217	acyl-coenzyme A oxidase
31	Q6CKK7	59799028	Acyl-coenzyme A oxidase (Acyl-CoA oxidase)
32	1W07B	58177067	Chain B, Arabidopsis Thaliana Acyl-Coa Oxidase 1
33	O65202	62286589	Acyl-coenzyme A oxidase 1, peroxisomal (AOX 1) (Long-chain acyl-CoA oxidase) (AtCX1)
34	CAA68660	2673	acyl-coenzyme A oxidase [Candida tropicalis]
35	NP_567513	18414744	ACX1 (ACYL-COA OXIDASE 1) [Arabidopsis thaliana]
36	H71434	7488059	probable apetala2 domain TINY - Arabidopsis thaliana
37	AAL01888	15553480	acyl-CoA oxidase [Glycine max]
38	AAL01887	15553478	acyl-CoA oxidase [Glycine max]

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39	ABE83706	92875906	acyl-CoA oxidase [Medicago truncatula]
40	BAF18456	113594582	Os06g0103500 [Oryza sativa (japonica cultivar-group)]
41	2FONC	109157678	Chain C, X-Ray Crystal Structure Of Leacx1, An Acyl-Coa Oxidase From Lycopersicon Esculentum (Tomato)
42	AAW78689	58531948	peroxisomal acyl-CoA oxidase 1A [Lycopersicon esculentum]
43	AAW78691	58531952	peroxisomal acyl-CoA oxidase 1A [Lycopersicon cheesmaniae]
44	Q9ZQP2	62286640	Putative acyl-coenzyme A oxidase 1.2, peroxisomal
45	NP_001...	54400372	hypothetical protein LOC449662 [Danio rerio]
46	XP_592892	76648807	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 1 [Bos taurus]
47	XP_879996	76648809	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 6 [Bos taurus]
48	AAH68891	46250227	MGC83074 protein [Xenopus laevis]
49	AAH97101	67678187	Zgc:92584 protein [Danio rerio]
50	XP_414406	50754485	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Gallus gallus]
51	NP_001...	55741614	acyl-Coenzyme A oxidase 1, palmitoyl [Gallus gallus]
52	XP_320717	58394415	ENSANGP00000020118 [Anopheles gambiae str. PEST]
53	NP_510603	17568313	F59F4.1 [Caenorhabditis elegans]
54	BAE25794	74188249	unnamed protein product [Mus musculus]
55	CAE69737	39596101	Hypothetical protein CBG16008 [Caenorhabditis briggsae]
56	AAH21339	18204156	Acox2 protein [Mus musculus]
57	CAJ83302	89271321	acyl-Coenzyme A oxidase 2, branched chain [Xenopus tropicalis]
58	XP_320718	58394417	ENSANGP00000020032 [Anopheles gambiae str. PEST]
59	Q9QXD1	17367045	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
60	AAH63727	39795632	MGC68531 protein [Xenopus laevis]
61	Q5RC19	62286600	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
62	AAW78690	58531950	peroxisomal acyl-CoA oxidase 1B [Lycopersicon esculentum]
63	XP_782824	72015136	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
64	AAH47700	28839704	Acyl-Coenzyme A oxidase 2, branched chain [Homo sapiens]
65	EAT39640	108875415	acyl-CoA oxidase [Aedes aegypti]
66	NP_001...	62751552	MGC108278 protein [Xenopus tropicalis]
67	CAH90691	55727877	hypothetical protein [Pongo pygmaeus]
68	XP_001...	109118312	PREDICTED: similar to acyl-Coenzyme A oxidase isoform b [Macaca mulatta]
69	Q15067	17380467	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) (Straight-chain acyl-CoA oxidase) (SCOX)
70	NP_009223	30089974	acyl-Coenzyme A oxidase isoform b [Homo sapiens]
71	AAA19113	458119	acyl-CoA oxidase

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72	AAB30019	7689914	peroxisomal acyl-coenzyme A oxidase [Homo sapiens]
73	XP_785210	72015040	PREDICTED: similar to Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX) [Strongylocentrotus purpuratus]
74	O02767	17366131	Acyl-coenzyme A oxidase 2, peroxisomal (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase) (3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase)
75	NP_004026	30089972	acyl-Coenzyme A oxidase isoform a [Homo sapiens]
76	AAA18595	495475	peroxisomal fatty acyl-coA oxidase
77	I38095	2117541	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal - human
78	AAH08767	14250616	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
79	B54942	1082171	acyl-CoA oxidase (EC 1.3.3.6), peroxisomal splice form II - human
80	NP_001...	78369480	acyl-Coenzyme A oxidase 1, palmitoyl [Bos taurus]
81	NP_499119	17552648	C48B4.1 [Caenorhabditis elegans]
82	NP_665713	21955130	acyl-Coenzyme A oxidase 2, branched chain [Rattus norvegicus]
83	CAD97622	31873262	hypothetical protein [Homo sapiens]
84	BAA86870	6429156	peroxisomal acyl-CoA oxidase [Mus musculus]
85	NP_056544	66793429	acyl-Coenzyme A oxidase 1, palmitoyl [Mus musculus]
86	AAH85743	55249685	Acyl-Coenzyme A oxidase 1, palmitoyl [Rattus norvegicus]
87	2DDHA	93279231	Chain A, Crystal Structure Of Acyl-Coa Oxidase Complexed With 3-Oh- Dodecanoate
88	Q9R0H0	51338830	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
89	XP_758355	71010163	hypothetical protein UM02208.1 [Ustilago maydis 521]
90	AAH10425	14714578	Acyl-Coenzyme A oxidase 1, palmitoyl [Homo sapiens]
91	AAB62926	2253380	peroxisomal acyl-CoA oxidase [Mus musculus]
92	CAE65171	39590798	Hypothetical protein CBG10043 [Caenorhabditis briggsae]
93	XP_625136	66556360	PREDICTED: similar to CG5009-PA, partial [Apis mellifera]
94	XP_540441	73965013	PREDICTED: similar to acyl-Coenzyme A oxidase isoform a [Canis familiaris]
95	Q8HYL8	34098564	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
96	CAE63476	39592399	Hypothetical protein CBG07943 [Caenorhabditis briggsae]
97	AAI08648	83318302	Unknown (protein for MGC:131363) [Xenopus laevis]
98	XP_879827	76648805	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) isoform 5 [Bos taurus]
99	AAF73843	8163758	acyl-CoA oxidase ACX3 [Arabidopsis thaliana]
100	Q9LLH9	62286634	Acyl-coenzyme A oxidase 3, peroxisomal precursor (AOX 3) (Medium-chain acyl-CoA oxidase) (AtCX3)
101	XP_973660	91082769	PREDICTED: similar to CG5009-PA [Tribolium castaneum]
102	EAS31618	90301987	hypothetical protein CIMG_07097 [Coccidioides immitis RS]
103	EAR95568	89297580	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
104	Q9Z1N0	17367267	Acyl-coenzyme A oxidase 1, peroxisomal (Palmitoyl-CoA oxidase) (AOX)
105	AAO15577	27462768	acyl-CoA oxidase type 2 [Phascolarctos cinereus]

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106	XP_541826	73985284	PREDICTED: similar to Acyl-coenzyme A oxidase 2, peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) [Canis familiaris]
107	CAE63479	39592402	Hypothetical protein CBG07946 [Caenorhabditis briggsae]
108	XP_511690	55645995	PREDICTED: similar to hypothetical protein [Pan troglodytes]
109	BAC26167	26324826	unnamed protein product [Mus musculus]
110	CAE63477	39592400	Hypothetical protein CBG07944 [Caenorhabditis briggsae]
111	NP_493264	17506535	F08A8.4 [Caenorhabditis elegans]
112	Q9LMI7	62286635	Putative acyl-coenzyme A oxidase 3.2, peroxisomal precursor
113	CAJ58493	85539740	Hypothetical protein F08A8.1c [Caenorhabditis elegans]
114	NP_001...	71983355	F08A8.1b [Caenorhabditis elegans]
115	NP_001...	71983346	F08A8.1a [Caenorhabditis elegans]
116	BAF19505	113595631	Os06g0354500 [Oryza sativa (japonica cultivar-group)]
117	NP_493263	17506533	F08A8.3 [Caenorhabditis elegans]
118	O64894	62286587	Acyl-coenzyme A oxidase, peroxisomal precursor (AOX) (Long-chain acyl-CoA oxidase)
119	NP_493262	17506531	F08A8.2 [Caenorhabditis elegans]
120	CAE63480	39592403	Hypothetical protein CBG07947 [Caenorhabditis briggsae]
121	AAF14635	6503198	acyl-CoA oxidase [Petroselinum crispum]
122	BAE55537	83765394	unnamed protein product [Aspergillus oryzae]
123	NP_998312	47085909	pristanoyl acyl-Coenzyme A oxidase 3 [Danio rerio]
124	O65201	62286588	Acyl-coenzyme A oxidase 2, peroxisomal precursor (AOX 2) (Long-chain acyl-CoA oxidase) (AtCX2)
125	AAC13497	3044212	acyl-CoA oxidase [Arabidopsis thaliana]
126	EAT87650	111066530	hypothetical protein SNOG_05259 [Phaeosphaeria nodorum SN15]
127	XP_587157	76620513	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Bos taurus]
128	EAT48205	108883980	acyl-CoA oxidase [Aedes aegypti]
129	EAT87454	111066334	hypothetical protein SNOG_05063 [Phaeosphaeria nodorum SN15]
130	XP_664356	67541164	hypothetical protein AN6752.2 [Aspergillus nidulans FGSC A4]
131	AAB67883	1575556	acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady']
132	AAR00586	37699750	acyl-CoA oxidase [Phalaenopsis cv. 'True Lady']
133	CAH91864	55730283	hypothetical protein [Pongo pygmaeus]
134	XP_636605	66805767	hypothetical protein DDBDRAFT_0188084 [Dictyostelium discoideum AX4]
135	NP_611264	24654595	CG5009-PA [Drosophila melanogaster]
136	EAS04704	89306716	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
137	XP_635946	66804335	hypothetical protein DDBDRAFT_0188674 [Dictyostelium discoideum AX4]
138	O15254	17366151	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
139	AAL39944	17862934	SD03592p [Drosophila melanogaster]
140	NP_523802	17647123	acyl-Coenzyme A oxidase at 57D proximal CG9707-PA [Drosophila melanogaster]
141	AAL28144	16767852	GH01266p [Drosophila melanogaster]
142	XP_382463	46110811	hypothetical protein FG02287.1 [Gibberella zeae PH-1]
143	EAL26359	54636956	GA18591-PA [Drosophila pseudoobscura]
144	CAA04688	2370232	putative acyl-CoA oxidase [Hordeum vulgare subsp. vulgare]

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145	XP_783450	72111190	PREDICTED: similar to acyl-Coenzyme A oxidase 1, palmitoyl [Strongylocentrotus purpuratus]
146	AAL48010	17944231	LD22081p [Drosophila melanogaster]
147	CAH91120	55728762	hypothetical protein [Pongo pygmaeus]
148	XP_646395	66826081	hypothetical protein DDBDRAFT_0216722 [Dictyostelium discoideum AX4]
149	XP_758113	71007469	hypothetical protein UM01966.1 [Ustilago maydis 521]
150	EAR99631	89301643	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
151	EAR89261	89291273	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
152	XP_637610	66807775	hypothetical protein DDBDRAFT_0187085 [Dictyostelium discoideum AX4]
153	ABA94670	108864573	Acyl-coenzyme A oxidase 2, peroxisomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
154	EAL26647	54637244	GA21980-PA [Drosophila pseudoobscura]
155	ZP_012...	90587482	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Flavobacterium johnsoniae UW101]
156	BAC35782	74197284	unnamed protein product [Mus musculus]
157	EAS02716	89304728	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
158	YP_634556	108758121	putative acyl-CoA dehydrogenase [Myxococcus xanthus DK 1622]
159	AAH54727	68262425	Acox1 protein [Mus musculus]
160	YP_445820	83816544	acyl-coenzyme A oxidase I, putative [Salinibacter ruber DSM 13855]
161	AAH44725	28703869	Acox3 protein [Mus musculus]
162	NP_109646	34328334	acyl-Coenzyme A oxidase 3, pristanoyl [Mus musculus]
163	XP_545908	73951751	PREDICTED: similar to Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) [Canis familiaris]
164	NP_001...	79332306	ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase [Arabidopsis thaliana]
165	EAR98581	89300593	Acyl-CoA oxidase family protein [Tetrahymena thermophila SB210]
166	XP_969513	91093755	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Tribolium castaneum]
167	ZP_012...	89890388	acyl-CoA oxidase [Flavobacteria bacterium BBFL7]
168	YP_290295	72162638	hypothetical protein Tfu_2239 [Thermobifida fusca YX]
169	BAC26136	26324764	unnamed protein product [Mus musculus]
170	BAE42553	74143079	unnamed protein product [Mus musculus]
171	EAL26648	54637245	GA21981-PA [Drosophila pseudoobscura]
172	NP_445791	16758056	acyl-Coenzyme A oxidase 3, pristanoyl [Rattus norvegicus]
173	Q9EPL9	17366740	Acyl-coenzyme A oxidase 3, peroxisomal (Pristanoyl-CoA oxidase) (Branched-chain acyl-CoA oxidase) (BRCACox)
174	XP_786025	72005645	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
175	XP_786081	72005647	PREDICTED: similar to pristanoyl acyl-Coenzyme A oxidase 3 [Strongylocentrotus purpuratus]
176	EAL32329	54643586	GA18278-PA [Drosophila pseudoobscura]
177	NP_724181	24585195	CG17544-PC, isoform C [Drosophila melanogaster]
178	AAL14003	16186117	SD05719p [Drosophila melanogaster]
179	CAA68661	2674	44 kD translation product [Candida tropicalis]

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180	NP_572371	24640268	CG4586-PA [Drosophila melanogaster]
181	ZP_011...	88854811	acyl-CoA oxidase [marine actinobacterium PHSC20C1]
182	EAL33335	54644594	GA14550-PA [Drosophila pseudoobscura]
183	EAS36523	90306892	hypothetical protein CIMG_01877 [Coccidioides immitis RS]
184	EAT48670	108884445	acyl-CoA oxidase [Aedes aegypti]
185	YP_702012	111019040	acyl-CoA oxidase [Rhodococcus sp. RHA1]
186	ZP_003...	62426247	COG1960: Acyl-CoA dehydrogenases [Brevibacterium linens BL2]
187	XP_317446	58390030	ENSANGP00000011863 [Anopheles gambiae str. PEST]
188	XP_317513	58390136	ENSANGP00000010039 [Anopheles gambiae str. PEST]
189	AAH17053	16877606	ACOX3 protein [Homo sapiens]
190	ZP_012...	90205075	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium vanbaalenii PYR-1]
191	ZP_011...	88803915	acyl-coenzyme A oxidase I, putative [Robiginitalea biformata HTCC2501]
192	XP_642669	66817952	hypothetical protein DDBDRAFT_0169270 [Dictyostelium discoideum AX4]
193	NP_508036	17560134	F25C8.1 [Caenorhabditis elegans]
194	ZP_006...	71369913	Acyl-CoA oxidase:Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase, N-terminal [Nocardioides sp. JS614]
195	BAE65934	83775815	unnamed protein product [Aspergillus oryzae]
196	ZP_012...	92908524	Acyl-CoA oxidase-like:Acyl-CoA dehydrogenase-like:Acyl-CoA dehydrogenase, central region [Mycobacterium sp. JLS]

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Table 40. Examples of triglyceride lipase (tgl4) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_505230	50555644	hypothetical protein [Yarrowia lipolytica].
2	XP_459553	50421985	hypothetical protein DEHA0E06127g [Debaryomyces hansenii CBS767]
3	XP_387731	46126355	hypothetical protein FG07555.1 [Gibberella zeae PH-1]
4	XP_717704	68476486	putative patatin-like phospholipase [Candida albicans SC5314]
5	XP_958750	85091127	hypothetical protein [Neurospora crassa OR74A]
6	NP_013015	6322942	Triacylglycerol lipase involved in triacylglycerol mobilization and degradation; found in lipid particles; potential Cdc28p substrate; Tgl4p [Saccharomyces cerevisiae]
7	XP_659317	67522513	hypothetical protein AN1713.2 [Aspergillus nidulans FGSC A4]
8	NP_984327	45188104	ADR231Cp [Eremothecium gossypii]
9	CAD60564	27764284	unnamed protein product [Podospora anserina]
10	EAT92134	111071014	hypothetical protein SNOG_00639 [Phaeosphaeria nodorum SN15]
11	BAE59228	83769091	unnamed protein product [Aspergillus oryzae]
12	XP_446465	50288073	unnamed protein product [Candida glabrata]
13	XP_751982	70994310	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
14	XP_451336	50302799	unnamed protein product [Kluyveromyces lactis]
15	EAS30095	90300464	hypothetical protein CIMG_08841 [Coccidioides immitis RS]
16	EAQ83092	88175624	hypothetical protein CHGG_10910 [Chaetomium globosum CBS 148.51]
17	NP_014724	6324655	Triacylglycerol lipase involved in TAG mobilization; localizes to lipid particles; potential Cdc28p substrate; Tgl5p [Saccharomyces cerevisiae]
18	XP_448470	50292075	unnamed protein product [Candida glabrata]
19	ABG79933	110628937	triacylglycerol lipase [Magnaporthe grisea]
20	NP_593197	19114109	hypothetical protein SPAC1A6.05c [Schizosaccharomyces pombe 972h-]
21	EAR86065	89288077	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
22	XP_463448	50902030	P0512C01.22 [Oryza sativa (japonica cultivar-group)]
23	BAF06239	113533856	Os01g0762000 [Oryza sativa (japonica cultivar-group)]
24	YP_433865	83645430	predicted esterase of the alpha-beta hydrolase superfamily [Hahella chejuensis KCTC 2396]
25	ZP_008...	77951643	conserved hypothetical protein [Marinobacter aquaeolei VT8]
26	AAM97135	22531263	putative protein [Arabidopsis thaliana]
27	BAF13581	113550138	Os03g0810900 [Oryza sativa (japonica cultivar-group)]
28	ABE78088	92867978	phospholipase, patatin family, putative [Medicago truncatula]
29	YP_693301	110834442	hypothetical protein ABO_1581 [Alcanivorax borkumensis SK2]
30	NP_974449	42572707	unknown protein [Arabidopsis thaliana]
31	BAE56507	83766364	unnamed protein product [Aspergillus oryzae]
32	EAR83738	89285729	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
33	ABE94194	92898449	Patatin [Medicago truncatula]
34	XP_752278	70995024	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
35	YP_046026	50084516	hypothetical protein ACIAD1335 [Acinetobacter sp. ADP1]
36	ZP_011...	88794068	predicted esterase of the alpha-beta hydrolase superfamily protein [Alteromonas macleodii 'Deep ecotype']
37	XP_380696	46107274	hypothetical protein FG00520.1 [Gibberella zeae PH-1]

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38	ZP_011...	88703608	Patatin-like phospholipase [gamma proteobacterium KT 71]
39	EAT85718	111064598	hypothetical protein SNOG_07067 [Phaeosphaeria nodorum SN15]
40	ZP_011...	88707125	Patatin-like phospholipase [gamma proteobacterium KT 71]
41	XP_757164	71004996	hypothetical protein UM01017.1 [Ustilago maydis 521]
42	YP_615253	103485692	Patatin [Sphingopyxis alaskensis RB2256]
43	XP_964502	85113293	hypothetical protein [Neurospora crassa OR74A]
44	NP_594022	63054585	hypothetical protein SPAC31G5.20c [Schizosaccharomyces pombe 972h-]
45	XP_502898	50550851	hypothetical protein [Yarrowia lipolytica]
46	XP_722550	68466709	putative patatin-like phospholipase [Candida albicans SC5314]
47	EAS31687	90302056	hypothetical protein CIMG_07166 [Coccidioides immitis RS]
48	BAE57969	83767830	unnamed protein product [Aspergillus oryzae]
49	XP_722412	68466994	putative patatin-like phospholipase [Candida albicans SC5314]
50	EAQ93362	88185894	hypothetical protein CHGG_01597 [Chaetomium globosum CBS 148.51]
51	ZP_010...	85708568	hypothetical protein NAP1_04995 [Erythrobacter sp. NAP1]
52	XP_457141	50412575	hypothetical protein DEHA0B04048g [Debaryomyces hansenii CBS767]
53	XP_658012	67516253	hypothetical protein AN0408.2 [Aspergillus nidulans FGSC A4]
54	EAS33873	90304242	hypothetical protein CIMG_04897 [Coccidioides immitis RS]
55	XP_805126	71404931	hypothetical protein [Trypanosoma cruzi strain CL Brener]
56	CAB88226	7630152	conserved hypothetical protein L5213T.05 [Leishmania major]
57	CAJ06433	68127889	hypothetical protein, conserved [Leishmania major]
58	XP_750246	70990794	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
59	ABG79934	110628939	triacylglycerol lipase [Magnaporthe grisea]
60	XP_386821	46124535	hypothetical protein FG06645.1 [Gibberella zeae PH-1]
61	EAT92413	111071293	hypothetical protein SNOG_00918 [Phaeosphaeria nodorum SN15]
62	NP_588315	19075815	hypothetical protein SPCC1450.16c [Schizosaccharomyces pombe 972h-]
63	EAQ90965	88183497	hypothetical protein CHGG_02900 [Chaetomium globosum CBS 148.51]
64	XP_957267	85084210	hypothetical protein [Neurospora crassa OR74A]
65	XP_451445	50303015	unnamed protein product [Kluyveromyces lactis]
66	CAB11704	2388971	SPAC31G5.20c [Schizosaccharomyces pombe]
67	XP_626587	66358818	hypothetical protein cgd2_4050 [Cryptosporidium parvum Iowa II]
68	XP_665308	67588018	hypothetical protein Chro.20432 [Cryptosporidium hominis TU502]
69	XP_449952	50295082	hypothetical protein CAGL0M13981g [Candida glabrata CBS138]
70	XP_722764	68466564	putative lipid particle triacylglycerol lipase fragment [Candida albicans SC5314]
71	NP_986330	45200760	AGL337Cp [Eremothecium gossypii]
72	CAE84405	39722369	Tgl3 protein [Kluyveromyces delphensis]
73	XP_807283	71409928	hypothetical protein [Trypanosoma cruzi strain CL Brener]
74	XP_807016	71409330	hypothetical protein [Trypanosoma cruzi strain CL Brener]
75	XP_502944	50550941	hypothetical protein [Yarrowia lipolytica]
76	NP_014044	6323973	Triacylglycerol lipase of the lipid particle, responsible for all the TAG lipase activity of the lipid particle; contains the consensus sequence motif GXSXG, which is found in lipolytic enzymes; Tgl3p [Saccharomyces cerevisiae]

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Table 41. Examples of triglyceride lipase (tgl3) polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_502944	50550941	hypothetical protein [Yarrowia lipolytica].
2	XP_752278	70995024	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
3	BAE56507	83766364	unnamed protein product [Aspergillus oryzae]
4	EAT85718	111064598	hypothetical protein SNOG_07067 [Phaeosphaeria nodorum SN15]
5	XP_380696	46107274	hypothetical protein FG00520.1 [Gibberella zeae PH-1]
6	XP_964502	85113293	hypothetical protein [Neurospora crassa OR74A]
7	EAQ93362	88185894	hypothetical protein CHGG_01597 [Chaetomium globosum CBS 148.51]
8	XP_722764	68466564	putative lipid particle triacylglycerol lipase fragment [Candida albicans SC5314]
9	NP_986330	45200760	AGL337Cp [Eremothecium gossypii]
10	CAE84405	39722369	Tgl3 protein [Kluyveromyces delphensis]
11	XP_449952	50295082	hypothetical protein CAGL0M13981g [Candida glabrata CBS138]
12	XP_451445	50303015	unnamed protein product [Kluyveromyces lactis]
13	NP_014044	6323973	Triacylglycerol lipase of the lipid particle, responsible for all the TAG lipase activity of the lipid particle; contains the consensus sequence motif GXSXG, which is found in lipolytic enzymes; Tgl3p [Saccharomyces cerevisiae]
14	EAS31687	90302056	hypothetical protein CIMG_07166 [Coccidioides immitis RS]
15	EAT92134	111071014	hypothetical protein SNOG_00639 [Phaeosphaeria nodorum SN15]
16	XP_387731	46126355	hypothetical protein FG07555.1 [Gibberella zeae PH-1]
17	NP_588315	19075815	hypothetical protein SPCC1450.16c [Schizosaccharomyces pombe 972h-]
18	XP_751982	70994310	patatin-like serine hydrolase [Aspergillus fumigatus Af293]
19	XP_958750	85091127	hypothetical protein [Neurospora crassa OR74A]
20	EAQ83092	88175624	hypothetical protein CHGG_10910 [Chaetomium globosum CBS 148.51]
21	BAE59228	83769091	unnamed protein product [Aspergillus oryzae]
22	YP_693301	110834442	hypothetical protein ABO_1581 [Alcanivorax borkumensis SK2]
23	XP_659317	67522513	hypothetical protein AN1713.2 [Aspergillus nidulans FGSC A4]
24	ZP_011...	88703608	Patatin-like phospholipase [gamma proteobacterium KT 71]
25	BAF06239	113533856	Os01g0762000 [Oryza sativa (japonica cultivar-group)]
26	XP_463448	50902030	P0512C01.22 [Oryza sativa (japonica cultivar-group)]
27	EAS30095	90300464	hypothetical protein CIMG_08841 [Coccidioides immitis RS]
28	YP_433865	83645430	predicted esterase of the alpha-beta hydrolase superfamily [Hahella chejuensis KCTC 2396]
29	XP_459553	50421985	hypothetical protein DEHA0E06127g [Debaryomyces hansenii CBS767]
30	CAD60564	27764284	unnamed protein product [Podospora anserina]
31	ZP_008...	77951643	conserved hypothetical protein [Marinobacter aquaeolei VT8]
32	XP_505230	50555644	hypothetical protein [Yarrowia lipolytica]
33	XP_446465	50288073	unnamed protein product [Candida glabrata]
34	AAM97135	22531263	putative protein [Arabidopsis thaliana]
35	BAF13581	113550138	Os03g0810900 [Oryza sativa (japonica cultivar-group)]
36	ABG79933	110628937	triacylglycerol lipase [Magnaporthe grisea]
37	XP_717704	68476486	putative patatin-like phospholipase [Candida albicans SC5314]

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38	NP_013015	6322942	Triacylglycerol lipase involved in triacylglycerol mobilization and degradation; found in lipid particles; potential Cdc28p substrate; Tgl4p [Saccharomyces cerevisiae]
39	NP_594022	63054585	hypothetical protein SPAC31G5.20c [Schizosaccharomyces pombe 972h-]
40	EAR83738	89285729	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
41	NP_984327	45188104	ADR231Cp [Eremothecium gossypii]
42	EAR86065	89288077	Patatin-like phospholipase family protein [Tetrahymena thermophila SB210]
43	NP_014724	6324655	Triacylglycerol lipase involved in TAG mobilization; localizes to lipid particles; potential Cdc28p substrate; Tgl5p [Saccharomyces cerevisiae]
44	YP_046026	50084516	hypothetical protein ACIAD1335 [Acinetobacter sp. ADP1]
45	XP_451336	50302799	unnamed protein product [Kluyveromyces lactis]
46	ZP_011...	88794068	predicted esterase of the alpha-beta hydrolase superfamily protein [Alteromonas macleodii 'Deep ecotype']
47	XP_722550	68466709	putative patatin-like phospholipase [Candida albicans SC5314]
48	XP_722412	68466994	putative patatin-like phospholipase [Candida albicans SC5314]
49	EAS33873	90304242	hypothetical protein CIMG_04897 [Coccidioides immitis RS]
50	ABG79934	110628939	triacylglycerol lipase [Magnaporthe grisea]
51	ZP_011...	88707125	Patatin-like phospholipase [gamma proteobacterium KT 71]
52	NP_593197	19114109	hypothetical protein SPAC1A6.05c [Schizosaccharomyces pombe 972h-]
53	YP_615253	103485692	Patatin [Sphingopyxis alaskensis RB2256]
54	ZP_010...	85708568	hypothetical protein NAP1_04995 [Erythrobacter sp. NAP1]
55	XP_658012	67516253	hypothetical protein AN0408.2 [Aspergillus nidulans FGSC A4]
56	XP_448470	50292075	unnamed protein product [Candida glabrata]
57	XP_807283	71409928	hypothetical protein [Trypanosoma cruzi strain CL Brener]
58	XP_386821	46124535	hypothetical protein FG06645.1 [Gibberella zeae PH-1]

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Table 42. Examples of acyl-coA-cholesterol polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_505086.1	50555355	hypothetical protein [Yarrowia lipolytica]
2	XP_449806	50294790	hypothetical protein CAGL0M10571g [Candida glabrata CBS138]
3	AAO32554	28564940	ARE2 [Saccharomyces kluyveri]
4	XP_461395	50425599	hypothetical protein DEHA0F25652g [Debaryomyces hansenii CBS767]
5	P84285	56404462	Sterol O-acyltransferase 2 (Sterol-ester synthase) (ASAT)
6	XP_714776	68482533	acyl-CoA cholesterol acyltransferase [Candida albicans SC5314]
7	AAO32474	28564191	ARE2 [Saccharomyces castellii]
8	NP_982606	45184888	AAR065Cp [Eremothecium gossypii]
9	NP_014416	6324346	Acyl-CoA:sterol acyltransferase, isozyme of Are1p; endoplasmic reticulum enzyme that contributes the major sterol esterification activity in the presence of oxygen; Are2p [Saccharomyces cerevisiae]
10	AAC49441	1389739	acyl-CoA:sterol acyltransferase
11	XP_452607	50305295	unnamed protein product [Kluyveromyces lactis]
12	Q876L2	34582301	Sterol O-acyltransferase 2 (Sterol-ester synthase 2)
13	Q876L3	34582302	Sterol O-acyltransferase 1 (Sterol-ester synthase 1)
14	AAT92940	51013293	YCR048W [Saccharomyces cerevisiae]
15	XP_445307	50285757	unnamed protein product [Candida glabrata]
16	NP_593707	19114619	hypothetical protein SPAC13G7.05 [Schizosaccharomyces pombe 972h-]
17	XP_370268	39977761	hypothetical protein MG06765.4 [Magnaporthe grisea 70-15]
18	EAQ84619	88177151	hypothetical protein CHGG_08633 [Chaetomium globosum CBS 148.51]
19	XP_961300	85102248	related to acyl-CoA sterol acyltransferase [MIPS] [Neurospora crassa OR74A]
20	XP_750354	70991010	sterol o-acyltransferase APE2 [Aspergillus fumigatus Af293]
21	EAT80792	111059672	hypothetical protein SNOG_11748 [Phaeosphaeria nodorum SN15]
22	XP_661812	67527926	hypothetical protein AN4208.2 [Aspergillus nidulans FGSC A4]
23	BAE54934	83764790	unnamed protein product [Aspergillus oryzae]
24	EAT89521	111068401	predicted protein [Phaeosphaeria nodorum SN15]
25	EAQ86094	88178626	hypothetical protein CHGG_07347 [Chaetomium globosum CBS 148.51]
26	NP_588558	19076058	hypothetical protein SPCP1E11.05c [Schizosaccharomyces pombe 972h-]
27	XP_956576	85080625	hypothetical protein [Neurospora crassa OR74A]
28	EAS32815	90303184	hypothetical protein CIMG_03839 [Coccidioides immitis RS]
29	XP_382192	46110268	hypothetical protein FG02016.1 [Gibberella zeae PH-1]
30	XP_761502	71022545	hypothetical protein UM05355.1 [Ustilago maydis 521]
31	EAL20032	50257323	hypothetical protein CNBF3580 [Cryptococcus neoformans var. neoformans B-3501A]
32	XP_571260	58268208	sterol O-acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
33	EAR83561	89285549	MBOAT family protein [Tetrahymena thermophila SB210]
34	EAS03424	89305436	MBOAT family protein [Tetrahymena thermophila SB210]
35	AAS72375	45642961	acyl-CoA:cholesterol acyltransferase alpha [Toxoplasma gondii]
36	AAS72376	45642963	acyl-CoA:cholesterol acyltransferase beta [Toxoplasma gondii]

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37	XP_640280	111226542	hypothetical protein DDBDRAFT_0205259 [Dictyostelium discoideum AX4]
38	XP_645633	66824557	hypothetical protein DDBDRAFT_0202877 [Dictyostelium discoideum AX4]
39	EAS35506	90305875	hypothetical protein CIMG_00860 [Coccidioides immitis RS]
40	XP_386864	46124621	hypothetical protein FG06688.1 [Gibberella zeae PH-1]
41	NP_649816	28571583	CG8112-PA [Drosophila melanogaster]
42	CAE75170	39591950	Hypothetical protein CBG23107 [Caenorhabditis briggsae]
43	NP_033256	84619697	sterol O-acyltransferase 1 [Mus musculus]
44	BAC34925	26342537	unnamed protein product [Mus musculus]
45	XP_359451	39939828	hypothetical protein MG05326.4 [Magnaporthe grisea 70-15]
46	Q61263	18202591	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
47	XP_975142	91083363	PREDICTED: similar to CG31991-PA, isoform A [Tribolium castaneum]
48	EAL28962	54639560	GA20833-PA [Drosophila pseudoobscura]
49	XP_957022	85082953	hypothetical protein [Neurospora crassa OR74A]
50	XP_547445	73961286	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1) [Canis familiaris]
51	EAQ89124	88181656	hypothetical protein CHGG_05743 [Chaetomium globosum CBS 148.51]
52	EAT78735	111057615	hypothetical protein SNOG_13711 [Phaeosphaeria nodorum SN15]
53	Q60457	18202585	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
54	XP_624754	110762262	PREDICTED: similar to midway CG31991-PA, isoform A [Apis mellifera]
55	O70536	18202126	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
56	XP_728984	82915156	hypothetical protein PY01256 [Plasmodium yoelii yoelii str. 17XNL]
57	NP_505828	71997360	H19N07.4 [Caenorhabditis elegans]
58	NP_001...	77735363	hypothetical protein LOC504287 [Bos taurus]
59	2201440A	1585676	acyl-CoA/cholesterol acyltransferase
60	XP_663763	67539978	hypothetical protein AN6159.2 [Aspergillus nidulans FGSC A4]
61	CAI13574	55960156	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 [Homo sapiens]
62	XP_514030	55588858	PREDICTED: hypothetical protein XP_514030 [Pan troglodytes]
63	AAL56227	18028942	cholesterol acyltransferase 1 [Gorilla gorilla]
64	AAL56228	18028944	cholesterol acyltransferase 1 [Pongo pygmaeus]
65	AAC37532	4878022	acyl-coenzyme A: cholesterol acyltransferase [Homo sapiens]
66	EAT47694	108883469	sterol o-acyltransferase [Aedes aegypti]
67	XP_390039	46136695	hypothetical protein FG09863.1 [Gibberella zeae PH-1]
68	BAE01048	67969393	unnamed protein product [Macaca fascicularis]
69	O77761	18202178	Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1)
70	AAH06263	34782946	DGAT1 protein [Homo sapiens]
71	XP_317656	31226099	ENSANGP00000002281 [Anopheles gambiae str. PEST]
72	XP_320320	58393809	ENSANGP00000016486 [Anopheles gambiae str. PEST]
73	XP_320321	58393811	ENSANGP00000016512 [Anopheles gambiae str. PEST]
74	BAE65302	83775179	unnamed protein product [Aspergillus oryzae]

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75	NP_724017	24584734	midway CG31991-PC, isoform C [Drosophila melanogaster]
76	NP_995724	45552403	midway CG31991-PD, isoform D [Drosophila melanogaster]
77	EAL33593	54644853	GA16599-PA [Drosophila pseudoobscura]
78	NP_586145	19074639	STEROL O-ACYLTRANSFERASE [Encephalitozoon cuniculi GB-M1]
79	XP_502557	50550169	hypothetical protein [Yarrowia lipolytica]
80	XP_885914	76617939	PREDICTED: similar to Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransferase 2) (ACAT-2) isoform 2 [Bos taurus]
81	XP_591251	76617937	PREDICTED: similar to Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransferase 2) (ACAT-2) isoform 1 [Bos taurus]
82	XP_624691	66564061	PREDICTED: similar to CG8112-PA [Apis mellifera]
83	O75908	18202149	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransferase 2) (ACAT-2)
84	XP_001...	109096888	PREDICTED: sterol O-acyltransferase 2 [Macaca mulatta]
85	AAK48829	13898623	acyl coenzyme A: cholesterol acyltransferase-2 [Homo sapiens]
86	AAH77916	50416229	Soat1-prov protein [Xenopus laevis]
87	AAH96091	64654094	Sterol O-acyltransferase 2 [Homo sapiens]
88	EAT38531	108874306	sterol o-acyltransferase [Aedes aegypti]
89	AAH96090	64652990	Sterol O-acyltransferase 2 [Homo sapiens]
90	NP_001...	50539976	hypothetical protein LOC436731 [Danio rerio]
91	NP_714950	40254723	sterol O-acyltransferase 2 [Rattus norvegicus]
92	XP_422267	50751122	PREDICTED: similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1) [Gallus gallus]
93	O88908	18202245	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransferase 2) (ACAT-2)
94	O77759	18202176	Sterol O-acyltransferase 2 (Cholesterol acyltransferase 2) (Acyl coenzyme A:cholesterol acyltransferase 2) (ACAT-2)
95	NP_666176	22122547	sterol O-acyltransferase 2 [Mus musculus]
96	BAC00846	21392392	AcylCoA:Cholesterol Acyltransferase 2 [Rattus norvegicus]
97	XP_692855	68364838	PREDICTED: similar to Soat1-prov protein [Danio rerio]
98	XP_543637	73996435	PREDICTED: similar to sterol O-acyltransferase 2 [Canis familiaris]
99	CAG11944	47225461	unnamed protein product [Tetraodon nigroviridis]
100	CAF96514	47222847	unnamed protein product [Tetraodon nigroviridis]
101	CAG10815	47219451	unnamed protein product [Tetraodon nigroviridis]
102	EAR94647	89296659	MBOAT family protein [Tetrahymena thermophila SB210]
103	AAP68322	31711932	At2g19450 [Arabidopsis thaliana]
104	EAR94441	89296453	MBOAT family protein [Tetrahymena thermophila SB210]
105	CAG07990	47225647	unnamed protein product [Tetraodon nigroviridis]
106	XP_788209	72085563	PREDICTED: similar to sterol O-acyltransferase 1 [Strongylocentrotus purpuratus]
107	AAO32475	28564193	ARE2 [Saccharomyces castellii]
108	XP_673128	68062248	hypothetical protein PB300300.00.0 [Plasmodium berghei strain ANKA]

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Table 43. Examples of phospholipid-diacylglycerol polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504038	50553256	hypothetical protein [Yarrowia lipolytica].
2	XP_458897	50420721	hypothetical protein DEHA0D10868g [Debaryomyces hansenii CBS767]
3	XP_718878	68473963	hypothetical protein CaO19_13439 [Candida albicans SC5314]
4	XP_447501	50290139	hypothetical protein CAGL0I05786g [Candida glabrata CBS138]
5	XP_455369	50310695	unnamed protein product [Kluyveromyces lactis]
6	NP_014405	6324335	Acyltransferase that catalyzes diacylglycerol esterification; one of several acyltransferases that contribute to triglyceride synthesis; putative homolog of human lecithin cholesterol acyltransferase; Lro1p [Saccharomyces cerevisiae]
7	NP_985371	45198342	AFL179Cp [Eremothecium gossypii]
8	BAE57684	83767545	unnamed protein product [Aspergillus oryzae]
9	EAS32928	90303297	hypothetical protein CIMG_03952 [Coccidioides immitis RS]
10	EAT89812	111068692	hypothetical protein SNOG_03081 [Phaeosphaeria nodorum SN15]
11	XP_662596	67537644	hypothetical protein AN4992.2 [Aspergillus nidulans FGSC A4]
12	XP_361017	39942960	hypothetical protein MG03560.4 [Magnaporthe grisea 70-15]
13	CAD60714	27803011	unnamed protein product [Podospora anserina]
14	XP_718980	68473754	hypothetical protein CaO19_6018 [Candida albicans SC5314]
15	XP_386551	46123995	hypothetical protein FG06375.1 [Gibberella zeae PH-1]
16	XP_959598	85092964	hypothetical protein [Neurospora crassa OR74A]
17	XP_754624	70999814	phospholipid:diacylglycerol acyltransferase [Aspergillus fumigatus Af293]
18	O94680	21362753	Phospholipid:diacylglycerol acyltransferase (PDAT) (Pombe LRO1 homolog 1)
19	EAQ92213	88184745	hypothetical protein CHGG_00448 [Chaetomium globosum CBS 148.51]
20	XP_756469	71003606	hypothetical protein UM00322.1 [Ustilago maydis 521]
21	EAL18953	50256226	hypothetical protein CNBI2140 [Cryptococcus neoformans var. neoformans B-3501A]
22	XP_568014	58261208	phospholipid:diacylglycerol acyltransferase [Cryptococcus neoformans var. neoformans JEC21]
23	AAP47635	37785695	lecithine cholesterol acyltransferase-like protein [Medicago truncatula]
24	AAS79590	45935132	putative phosphatidylcholine-sterol acyltransferase [Ipomoea trifida]
25	BAF25212	113631531	Os09g0444200 [Oryza sativa (japonica cultivar-group)]
26	AAK96619	15450695	AT5g13640/MSH12_10 [Arabidopsis thaliana]
27	XP_829379	74025626	phospholipid:diacylglycerol acyltransferase-like protein [Trypanosoma brucei TREU927]
28	XP_816552	71655997	phospholipid:diacylglycerol acyltransferase [Trypanosoma cruzi strain CL Brener]
29	AAO17787	37724553	lecithine cholesterol acyltransferase-like protein [Arabidopsis thaliana]
30	XP_821756	71660075	phospholipid:diacylglycerol acyltransferase [Trypanosoma cruzi strain CL Brener]
31	CAD38153	27552462	putative phosphatidylcholine-sterol acetyltransferase [Physcomitrella patens]
32	NP_190069	15230521	phosphatidylcholine-sterol O-acyltransferase [Arabidopsis

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			thaliana]
33	CAD38155	27552466	putative acetyltransferase [Physcomitrella patens]
34	CAJ02843	68124573	phospholipid:diacylglycerol acyltransferase, putative [Leishmania major]

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Table 44. Examples of malate dehydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503933.1	50553046	hypothetical protein [Yarrowia lipolytica].
2	EAT83219	111062099	predicted protein [Phaeosphaeria nodorum SN15]
3	XP_747556	70984070	malate dehydrogenase, NAD-dependent [Aspergillus fumigatus Af293]
4	BAE61776	83771646	unnamed protein product [Aspergillus oryzae]
5	EAQ89010	88181542	malate dehydrogenase, mitochondrial precursor [Chaetomium globosum CBS 148.51]
6	EAS37226	90307595	hypothetical protein CIMG_02580 [Coccidioides immitis RS]
7	XP_572013	58269714	L-malate dehydrogenase [Cryptococcus neoformans var. neoformans JEC21]
8	XP_748936	70986899	malate dehydrogenase, NAD-dependent [Aspergillus fumigatus Af293]
9	BAE55502	83765359	unnamed protein product [Aspergillus oryzae]
10	EAQ88553	88181085	malate dehydrogenase, mitochondrial precursor [Chaetomium globosum CBS 148.51]
11	ABH10641	111606553	malate dehydrogenase [Coccidioides posadasii]
12	XP_321163	58395331	ENSANGP00000020184 [Anopheles gambiae str. PEST]
13	XP_717047	68477790	putative peroxisomal malate dehydrogenase [Candida albicans SC5314]
14	AAY63978	67043759	mitochondrial malate dehydrogenase [Lysiphlebus testaceipes]
15	AAX19496	60393102	mitochondrial malate dehydrogenase 2b [Xenopus laevis]
16	EAT40089	108875864	malate dehydrogenase [Aedes aegypti]
17	AAI06696	76780392	Mdh2a protein [Xenopus laevis]
18	XP_572038	58269764	malate dehydrogenase [Cryptococcus neoformans var. neoformans JEC21]
19	XP_392478	66513092	PREDICTED: similar to mitochondrial malate dehydrogenase precursor isoform 1 [Apis mellifera]
20	XP_973533	91085015	PREDICTED: similar to mitochondrial malate dehydrogenase precursor [Tribolium castaneum]
21	CAG12894	47224065	unnamed protein product [Tetraodon nigroviridis]
22	NP_001...	58332672	mitochondrial malate dehydrogenase 2 [Xenopus tropicalis]
23	XP_819104	71664243	malate dehydrogenase [Trypanosoma cruzi strain CL Brener]
24	CAJ07715	68129178	malate dehydrogenase [Leishmania major]
25	EAL29124	54639722	GA20754-PA [Drosophila pseudoobscura]
26	XP_708782	68367713	PREDICTED: similar to malate dehydrogenase, mitochondrial isoform 6 [Danio rerio]
27	XP_708779	68367700	PREDICTED: similar to malate dehydrogenase, mitochondrial isoform 3 [Danio rerio]
28	AAW79319	58613465	malate dehydrogenase [Isochrysis galbana]
29	CAI29601	56403598	hypothetical protein [Pongo pygmaeus]
30	XP_460754	50424335	hypothetical protein DEHA0F09911g [Debaryomyces hansenii CBS767]
31	XP_001...	109066259	PREDICTED: similar to mitochondrial malate dehydrogenase precursor [Macaca mulatta]
32	AAK69767	14583133	malate dehydrogenase [Sphyraena idiastes]
33	XP_708778	68367696	PREDICTED: similar to malate dehydrogenase, mitochondrial isoform 2 [Danio rerio]
34	NP_001...	79327392	PMDH2 [Arabidopsis thaliana]
35	ABE84799	92877831	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Medicago truncatula]

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36	AAU29200	52139820	glyoxisomal malate dehydrogenase [Lycopersicon esculentum]
37	AAW27425	56758570	SJCHGC06124 protein [Schistosoma japonicum]
38	XP_708781	68367709	PREDICTED: similar to malate dehydrogenase, mitochondrial isoform 5 [Danio rerio]
39	1SMKH	60593494	Chain H, Mature And Translocatable Forms Of Glyoxysomal Malate Dehydrogenase Have Different Activities And Stabilities But Similar Crystal Structures
40	XP_822509	71746908	mitochondrial malate dehydrogenase [Trypanosoma brucei TREU927]
41	1SEVB	60593476	Chain B, Mature And Translocatable Forms Of Glyoxysomal Malate Dehydrogenase Have Different Activities And Stabilities But Similar Crystal Structures
42	XP_708780	68367705	PREDICTED: similar to malate dehydrogenase, mitochondrial isoform 4 [Danio rerio]
43	ABD77290	89574129	mitochondrial malate dehydrogenase 2, NAD [Homo sapiens]
44	ABD77284	89574117	mitochondrial malate dehydrogenase 2, NAD [Rattus norvegicus]
45	ABD77283	89574115	mitochondrial malate dehydrogenase 2, NAD [Mus musculus]
46	ABD77287	89574123	mitochondrial malate dehydrogenase 2, NAD [Oryctolagus cuniculus]
47	ABD77280	89574109	mitochondrial malate dehydrogenase 2, NAD [Loxodonta africana]
48	ABD77288	89574125	mitochondrial malate dehydrogenase 2, NAD [Lepus europaeus]
49	XP_792004	72025672	PREDICTED: similar to mitochondrial malate dehydrogenase precursor [Strongylocentrotus purpuratus]
50	ABD77293	89574135	mitochondrial malate dehydrogenase 2, NAD [Canis familiaris]
51	ABD77294	89574137	mitochondrial malate dehydrogenase 2, NAD [Felis catus]
52	ABD77278	89574105	mitochondrial malate dehydrogenase 2, NAD [Didelphis virginiana]
53	XP_809210	71414199	mitochondrial malate dehydrogenase [Trypanosoma cruzi strain CL Brener]
54	ABD77301	89574151	mitochondrial malate dehydrogenase 2, NAD [Sus scrofa]
55	ABD77286	89574121	mitochondrial malate dehydrogenase 2, NAD [Mesocricetus auratus]
56	ABD77298	89574145	mitochondrial malate dehydrogenase 2, NAD [Bos taurus]
57	AAT35230	47531133	mitochondrial malate dehydrogenase [Clonorchis sinensis]
58	ABD77281	89574111	mitochondrial malate dehydrogenase 2, NAD [Dasypus novemcinctus]
59	ABD77296	89574141	mitochondrial malate dehydrogenase 2, NAD [Ceratotherium simum]
60	ABA99939	108863014	Malate dehydrogenase, glyoxysomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
61	AAU29198	52139816	mitochondrial malate dehydrogenase [Lycopersicon esculentum]
62	ABD77279	89574107	mitochondrial malate dehydrogenase 2, NAD [Sminthopsis douglasi]
63	CAJ07717	68129180	malate dehydrogenase, putative [Leishmania major]
64	XP_519160	55628772	PREDICTED: similar to mitochondrial malate dehydrogenase precursor [Pan troglodytes]
65	ABD72702	89473780	putative mitochondrial malate dehydrogenase [Acyrthosiphon

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			pisum]
66	ABD77299	89574147	mitochondrial malate dehydrogenase 2, NAD [Balaenoptera physalus]
67	BAF23792	113623847	Os08g0434300 [Oryza sativa (japonica cultivar-group)]
68	CAI11361	57337458	putative malate dehydrogenase [Orpinomyces sp. OUS1]
69	ABD77289	89574127	mitochondrial malate dehydrogenase 2, NAD [Tadarida brasiliensis]
70	BAF06605	113534222	Os01g0829800 [Oryza sativa (japonica cultivar-group)]
71	ABD77292	89574133	mitochondrial malate dehydrogenase 2, NAD [Tupaia glis]
72	ABD77285	89574119	mitochondrial malate dehydrogenase 2, NAD [Cavia porcellus]
73	BAF18303	113579940	Os05g0574400 [Oryza sativa (japonica cultivar-group)]
74	ZP_010...	85712491	malate dehydrogenase [Idiomarina baltica OS145]
75	XP_539718	57097207	PREDICTED: similar to malate dehydrogenase 2, NAD (mitochondrial) [Canis familiaris]
76	ABD77277	89574103	mitochondrial malate dehydrogenase 2, NAD [Monodelphis domestica]
77	Q5R030	62286970	Malate dehydrogenase
78	YP_660122	109896867	malate dehydrogenase, NAD-dependent [Pseudoalteromonas atlantica T6c]
79	Q87SU7	48428249	Malate dehydrogenase
80	ABD77291	89574131	mitochondrial malate dehydrogenase 2, NAD [Aotus trivirgatus]
81	ZP_007...	75854582	COG0039: Malate/lactate dehydrogenases [Vibrio sp. Ex25]
82	ZP_011...	88795318	malate dehydrogenase [Alteromonas macleodii 'Deep ecotype']
83	ZP_012...	91228842	malate dehydrogenase [Vibrio alginolyticus 12G01]
84	ZP_011...	89075547	malate dehydrogenase [Photobacterium sp. SKA34]
85	ZP_012...	90580811	malate dehydrogenase [Vibrio angustum S14]
86	YP_671200	110643470	malate dehydrogenase [Escherichia coli 536]
87	ABD77295	89574139	mitochondrial malate dehydrogenase 2, NAD [Equus caballus]
88	Q5E875	66774139	Malate dehydrogenase
89	ZP_007...	75209673	COG0039: Malate/lactate dehydrogenases [Escherichia coli B171]
90	ZP_009...	84394039	malate dehydrogenase [Vibrio splendidus 12B01]
91	ZP_007...	75228638	COG0039: Malate/lactate dehydrogenases [Escherichia coli B7A]
92	ZP_010...	86147822	malate dehydrogenase [Vibrio sp. MED222]
93	BAD30064	50508045	malate dehydrogenase [Moritella sp. 36B1]
94	Q4QL89	73621201	Malate dehydrogenase
95	YP_404893	82778544	malate dehydrogenase [Shigella dysenteriae Sd197]
96	BAD30059	50508035	malate dehydrogenase [Moritella sp. 47A1]
97	BAD30066	50508049	malate dehydrogenase [Moritella sp. 36G1]
98	ZP_008...	77958772	COG0039: Malate/lactate dehydrogenases [Yersinia bercovieri ATCC 43970]
99	BAD30071	50508059	malate dehydrogenase [Moritella sp. 38F1]
100	ZP_008...	77973999	COG0039: Malate/lactate dehydrogenases [Yersinia frederiksenii ATCC 33641]
101	ZP_008...	77977600	COG0039: Malate/lactate dehydrogenases [Yersinia intermedia ATCC 29909]
102	P48364	1346511	Malate dehydrogenase
103	BAD30062	50508041	malate dehydrogenase [Moritella sp. 16H2]
104	BAD30069	50508055	malate dehydrogenase [Moritella sp. 56A1]

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105	ZP_008...	77961850	COG0039: Malate/lactate dehydrogenases [Yersinia mollaretii ATCC 43969]
106	ZP_012...	90411956	putative malate dehydrogenase [Photobacterium profundum 3TCK]
107	Q6AW21	57012891	Malate dehydrogenase
108	Q57JA9	68052390	Malate dehydrogenase
109	ZP_012...	90407531	malate dehydrogenase [Psychromonas sp. CNPT3]
110	BAD36746	51172588	malate dehydrogenase [Moritella yayanosii]
111	Q6AW23	57012892	Malate dehydrogenase
112	ABG22106	108863015	Malate dehydrogenase, glyoxysomal precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
113	ZP_005...	68546610	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella amazonensis SB2B]
114	BAD30060	50508037	malate dehydrogenase [Moritella sp. 47B1]
115	EAL31008	54642259	GA10540-PA [Drosophila pseudoobscura]
116	YP_736674	114046124	malate dehydrogenase, NAD-dependent [Shewanella sp. MR-7]
117	CAJ07716	68129179	malate dehydrogenase, putative [Leishmania major]
118	ZP_009...	82743617	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella sp. W3-18-1]
119	Q47VL0	83288301	Malate dehydrogenase
120	ZP_011...	88859032	malate dehydrogenase [Pseudoalteromonas tunicata D2]
121	YP_561838	91792187	malate dehydrogenase, NAD-dependent [Shewanella denitrificans OS217]
122	ZP_005...	68544347	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella baltica OS155]
123	ZP_007...	75429373	malate dehydrogenase [Actinobacillus succinogenes 130Z]
124	AAW29940	56788316	malate dehydrogenase [Pasteurella trehalosi]
125	BAD30063	50508043	malate dehydrogenase [Shewanella sp. T4609]
126	EAL31009	54642260	GA10541-PA [Drosophila pseudoobscura]
127	ZP_006...	69950735	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella frigidimarina NCIMB 400]
128	YP_341148	77361573	malate dehydrogenase [Pseudoalteromonas haloplanktis TAC125]
129	ZP_013...	106882260	malate dehydrogenase, NAD-dependent [Psychromonas ingrahamii 37]
130	BAD30068	50508053	malate dehydrogenase [Shewanella sp. 33H2]
131	ZP_008...	78368581	Malate dehydrogenase, NAD-dependent, eukaryotes and gamma proteobacteria [Shewanella sp. PV-4]
132	XP_851105	74004024	PREDICTED: similar to malate dehydrogenase, mitochondrial [Canis familiaris]
133	ABD77300	89574149	mitochondrial malate dehydrogenase 2, NAD [Hippopotamus amphibius]
134	XP_816948	71656813	glycosomal malate dehydrogenase [Trypanosoma cruzi strain CL Brener]
135	CAJ19596	82655060	malate dehydrogenase [Klebsiella pneumoniae]
136	AAW29939	56788314	malate dehydrogenase [Mannheimia glucosida]
137	CAJ19583	82655034	malate dehydrogenase [Klebsiella pneumoniae]
138	CAJ19589	82655046	malate dehydrogenase [Klebsiella pneumoniae]
139	CAJ19580	82655028	malate dehydrogenase [Klebsiella pneumoniae]
140	CAJ19591	82655050	malate dehydrogenase [Klebsiella pneumoniae]
141	CAJ19595	82655058	malate dehydrogenase [Klebsiella pneumoniae]

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142	CAJ19593	82655054	malate dehydrogenase [Klebsiella pneumoniae]
143	AAW29937	56788310	malate dehydrogenase [Mannheimia haemolytica]
144	XP_812467	71423452	glycosomal malate dehydrogenase [Trypanosoma cruzi strain CL Brener]
145	AAW29938	56788312	malate dehydrogenase [Mannheimia haemolytica]
146	AAW29936	56788308	malate dehydrogenase [Mannheimia haemolytica]
147	XP_849858	73993436	PREDICTED: similar to malate dehydrogenase, mitochondrial [Canis familiaris]
148	AAW28048	56718658	malate dehydrogenase [Vibrio cholerae]
149	AAU88998	52856248	malate dehydrogenase [Shigella flexneri]
150	AAW28041	56718644	malate dehydrogenase [Vibrio cholerae]
151	AAW28047	56718656	malate dehydrogenase [Vibrio mimicus]
152	AAW28045	56718652	malate dehydrogenase [Vibrio mimicus]
153	ABD77282	89574113	mitochondrial malate dehydrogenase 2, NAD [Tamandua tetradactyla]
154	AAU89018	52856288	malate dehydrogenase [Shigella boydii]
155	AAU89003	52856258	malate dehydrogenase [Escherichia coli]
156	AAU88960	52856172	malate dehydrogenase [Escherichia coli]
157	AAU88962	52856176	malate dehydrogenase [Shigella flexneri]
158	AAU88996	52856244	malate dehydrogenase [Escherichia coli]
159	AAU88972	52856196	malate dehydrogenase [Shigella boydii]
160	AAU88969	52856190	malate dehydrogenase [Shigella boydii]
161	ZP_007...	75822170	COG0039: Malate/lactate dehydrogenases [Vibrio cholerae RC385]
162	AAU89062	52856376	malate dehydrogenase [Shigella boydii]
163	AAU88982	52856216	malate dehydrogenase [Shigella dysenteriae]
164	AAU88995	52856242	malate dehydrogenase [Escherichia coli]
165	AAU88993	52856238	malate dehydrogenase [Escherichia coli]
166	AAU89044	52856340	malate dehydrogenase [Shigella flexneri]
167	AAU89015	52856282	malate dehydrogenase [Shigella boydii]
168	AAU88971	52856194	malate dehydrogenase [Shigella sonnei]
169	AAW28034	56718629	malate dehydrogenase [Vibrio cholerae]
170	AAU89011	52856274	malate dehydrogenase [Shigella flexneri]
171	AAU88958	52856168	malate dehydrogenase [Escherichia coli]
172	AAU88976	52856204	malate dehydrogenase [Shigella dysenteriae]
173	AAU88991	52856234	malate dehydrogenase [Escherichia coli]
174	XP_850818	73988067	PREDICTED: similar to mitochondrial malate dehydrogenase precursor [Canis familiaris]
175	AAU86550	52697626	malate dehydrogenase [Shigella boydii]
176	AAU88979	52856210	malate dehydrogenase [Shigella dysenteriae]
177	AAU89005	52856262	malate dehydrogenase [Escherichia coli]
178	AAU89019	52856290	malate dehydrogenase [Shigella dysenteriae]
179	AAU88983	52856218	malate dehydrogenase [Shigella dysenteriae]
180	AAU86549	52697624	malate dehydrogenase [Escherichia albertii]
181	AAX85842	62532910	Mdh [Escherichia coli]
182	AAU89007	52856266	malate dehydrogenase [Shigella flexneri]
183	AAU88980	52856212	malate dehydrogenase [Shigella flexneri]
184	AAU89000	52856252	malate dehydrogenase [Shigella flexneri]
185	AAU88968	52856188	malate dehydrogenase [Shigella boydii]
186	AAU88988	52856228	malate dehydrogenase [Escherichia coli]
187	AAX85856	62532938	Mdh [Escherichia coli]
188	AAU86566	52697658	malate dehydrogenase [Shigella boydii]

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189	AAU86571	52697668	malate dehydrogenase [Escherichia albertii]
190	ABF20150	94468239	Mdh [Escherichia coli]
191	AAU89051	52856354	malate dehydrogenase [Shigella boydii]
192	AAU89059	52856370	malate dehydrogenase [Shigella boydii]
193	AAU89057	52856366	malate dehydrogenase [Shigella boydii]
194	AAU89036	52856324	malate dehydrogenase [Shigella flexneri]
195	AAU86559	52697644	malate dehydrogenase [Shigella boydii]
196	ABF20151	94468241	Mdh [Escherichia coli]
197	ABF20142	94468223	Mdh [Escherichia coli]
198	AAU88990	52856232	malate dehydrogenase [Escherichia coli]
199	AAU86567	52697660	malate dehydrogenase [Shigella boydii]
200	AAU89032	52856316	malate dehydrogenase [Shigella dysenteriae]
201	AAU89012	52856276	malate dehydrogenase [Shigella flexneri]

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Table 45. Examples of glucose-6-phosphate dehydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_504275	50553728	hypothetical protein [Yarrowia lipolytica]
2	XP_365081	39965237	hypothetical protein MG09926.4 [Magnaporthe grisea 70-15]
3	XP_381455	46108794	G6PD_ASPNG Glucose-6-phosphate 1-dehydrogenase (G6PD) [Gibberella zeae PH-1]
4	XP_660585	67525047	glucose-6-phosphate 1-dehydrogenase [Aspergillus nidulans FGSC A4]
5	P48826	1346070	Glucose-6-phosphate 1-dehydrogenase (G6PD)
6	CAA54840	1523782	glucose-6-phosphate 1-dehydrogenase [Aspergillus niger]
7	EAU38380	114196680	glucose-6-phosphate 1-dehydrogenase [Aspergillus terreus NIH2624]
8	EAT83608	111062488	predicted protein [Phaeosphaeria nodorum SN15]
9	EAS28915	90299284	glucose-6-phosphate 1-dehydrogenase [Coccidioides immitis RS]
10	XP_754767	71000100	glucose-6-phosphate 1-dehydrogenase [Aspergillus fumigatus Af293]
11	XP_958320	85090234	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (G6PD) [Neurospora crassa OR74A]
12	EAQ93370	88185902	glucose-6-phosphate 1-dehydrogenase [Chaetomium globosum CBS 148.51]
13	CAA58825	642160	unnamed protein product [Emericella nidulans]
14	XP_458129	50419213	hypothetical protein DEHA0C11286g [Debaryomyces hansenii CBS767]
15	AAB25541	299248	glucose-6-phosphate dehydrogenase [Pichia jadinii=yeast, Peptide, 495 aa]
16	XP_723251	68465104	putative glucose-6-phosphate dehydrogenase [Candida albicans SC5314]
17	XP_723440	68464725	putative glucose-6-phosphate dehydrogenase [Candida albicans SC5314]
18	XP_453944	50307901	G6PD_KLULA [Kluyveromyces lactis]
19	NP_982741	45185024	ABL206Cp [Eremothecium gossypii]
20	XP_448038	50291211	unnamed protein product [Candida glabrata]
21	XP_572045	58269778	glucose-6-phosphate 1-dehydrogenase [Cryptococcus neoformans var. neoformans JEC21]
22	NP_014158	6324088	Glucose-6-phosphate dehydrogenase (G6PD), catalyzes the first step of the pentose phosphate pathway; involved in adapting to oxidatve stress; homolog of the human G6PD which is deficient in patients with hemolytic anemia; Zwf1p [Saccharomyces cerevisiae]
23	AAT93017	51013447	YNL241C [Saccharomyces cerevisiae]
24	AAA34619	171545	glucose-6-phosphate dehydrogenase (ZWF1) (EC 1.1.1.49)
25	XP_761077	71021693	hypothetical protein UM04930.1 [Ustilago maydis 521]
26	NP_593344	63054535	glucose-6-phosphate 1-dehydrogenase [Schizosaccharomyces pombe 972h-]

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27	XP_644814	66822919	glucose 6-phosphate-1-dehydrogenase [Dictyostelium discoideum AX4]
28	ABD72519	89357348	glucose 6-phosphate dehydrogenase [Trypanosoma cruzi]
29	BAE99888	110735823	glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
30	CAB52675	5732197	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
31	CAB08746	2104434	SPAC3A12.18 [Schizosaccharomyces pombe]
32	ABD72517	89357344	glucose 6-phosphate dehydrogenase [Trypanosoma cruzi]
33	ABD72518	89357346	glucose 6-phosphate dehydrogenase [Trypanosoma cruzi]
34	BAB96757	21262179	glucose-6-phosphate dehydrogenase 1 [Chlorella vulgaris]
35	XP_822502	71746894	glucose-6-phosphate 1-dehydrogenase [Trypanosoma brucei TREU927]
36	CAJ07708	68129171	glucose-6-phosphate dehydrogenase [Leishmania major]
37	CAC07816	10045209	glucose-6-phosphate 1-dehydrogenase [Trypanosoma brucei]
38	BAF15046	113564703	Os04g0485300 [Oryza sativa (japonica cultivar-group)]
39	AAO37825	28261397	glucose-6-phosphate dehydrogenase [Leishmania mexicana]
40	AAM64228	27434608	glucose-6-phosphate dehydrogenase [Leishmania mexicana amazonensis]
41	XP_001...	110750934	PREDICTED: similar to Zwischenferment CG12529-PA, isoform A [Apis mellifera]
42	XP_974096	91082561	PREDICTED: similar to CG12529-PA, isoform A [Tribolium castaneum]
43	ABE83959	92876243	Glucose-6-phosphate dehydrogenase [Medicago truncatula]
44	BAE38077	74138546	unnamed protein product [Mus musculus]
45	NP_001...	79313844	G6PD5; glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
46	CAB52674	5732195	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
47	AAD11426	4206114	cytoplasmic glucose-6-phosphate 1-dehydrogenase [Mesembryanthemum crystallinum]
48	Q42919	3023815	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD)
49	AAL79959	19071787	glucose-6-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
50	CAE62054	39593761	Hypothetical protein CBG06072 [Caenorhabditis briggsae]
51	EAL31619	54642875	GA11679-PA [Drosophila pseudoobscura]
52	Q00612	54037161	Glucose-6-phosphate 1-dehydrogenase X (G6PD)
53	AAH75663	49523350	Glucose-6-phosphate dehydrogenase X-linked [Mus musculus]
54	AAB69319	2352923	cytosolic glucose-6-phosphate dehydrogenase 2 [Petroselinum crispum]
55	AAM64230	27434612	glucose-6-phosphate dehydrogenase [Leishmania guyanensis]
56	ABB29564	78183137	putative Zwischenferment [Drosophila yakuba]

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57	AAL57688	18086470	AT3g27300/K17E12_12 [Arabidopsis thaliana]
58	NP_728287	24643352	Zwischenferment CG12529-PB, isoform B [Drosophila melanogaster]
59	EAT38627	108874402	glucose-6-phosphate 1-dehydrogenase [Aedes aegypti]
60	AAR26303	89214190	glucose-6-phosphate dehydrogenase [Populus suaveolens]
61	AAA99073	1304700	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
62	AAK93503	15292469	SD03244p [Drosophila melanogaster]
63	AAB02809	1304686	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
64	NP_523411	24643350	Zwischenferment CG12529-PA, isoform A [Drosophila melanogaster]
65	AAA99107	1305086	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
66	ABB29562	78183133	putative Zwischenferment [Drosophila simulans]
67	NP_502129	17538218	B0035.5 [Caenorhabditis elegans]
68	AAZ23850	71089991	glucose-6-phosphate dehydrogenase [Boophilus microplus]
69	P37830	585165	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD)
70	AAB02812	1304692	glucose-6-phosphate 1-dehydrogenase [Drosophila melanogaster]
71	ABB55386	81075965	glucose-6-phosphate 1-dehydrogenase cytoplasmic isoform-like [Solanum tuberosum]
72	CAJ83683	89273424	glucose-6-phosphate dehydrogenase [Xenopus tropicalis]
73	NP_001...	62859893	glucose-6-phosphate dehydrogenase 2 [Xenopus tropicalis]
74	ABB29563	78183135	putative Zwischenferment [Drosophila teissieri]
75	AAX45785	61394184	glucose-6-phosphate dehydrogenase isoform B [Ips typographus]
76	AAX45784	61394183	glucose-6-phosphate dehydrogenase isoform A [Ips typographus]
77	AAH81820	51980296	Glucose-6-phosphate dehydrogenase X-linked [Rattus norvegicus]
78	XP_311452	58381765	ENSANGP00000018551 [Anopheles gambiae str. PEST]
79	XP_538209	74009187	PREDICTED: similar to Glucose-6-phosphate 1-dehydrogenase (G6PD) [Canis familiaris]
80	AAH59324	111185531	Unknown (protein for MGC:69058) [Xenopus laevis]
81	ABB29560	78183129	putative Zwischenferment [Drosophila erecta]
82	Q27638	3023810	Glucose-6-phosphate 1-dehydrogenase (G6PD)
83	Q29492	2494652	Glucose-6-phosphate 1-dehydrogenase (G6PD)
84	BAF09259	113536876	Os02g0600400 [Oryza sativa (japonica cultivar-group)]
85	O55044	62510568	Glucose-6-phosphate 1-dehydrogenase (G6PD)
86	CAA04993	3021510	glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

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87	ABB29561	78183131	putative Zwischenferment [Drosophila orena]
88	BAA97662	8918502	glucose-6-phosphate dehydrogenase [Triticum aestivum]
89	BAD17920	46849421	glucose-6-phosphate 1-dehydrogenase [Acipenser baerii]
90	XP_699168	68440567	PREDICTED: similar to glucose-6-phosphate dehydrogenase [Danio rerio]
91	AAB96363	2734869	glucose-6-phosphate dehydrogenase [Takifugu rubripes]
92	NP_000393	109389365	glucose-6-phosphate dehydrogenase isoform a [Homo sapiens]
93	NP_001...	108773793	glucose-6-phosphate dehydrogenase isoform b [Homo sapiens]
94	AAA52500	182871	glucose-6-phosphate dehydrogenase variant A- (EC 1.1.1.49)
95	P11413	120731	Glucose-6-phosphate 1-dehydrogenase (G6PD)
96	AAA92653	1203978	G6PD [Homo sapiens]
97	AAX43335	61369430	glucose-6-phosphate dehydrogenase [synthetic construct]
98	P41571	1169799	Glucose-6-phosphate 1-dehydrogenase (G6PD) (Zwischenferment)
99	2BHLB	66361518	Chain B, X-Ray Structure Of Human Glucose-6-Phosphate Dehydrogenase (Deletion Variant) Complexed With Glucose-6-Phosphate
100	ABC74527	85700174	glucose-6-phosphate dehydrogenase [Populus trichocarpa]
101	ABC74528	85700176	glucose-6-phosphate dehydrogenase [Populus trichocarpa]
102	AAA51463	157470	glucose-6-phosphate dehydrogenase
103	XP_001...	109132852	PREDICTED: glucose-6-phosphate dehydrogenase isoform 1 [Macaca mulatta]
104	1QKIH	7546530	Chain H, X-Ray Structure Of Human Glucose 6-Phosphate Dehydrogenase (Variant Canton R459l) Complexed With Structural Nadp+
105	XP_001...	109132850	PREDICTED: glucose-6-phosphate dehydrogenase isoform 2 [Macaca mulatta]
106	BAA97663	8918504	glucose-6-phosphate dehydrogenase [Triticum aestivum]
107	CAA04992	3021508	glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
108	AAB69318	2352921	cytosolic glucose-6-phosphate dehydrogenase 1 [Petroselinum crispum]
109	XP_307095	58375370	ENSANGP00000012074 [Anopheles gambiae str. PEST]
110	AAA41179	204197	glucose-6-phosphate dehydrogenase
111	AAA63175	182890	glucose-6-phosphate dehydrogenase [Homo sapiens]
112	BAA97664	8918506	glucose-6-phosphate dehydrogenase [Triticum aestivum]
113	AAW24823	56753227	SJCHGC02527 protein [Schistosoma japonicum]
114	CAA58590	5459313	glucose-6-phosphate 1-dehydrogenase [Takifugu rubripes]
115	CAG07451	47228719	unnamed protein product [Tetraodon nigroviridis]
116	CAJ28912	113207852	glucose-6-phosphate 1-dehydrogenase [Crassostrea gigas]

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117	ABC25881	83628088	glucose-6-phosphate 1-dehydrogenase [Homo sapiens]
118	ABC25981	83628208	glucose-6-phosphate 1-dehydrogenase [Homo sapiens]
119	ABC25826	83628022	glucose-6-phosphate 1-dehydrogenase [Homo sapiens]
120	BAD17912	46849405	glucose-6-phosphate 1-dehydrogenase [Amia calva]
121	BAD17877	46849335	glucose-6-phosphate 1-dehydrogenase [Protopterus annectens]
122	BAD17947	46849475	glucose-6-phosphate 1-dehydrogenase [Callorhinchus callorynchus]
123	AAI20828	111306848	Glucose-6-phosphate dehydrogenase 2 [Mus musculus]
124	BAD17927	46849435	glucose-6-phosphate 1-dehydrogenase [Polypterus ornatipinnis]
125	BAD17898	46849377	glucose-6-phosphate 1-dehydrogenase [Oryzias latipes]
126	BAD17891	46849363	glucose-6-phosphate 1-dehydrogenase [Ambystoma mexicanum]
127	BAD17951	46849483	glucose-6-phosphate 1-dehydrogenase [Lethenteron reissneri]
128	AAF19030	7629275	glucose-6-phosphate-1-dehydrogenase; G6PD [Pimephales promelas]
129	BAD17941	46849463	glucose-6-phosphate 1-dehydrogenase [Potamotrygon motoro]
130	BAD17954	46849489	glucose-6-phosphate 1-dehydrogenase [Branchiostoma belcheri]
131	BAD17905	46849391	glucose-6-phosphate 1-dehydrogenase [Lepisosteus osseus]
132	BAD17884	46849349	glucose-6-phosphate 1-dehydrogenase [Lepidosiren paradoxa]
133	BAD17934	46849449	glucose-6-phosphate 1-dehydrogenase [Cephaloscyllium umbratile]
134	ABC74529	85700178	glucose-6-phosphate dehydrogenase [Populus trichocarpa]
135	CAB52685	5734379	plastidic glucose-6-phosphate dehydrogenase [Dunaliella bioculata]
136	Q43793	3023817	Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (G6PD)
137	AAF87216	9392607	plastidic glucose 6-phosphate dehydrogenase [Nicotiana tabacum]
138	BAC23041	24745908	glucose 6-phosphate dehydrogenase [Solanum tuberosum]
139	CAB52708	5734502	glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]
140	BAF21344	113610966	Os07g0406300 [Oryza sativa (japonica cultivar-group)]
141	AAQ02671	33304517	putative plastidic glucose-6-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
142	AAW82643	58803037	hepatic glucose-6-phosphate dehydrogenase [Rhabdosargus sarba]
143	BAF12270	113548827	Os03g0412800 [Oryza sativa (japonica cultivar-group)]
144	AAN72144	25083966	glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
145	AAB69317	2352919	plastidic glucose-6-phosphate dehydrogenase [Petroselinum crispum]
146	O24357	3334193	Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (G6PD)

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147	AAO23597	27764952	At1g24280/F3I6_22 [Arabidopsis thaliana]
148	Q8L743	25452975	Glucose-6-phosphate 1-dehydrogenase 3, chloroplast precursor (G6PD3) (G6PDH3)
149	CAA59011	1166405	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
150	CAA59012	1174336	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
151	CAC05439	9955555	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
152	Q9FY99	25452980	Glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor (G6PD2) (G6PDH2)
153	AAL57678	18086448	AT5g13110/T19L5_70 [Arabidopsis thaliana]
154	Q43839	3023818	Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (G6PD)
155	CAA04696	3021305	plastidic glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
156	CAB52681	5734372	glucose-6-phosphate 1-dehydrogenase [Cyanidium caldarium]
157	CAA04994	3021532	glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
158	Q7YS37	62510624	Glucose-6-phosphate 1-dehydrogenase (G6PD)
159	CAG04059	47229307	unnamed protein product [Tetraodon nigroviridis]
160	CAD28862	29149997	glucose 6 phosphate dehydrogenase [Acraea encedana]
161	CAD28863	29149999	glucose 6 phosphate dehydrogenase [Acraea encedana]
162	AAM64231	27434614	glucose-6-phosphate dehydrogenase [Leishmania braziliensis]
163	AAG28728	11066848	glucose-6-phosphate-dehydrogenase [Drosophila mauritiana]
164	AAG28730	11066852	glucose-6-phosphate-dehydrogenase [Drosophila sechellia]
165	ABF96583	108708788	Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor, putative, expressed [Oryza sativa (japonica cultivar-group)]
166	CAA03941	2276348	Glucose-6-phosphate dehydrogenase [Spinacia oleracea]
167	XP_583628	76658972	PREDICTED: similar to Glucose-6-phosphate 1-dehydrogenase (G6PD) [Bos taurus]
168	AAA52499	182869	glucose-6-phosphate dehydrogenase
169	AAM64229	27434610	glucose-6-phosphate dehydrogenase [Leishmania mexicana]
170	NP_587749	19075249	hypothetical protein SPCC794.01c [Schizosaccharomyces pombe 972h-]
171	AAR12945	38156652	glucose-6-phosphate dehydrogenase [Drosophila mojavensis]
172	AAR12953	38156668	glucose-6-phosphate dehydrogenase [Drosophila mojavensis]
173	AAR12946	38156654	glucose-6-phosphate dehydrogenase [Drosophila mojavensis]
174	AAR12943	38156648	glucose-6-phosphate dehydrogenase [Drosophila mojavensis]
175	AAR12952	38156666	glucose-6-phosphate dehydrogenase [Drosophila mojavensis]
176	BAF11858	113548415	Os03g0318500 [Oryza sativa (japonica cultivar-group)]
177	XP_559252	57942974	ENSANGP00000028421 [Anopheles gambiae str. PEST]

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178	NP_593614	19114526	hypothetical protein SPAC3C7.13c [Schizosaccharomyces pombe 972h-]
179	BAD94743	62321397	glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]
180	CAJ20381	95007160	glucose-6-phosphate-1-dehydrogenase [Toxoplasma gondii]
181	YP_605437	94986073	glucose-6-phosphate 1-dehydrogenase [Deinococcus geothermalis DSM 11300]
182	CAE51228	37651949	glucose 6 phosphate dehydrogenase [Adalia bipunctata]
183	YP_007820	46446455	putative glucose-6-phosphate [Candidatus Protochlamydia amoebophila UWE25]
184	NP_295319	15806604	glucose-6-phosphate 1-dehydrogenase [Deinococcus radiodurans R1]
185	CAE51222	37651937	glucose 6 phosphate dehydrogenase [Adalia bipunctata]
186	CAE51229	37651951	glucose 6 phosphate dehydrogenase [Adalia decempunctata]
187	ZP_007...	76260057	Glucose-6-phosphate dehydrogenase [Chloroflexus aurantiacus J-10-fl]
188	ZP_002...	47096622	glucose-6-phosphate 1-dehydrogenase [Listeria monocytogenes str. 1/2a F6854]
189	ZP_004...	66965919	Glucose-6-phosphate dehydrogenase [Arthrobacter sp. FB24]
190	ZP_002...	47093301	glucose-6-phosphate 1-dehydrogenase [Listeria monocytogenes str. 4b H7858]
191	NP_471419	16801151	hypothetical protein lin2085 [Listeria innocua Clip11262]
192	NP_693860	23100393	glucose-6-phosphate 1-dehydrogenase [Oceanobacillus iheyensis HTE831]
193	NP_829405	29840299	glucose-6-phosphate 1-dehydrogenase [Chlamydophila caviae GPIC]
194	CAJ71041	91203388	strongly similar to glucose-6-phosphate dehydrogenase [Candidatus Kuenenia stuttgartiensis]
195	YP_629214	108761123	glucose-6-phosphate 1-dehydrogenase [Myxococcus xanthus DK 1622]
196	ZP_009...	84387050	glucose-6-phosphate 1-dehydrogenase [Vibrio splendidus 12B01]
197	ZP_011...	88856188	glucose-6-phosphate 1-dehydrogenase [marine actinobacterium PHSC20C1]
198	NP_827489	29832855	glucose-6-phosphate 1-dehydrogenase [Streptomyces avermitilis MA-4680]
199	CAH10104	88319768	putative glucose-6-phosphate-1-dehydrogenase [Streptomyces sp. SCC 2136]
200	YP_148187	56420869	glucose-6-phosphate 1-dehydrogenase [Geobacillus kaustophilus HTA426]
201	ZP_006...	71368421	Glucose-6-phosphate dehydrogenase [Nocardioides sp. JS614]

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Table 46. Examples of 6-phosphogluconate dehydrogenase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_500938	50546937	hypothetical protein [Yarrowia lipolytica].
2	XP_458726	50420381	hypothetical protein DEHA0D06820g [Debaryomyces hansenii CBS767]
3	XP_451408	50302941	unnamed protein product [Kluyveromyces lactis]
4	O13287	3334110	6-phosphogluconate dehydrogenase, decarboxylating
5	XP_722227	68467588	hypothetical protein CaO19_5024 [Candida albicans SC5314]
6	NP_012053	6321977	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress; Gnd1p [Saccharomyces cerevisiae]
7	AAO32396	28564035	GND1 [Saccharomyces bayanus]
8	XP_750696	70991695	6-phosphogluconate dehydrogenase, decarboxylating [Aspergillus fumigatus Af293]
9	CAD80254	29409963	6-phosphogluconate dehydrogenase [Aspergillus niger]
10	XP_661558	67526993	hypothetical protein AN3954.2 [Aspergillus nidulans FGSC A4]
11	AAO32456	28564155	GND1 [Saccharomyces servazzii]
12	AAO32497	28564385	GND1 [Saccharomyces castellii]
13	BAE57349	83767210	unnamed protein product [Aspergillus oryzae]
14	AAT92830	51013073	YGR256W [Saccharomyces cerevisiae]
15	XP_449923	50295024	hypothetical protein CAGL0M13343g [Candida glabrata CBS138]
16	NP_985676	45198647	AFR129Wp [Eremothecium gossypii]
17	EAS35799	90306168	6-phosphogluconate dehydrogenase, decarboxylating [Coccidioides immitis RS]
18	XP_758724	71014537	hypothetical protein UM02577.1 [Ustilago maydis 521]
19	O60037	12229635	6-phosphogluconate dehydrogenase, decarboxylating
20	XP_964959	85115938	hypothetical protein [Neurospora crassa OR74A]
21	XP_381287	46108458	hypothetical protein FG01111.1 [Gibberella zeae PH-1]
22	EAT76717	111055597	predicted protein [Phaeosphaeria nodorum SN15]
23	XP_369069	39975357	hypothetical protein MG00175.4 [Magnaporthe grisea 70-15]
24	XP_567793	58260766	phosphogluconate dehydrogenase (decarboxylating) [Cryptococcus neoformans var. neoformans JEC21]
25	NP_595095	19111887	6-phosphogluconate dehydrogenase [Schizosaccharomyces pombe 972h-]
26	EAQ92608	88185140	hypothetical protein CHGG_00843 [Chaetomium globosum CBS 148.51]
27	T42523	11251352	probable phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - fission yeast (Schizosaccharomyces pombe) (fragment)
28	XP_781394	72005545	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating [Strongylocentrotus purpuratus]
29	BAD98151	63003720	6-phosphogluconate dehydrogenase [Ascidia sydneiensis samea]
30	XP_625090	66547531	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating, partial [Apis mellifera]
31	CAG32303	53134115	hypothetical protein [Gallus gallus]
32	2PGD	999886	Chain , 6-Phosphogluconate Dehydrogenase (6-Pgdh) (E.C.1.1.1.44)

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33	NP_001...	57164179	6-phosphogluconate dehydrogenase (decarboxylating) [Ovis aries]
34	XP_911640	82896232	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating isoform 6 [Mus musculus]
35	BAE31577	74225286	unnamed protein product [Mus musculus]
36	AAX43359	61369608	phosphogluconate dehydrogenase [synthetic construct]
37	CAI95751	66347393	phosphogluconate dehydrogenase [Homo sapiens]
38	XP_993478	94374014	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating isoform 4 [Mus musculus]
39	AAH11329	15030150	Phosphogluconate dehydrogenase [Mus musculus]
40	AAI02179	73586529	LOC514939 protein [Bos taurus]
41	AAA75302	984325	phosphogluconate dehydrogenase [Homo sapiens]
42	AAH59958	37747616	MGC68486 protein [Xenopus laevis]
43	ZP_005...	67931108	6-phosphogluconate dehydrogenase, decarboxylating [Solibacter usitatus Ellin6076]
44	EAT42557	108878332	6-phosphogluconate dehydrogenase [Aedes aegypti]
45	XP_535411	73950940	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating isoform 1 [Canis familiaris]
46	XP_313091	58384192	ENSANGP00000012857 [Anopheles gambiae str. PEST]
47	CAG07546	47228814	unnamed protein product [Tetraodon nigroviridis]
48	YP_007316	46445951	6-phosphogluconate dehydrogenase [Candidatus Protochlamydia amoebophila UWE25]
49	NP_998717	47087205	phosphogluconate hydrogenase isoform 2 [Danio rerio]
50	XP_972051	91094851	PREDICTED: similar to phosphogluconate hydrogenase isoform 2 [Tribolium castaneum]
51	CAE70848	39594980	Hypothetical protein CBG17632 [Caenorhabditis briggsae]
52	XP_001...	94372948	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating isoform 9 [Mus musculus]
53	NP_998618	47087439	phosphogluconate hydrogenase isoform 1 [Danio rerio]
54	AAH95571	63102189	Pgd protein [Danio rerio]
55	XP_993446	94374016	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating isoform 3 [Mus musculus]
56	EAL31500	54642755	GA17642-PA [Drosophila pseudoobscura]
57	Q17761	74962414	6-phosphogluconate dehydrogenase, decarboxylating
58	P41573	1168233	6-phosphogluconate dehydrogenase, decarboxylating
59	AAL90185	19528141	AT26455p [Drosophila melanogaster]
60	NP_476860	24639279	Phosphogluconate dehydrogenase CG3724-PA [Drosophila melanogaster]
61	NP_001...	114053253	6-phosphogluconate dehydrogenase [Bombyx mori]
62	P41570	1168228	6-phosphogluconate dehydrogenase, decarboxylating
63	CAJ43391	95140247	6-phosphogluconate dehydrogenase [Bactrocera oleae]
64	CAJ43390	95140245	6-phosphogluconate dehydrogenase [Ceratitis capitata]
65	AAP92648	33086672	Cc2-27 [Rattus norvegicus]
66	YP_661682	109898427	6-phosphogluconate dehydrogenase, decarboxylating [Pseudoalteromonas atlantica T6c]
67	XP_592859	76637462	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating [Bos taurus]
68	YP_526109	90020282	6-phosphogluconate dehydrogenase, decarboxylating [Saccharophagus degradans 2-40]
69	ZP_001...	53733078	COG0362: 6-phosphogluconate dehydrogenase [Haemophilus influenzae R2846]
70	NP_761502	27365974	6-phosphogluconate dehydrogenase [Vibrio vulnificus CMCP6]

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71	YP_391484	78485559	6-phosphogluconate dehydrogenase, decarboxylating [Thiomicrospira crunogena XCL-2]
72	YP_248262	68249150	6-phosphogluconate dehydrogenase [Haemophilus influenzae 86-028NP]
73	NP_934400	37679791	6-phosphogluconate dehydrogenase [Vibrio vulnificus YJ016]
74	ZP_007...	75857693	COG0362: 6-phosphogluconate dehydrogenase [Vibrio sp. Ex25]
75	NP_798087	28898482	6-phosphogluconate dehydrogenase [Vibrio parahaemolyticus RIMD 2210633]
76	YP_206428	59713653	6-phosphogluconate dehydrogenase [Vibrio fischeri ES114]
77	ZP_001...	53733322	COG0362: 6-phosphogluconate dehydrogenase [Haemophilus influenzae R2866]
78	ZP_012...	91224436	6-phosphogluconate dehydrogenase [Vibrio alginolyticus 12G01]
79	AAB20377	239383	6-phosphogluconate dehydrogenase [sheep, Peptide, 466 aa]
80	ZP_010...	86145883	6-phosphogluconate dehydrogenase [Vibrio sp. MED222]
81	ZP_007...	75432781	Phosphogluconate dehydrogenase (decarboxylating) [Actinobacillus succinogenes 130Z]
82	ZP_001...	46143450	COG0362: 6-phosphogluconate dehydrogenase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
83	ZP_012...	90578957	6-phosphogluconate dehydrogenase [Vibrio angustum S14]
84	YP_087205	52424068	6-phosphogluconate dehydrogenase [Mannheimia succiniciproducens MBEL55E]
85	ZP_011...	89073009	6-phosphogluconate dehydrogenase [Photobacterium sp. SKA34]
86	NP_273081	15675963	6-phosphogluconate dehydrogenase [Neisseria meningitidis MC58]
87	ZP_007...	75825242	COG0362: 6-phosphogluconate dehydrogenase [Vibrio cholerae O395]
88	ZP_007...	75822319	COG0362: 6-phosphogluconate dehydrogenase [Vibrio cholerae RC385]
89	ZP_007...	75831146	COG0362: 6-phosphogluconate dehydrogenase [Vibrio cholerae MO10]
90	YP_719859	113461790	6-phosphogluconate dehydrogenase [Haemophilus somnus 129PT]
91	ZP_012...	90411828	6-phosphogluconate dehydrogenase [Photobacterium profundum 3TCK]
92	YP_129657	54308637	6-phosphogluconate dehydrogenase [Photobacterium profundum SS9]
93	ZP_001...	53728695	COG0362: 6-phosphogluconate dehydrogenase [Haemophilus somnus 2336]
94	BAD36766	51241757	6-phosphogluconate dehydrogenase [Cyanidioschyzon merolae]
95	P70718	2492494	6-phosphogluconate dehydrogenase, decarboxylating
96	XP_642122	66816225	6-phosphogluconate dehydrogenase (decarboxylating) [Dictyostelium discoideum AX4]
97	Q7VMX4	71152205	6-phosphogluconate dehydrogenase, decarboxylating
98	NP_283102	15793280	6-phosphogluconate dehydrogenase [Neisseria meningitidis Z2491]
99	NP_246493	15603419	6-phosphogluconate dehydrogenase [Pasteurella multocida subsp. multocida str. Pm70]
100	AAO19943	27573087	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]

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101	AAO19944	27573089	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]
102	YP_208939	59802227	6-phosphogluconate dehydrogenase [Neisseria gonorrhoeae FA 1090]
103	AAO19934	27573069	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]
104	AAO19942	27573085	6-phosphogluconate dehydrogenase, decarboxylating [Neisseria gonorrhoeae]
105	ZP_013...	106881674	6-phosphogluconate dehydrogenase, decarboxylating [Psychromonas ingrahamii 37]
106	XP_515670	55599346	PREDICTED: similar to 6-phosphogluconate dehydrogenase, decarboxylating [Pan troglodytes]
107	ZP_010...	87309497	6-phosphogluconate dehydrogenase [Blastopirellula marina DSM 3645]
108	NP_865160	32472166	6-phosphogluconate dehydrogenase [Rhodopirellula baltica SH 1]
109	AAW29923	56788282	6-phosphogluconate dehydrogenase [Mannheimia haemolytica]
110	AAW29924	56788284	6-phosphogluconate dehydrogenase [Mannheimia glucosida]
111	AAW29925	56788286	6-phosphogluconate dehydrogenase [Pasteurella trehalosi]
112	NP_218771	15639322	6-phosphogluconate dehydrogenase [Treponema pallidum subsp. pallidum str. Nichols]
113	YP_148197	56420879	6-phosphogluconate dehydrogenase [Geobacillus kaustophilus HTA426]
114	YP_356348	77918533	probable phosphogluconate dehydrogenase (decarboxylating) [Pelobacter carbinolicus DSM 2380]
115	NP_390267	50812264	6-phosphogluconate dehydrogenase [Bacillus subtilis subsp. subtilis str. 168]
116	YP_092134	52786305	6-phosphogluconate dehydrogenase [Bacillus licheniformis ATCC 14580]
117	ZP_011...	89099010	6-phosphogluconate dehydrogenase [Bacillus sp. NRRL B-14911]
118	NP_691106	23097640	6-phosphogluconate dehydrogenase [Oceanobacillus iheyensis HTE831]
119	YP_219832	62185047	6-phosphogluconate dehydrogenase [Chlamydophila abortus S26/3]
120	ZP_002...	47565365	6-phosphogluconate dehydrogenase, decarboxylating [Bacillus cereus G9241]
121	YP_026451	49183199	6-phosphogluconate dehydrogenase [Bacillus anthracis str. Sterne]
122	YP_034514	49476731	6-phosphogluconate dehydrogenase [Bacillus thuringiensis serovar konkukian str. 97-27]
123	YP_081773	52145056	6-phosphogluconate dehydrogenase [Bacillus cereus E33L]
124	YP_515493	89898383	6-phosphogluconate dehydrogenase [Chlamydophila felis Fe/C-56]
125	NP_814782	29375628	6-phosphogluconate dehydrogenase [Enterococcus faecalis V583]
126	ZP_003...	65317607	COG0362: 6-phosphogluconate dehydrogenase [Bacillus anthracis str. A2012]
127	YP_175422	56963691	6-phosphogluconate dehydrogenase [Bacillus clausii KSM-K16]
128	ZP_006...	69247351	6-phosphogluconate dehydrogenase, decarboxylating [Enterococcus faecium DO]

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129	NP_810135	29346632	6-phosphogluconate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482]
130	NP_829300	29840194	6-phosphogluconate dehydrogenase [Chlamydophila caviae GPIC]
131	AAL76325	18644678	6-phosphogluconate dehydrogenase [Porphyra yezoensis]
132	YP_546705	91776949	6-phosphogluconate dehydrogenase, decarboxylating [Methylobacillus flagellatus KT]
133	ZP_004...	67546118	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia vietnamiensis G4]
134	Q9CHU6	18202802	6-phosphogluconate dehydrogenase, decarboxylating
135	ZP_006...	74014955	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia ambifaria AMMD]
136	YP_372936	78063028	6-phosphogluconate dehydrogenase [Burkholderia sp. 383]
137	YP_624314	107026803	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia cenocepacia AU 1054]
138	NP_928851	37525507	6-phosphogluconate dehydrogenase [Photorhabdus luminescens subsp. laumondii TTO1]
139	ZP_002...	47095960	6-phosphogluconate dehydrogenase, decarboxylating [Listeria monocytogenes str. 1/2a F6854]
140	YP_438830	83717630	6-phosphogluconate dehydrogenase, decarboxylating [Burkholderia thailandensis E264]
141	P96789	8134294	6-phosphogluconate dehydrogenase, decarboxylating
142	NP_924063	37520686	6-phosphogluconate dehydrogenase [Gloeobacter violaceus PCC 7421]
143	AAA24207	146938	6-phosphogluconate dehydrogenase
144	ZP_009...	84360352	COG0362: 6-phosphogluconate dehydrogenase [Burkholderia dolosa AUO158]
145	YP_335987	76817886	6-phosphogluconate dehydrogenase [Burkholderia pseudomallei 1710b]
146	AAA24495	147501	6-phosphogluconate dehydrogenase
147	NP_310857	15832084	6-phosphogluconate dehydrogenase [Escherichia coli O157:H7 str. Sakai]
148	ZP_009...	83571257	COG0362: 6-phosphogluconate dehydrogenase [Shigella dysenteriae 1012]
149	ZP_007...	75229110	COG0362: 6-phosphogluconate dehydrogenase [Escherichia coli B7A]
150	ZP_013...	100915196	hypothetical protein Bmal10_03003493 [Burkholderia mallei 10399]
151	AAG35219	11464518	6-phosphogluconate dehydrogenase [Escherichia coli]
152	ZP_013...	100236192	hypothetical protein Bpse4_03000697 [Burkholderia pseudomallei 406e]
153	YP_669972	110642242	6-phosphogluconate dehydrogenase, decarboxylating [Escherichia coli 536]
154	ZP_013...	100062231	hypothetical protein BpseP_03002198 [Burkholderia pseudomallei Pasteur]
155	YP_114383	53803994	6-phosphogluconate dehydrogenase [Methylococcus capsulatus str. Bath]
156	AAA24208	146940	6-phosphogluconate dehydrogenase
157	YP_310991	74312572	gluconate-6-phosphate dehydrogenase, decarboxylating [Shigella sonnei Ss046]
158	ZP_003...	48870455	COG0362: 6-phosphogluconate dehydrogenase [Pediococcus pentosaceus ATCC 25745]
159	ZP_007...	75514070	COG0362: 6-phosphogluconate dehydrogenase [Escherichia

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			coli 53638]
160	YP_049550	50120383	6-phosphogluconate dehydrogenase [Erwinia carotovora subsp. atroseptica SCRI1043]
161	AP_002630	89108850	gluconate-6-phosphate dehydrogenase, decarboxylating [Escherichia coli W3110]
162	ZP_007...	75259178	COG0362: 6-phosphogluconate dehydrogenase [Escherichia coli E22]
163	YP_541301	91211315	6-phosphogluconate dehydrogenase, decarboxylating [Escherichia coli UTI89]
164	YP_013993	46907604	6-phosphogluconate dehydrogenase [Listeria monocytogenes str. 4b F2365]
165	YP_403788	82777439	gluconate-6-phosphate dehydrogenase [Shigella dysenteriae Sd197]
166	ZP_009...	83588030	COG0362: 6-phosphogluconate dehydrogenase [Escherichia coli 101-1]
167	AAD50492	5739470	6-phosphogluconate dehydrogenase Gnd [Escherichia coli]
168	ZP_006...	75177157	COG0362: 6-phosphogluconate dehydrogenase [Shigella boydii BS512]
169	AAA24209	146942	6-phosphogluconate dehydrogenase
170	AAG35221	11464522	6-phosphogluconate dehydrogenase [Escherichia coli]
171	ZP_007...	75186836	COG0362: 6-phosphogluconate dehydrogenase [Escherichia coli E24377A]
172	YP_689521	110806001	gluconate-6-phosphate dehydrogenase [Shigella flexneri 5 str. 8401]
173	ZP_008...	77959279	COG0362: 6-phosphogluconate dehydrogenase [Yersinia bercovieri ATCC 43970]
174	AAG35224	11464528	6-phosphogluconate dehydrogenase [Escherichia coli]
175	ZP_007...	77636293	COG0362: 6-phosphogluconate dehydrogenase [Yersinia pestis Angola]
176	ZP_008...	77962467	COG0362: 6-phosphogluconate dehydrogenase [Yersinia mollaretii ATCC 43969]
177	ZP_008...	77978861	COG0362: 6-phosphogluconate dehydrogenase [Yersinia intermedia ATCC 29909]
178	AAG35218	11464516	6-phosphogluconate dehydrogenase [Escherichia coli]
179	BAA77736	4867927	6-phosphogluconate dehydrogenase [Escherichia coli]
180	AAA24490	147491	6-phosphogluconate dehydrogenase
181	YP_648367	108812600	6-phosphogluconate dehydrogenase, decarboxylating [Yersinia pestis Nepal516]
182	NP_669932	22126509	6-phosphogluconate dehydrogenase [Yersinia pestis KIM]
183	AAA23918	146232	6-phosphogluconate dehydrogenase (EC 1.1.1.44)
184	CAJ71042	91203389	strongly similar to 6-phosphogluconate dehydrogenase (decarboxylating) [Candidatus Kuenenia stuttgartiensis]
185	AAA24206	146936	6-phosphogluconate dehydrogenase
186	AAA24494	147499	6-phosphogluconate dehydrogenase
187	AAA24492	147495	6-phosphogluconate dehydrogenase
188	YP_099135	53713143	6-phosphogluconate dehydrogenase [Bacteroides fragilis YCH46]
189	AAA23925	146246	6-phosphogluconate dehydrogenase
190	YP_211552	60681408	6-phosphogluconate dehydrogenase [Bacteroides fragilis NCTC 9343]
191	AAV74381	56122509	Gnd [Escherichia coli]
192	NP_992794	45441255	6-phosphogluconate dehydrogenase [Yersinia pestis biovar Microtus str. 91001]

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193	YP_650749	108806833	6-phosphogluconate dehydrogenase, decarboxylating [Yersinia pestis Antiqua]
194	NP_876643	33241702	6-phosphogluconate dehydrogenase [Chlamydophila pneumoniae TW-183]
195	NP_357929	15902379	6-phosphogluconate dehydrogenase [Streptococcus pneumoniae R6]
196	ZP_014...	111658214	hypothetical protein SpneT_02000606 [Streptococcus pneumoniae TIGR4]
197	NP_782446	28211502	6-phosphogluconate dehydrogenase [Clostridium tetani E88]
198	AAG35223	11464526	6-phosphogluconate dehydrogenase [Escherichia coli]
199	AAA24493	147497	6-phosphogluconate dehydrogenase
200	ZP_007...	75214880	COG0362: 6-phosphogluconate dehydrogenase [Escherichia coli E110019]

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Table 47. Examples of Fructose 1,6 bisphosphatase polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_500111	50545147	hypothetical protein [Yarrowia lipolytica].
2	AAP85294	32492043	fructose-1,6-bisphosphatase [Yarrowia lipolytica]
3	XP_460410	50423651	hypothetical protein DEHA0F01309g [Debaryomyces hansenii CBS767]
4	CAC69139	15528447	putative fructose-1,6-bisphosphatase [Pichia anomala]
5	XP_447425	50289987	hypothetical protein CAGL0I04048g [Candida glabrata CBS138]
6	NP_986140	45199111	AFR593Cp [Eremothecium gossypii]
7	XP_454003	50308005	F16P_KLULA [Kluyveromyces lactis]
8	EAT78213	111057093	predicted protein [Phaeosphaeria nodorum SN15]
9	XP_710934	68490480	fructose-1,6-bisphosphatase [Candida albicans SC5314]
10	AAT92835	51013083	YLR377C [Saccharomyces cerevisiae]
11	XP_364050	39954137	hypothetical protein MG08895.4 [Magnaporthe grisea 70-15]
12	NP_001...	68006542	fructose-1,6-bisphosphatase [Schizosaccharomyces pombe 972h-]
13	NP_595083	19111875	hypothetical protein SPBC1198.14c [Schizosaccharomyces pombe 972h-]
14	XP_751698	70993702	fructose-1,6-bisphosphatase [Aspergillus fumigatus Af293]
15	XP_447010	50289161	unnamed protein product [Candida glabrata]
16	BAE58185	83768046	unnamed protein product [Aspergillus oryzae]
17	EAQ84924	88177456	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
18	AAF34693	6980006	fructose 1,6-bisphosphatase [Candida albicans]
19	BAB12208	9955389	fructose-1,6-bisphosphatase [Aspergillus oryzae]
20	XP_663208	67538868	hypothetical protein AN5604.2 [Aspergillus nidulans FGSC A4]
21	XP_389456	46134281	conserved hypothetical protein [Gibberella zeae PH-1]
22	XP_960423	85097320	hypothetical protein [Neurospora crassa OR74A]
23	EAS36192	90306561	fructose-1,6-bisphosphatase [Coccidioides immitis RS]
24	XP_566475	58258125	fructose-bisphosphatase [Cryptococcus neoformans var. neoformans JEC21]
25	XP_758850	71015920	hypothetical protein UM02703.1 [Ustilago maydis 521]
26	P14766	119748	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
27	AAZ86538	73811203	fructose 1,6-bisphosphatase [Brassica rapa subsp. pekinensis]
28	Q9MA79	75312318	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
29	Q9SDL8	75313310	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
30	BAD81916	56785198	fructose-1,6-bisphosphatase [Oryza sativa (japonica cultivar-group)]
31	P46267	1169585	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
32	P46276	1169586	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) (CY-F1)
33	Q8RW99	75303233	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
34	Q43139	76363515	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
35	CAB46084	5305145	fructose-1,6-bisphosphatase [Pisum sativum]

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36	BAF06820	113534437	Os01g0866400 [Oryza sativa (japonica cultivar-group)]
37	Q42649	76789650	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
38	Q9XF47	75315047	Fructose-1,6-bisphosphatase, cytosolic (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
39	CAA61409	895909	fructose-1, 6-bisphosphatase [Saccharum hybrid cultivar H65-7052]
40	1906373A	444324	cytosolic fructose bisphosphatase
41	EAR87347	89289359	fructose-1,6-bisphosphatase family protein [Tetrahymena thermophila SB210]
42	NP_915641	34908588	fructose-1,6-bisphosphatase [Oryza sativa (japonica cultivar-group)]
43	XP_475314	50931573	putative fructose-1,6-bisphosphatase [Oryza sativa (japonica cultivar-group)]
44	NP_491004	17508131	K07A3.1 [Caenorhabditis elegans]
45	XP_782411	72013871	PREDICTED: similar to fructose-1,6-bisphosphatase 1, like [Strongylocentrotus purpuratus]
46	CAE60538	39595500	Hypothetical protein CBG04165 [Caenorhabditis briggsae]
47	NP_610001	19921562	fructose-1,6-bisphosphatase CG31692-PA, isoform A [Drosophila melanogaster]
48	NP_724223	45550998	fructose-1,6-bisphosphatase CG31692-PB, isoform B [Drosophila melanogaster]
49	XP_319937	58393257	ENSANGP00000016841 [Anopheles gambiae str. PEST]
50	AAN31471	23394363	fructose-1 6-biphosphatase [Phytophthora infestans]
51	XP_425040	50762393	PREDICTED: similar to fructose 1,6-bisphosphatase [Gallus gallus]
52	EAT47721	108883496	fructose-1,6-bisphosphatase [Aedes aegypti]
53	EAT47722	108883497	fructose-1,6-bisphosphatase [Aedes aegypti]
54	AAH53784	32450356	Fbp-prov protein [Xenopus laevis]
55	YP_001659	45657573	fructose-1,6-bisphosphatase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]
56	NP_989145	45361017	Fructose-1,6-bisphosphatase [Xenopus tropicalis]
57	1YZ0B	62738852	Chain B, R-State Amp Complex Reveals Initial Steps Of The Quaternary Transition Of Fructose-1,6-Bisphosphatase
58	1Q9DB	39654661	Chain B, Fructose-1,6-Bisphosphatase Complexed With A New Allosteric Site Inhibitor (I-State)
59	NP_999144	47522784	fructose 1,6-bisphosphatase [Sus scrofa]
60	EAL32807	54644065	GA16400-PA [Drosophila pseudoobscura]
61	XP_848306	73946392	PREDICTED: similar to fructose-1,6-bisphosphatase 1 isoform 3 [Canis familiaris]
62	1FJ9B	11514534	Chain B, Fructose-1,6-Bisphosphatase (Mutant Y57w) ProductsZNAMP Complex (T-State)
63	1LEVF	24987566	Chain F, Porcine Kidney Fructose-1,6-Bisphosphatase Complexed With An Amp-Site Inhibitor
64	1BK4A	6729708	Chain A, Crystal Structure Of Rabbit Liver Fructose-1,6-Bisphosphatase At 2.3 Angstrom Resolution
65	Q3SZB7	110808224	Fructose-1,6-bisphosphatase 1 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 1) (FBPase 1)
66	AAA41131	310111	fructose-biphosphatase
67	P46275	2506391	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
68	2F3HB	99032142	Chain B, Mechanism Of Displacement Of A Catalytically Essential Loop From The Active Site Of Fructose-1,6-

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			Bisphosphatase
69	NP_036690	51036635	fructose-1,6- biphosphatase 1 [Rattus norvegicus]
70	AAC25597	3288991	fructose-1,6-bisphosphatase [Sus scrofa]
71	XP_967802	91077758	PREDICTED: similar to CG31692-PA, isoform A [Tribolium castaneum]
72	AAK59929	14318171	fructose-1,6-bisphosphatase [Pisum sativum]
73	1DCUD	6730314	Chain D, Redox Signaling In The Chloroplast: Structure Of Oxidized Pea Fructose-1,6-Bisphosphate Phosphatase
74	1DBZD	6730306	Chain D, C153s Mutant Of Pea Fructose-1,6-Bisphosphatase
75	CAB39759	4539148	fructose-1,6-bisphosphatase [Pisum sativum]
76	P09199	20141075	Fructose-1,6-bisphosphatase 1 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 1) (FBPase 1)
77	CAA48719	20717	fructose-bisphosphatase [Pisum sativum]
78	1FPIB	1633402	Chain B, Fructose-1,6-Bisphosphatase (D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase) Complexed With Amp, 2,5-Anhydro-D-Glucitol-1,6-Bisphosphate And Potassium Ions (100 Mm)
79	AAB30523	546354	fructose-1,6-biphosphatase, FBPase {EC 3.1.3.11} [Pisum sativum=peas, Lincoln, Peptide Chloroplast, 357 aa]
80	1KZ8F	24987484	Chain F, Crystal Structure Of Porcine Fructose-1,6-Bisphosphatase Complexed With A Novel Allosteric-Site Inhibitor
81	AAW25416	56754457	SJCHGC06706 protein [Schistosoma japonicum]
82	1FRPB	809402	Chain B, Fructose-1,6-Bisphosphatase (D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase) (E.C.3.1.3.11) Complexed With Fructose-2,6-Bisphosphate, Adenosine Monophosphate (Amp), And Zinc
83	XP_425039	50762391	PREDICTED: similar to fructose-1,6-bisphosphatase [Gallus gallus]
84	NP_998297	47085885	fructose-1,6-bisphosphatase 1 [Danio rerio]
85	1RDZB	1942591	Chain B, T-State Structure Of The Arg 243 To Ala Mutant Of Pig Kidney Fructose 1,6-Bisphosphatase Expressed In E. Coli
86	1FSAB	2554913	Chain B, The T-State Structure Of Lys 42 To Ala Mutant Of The Pig Kidney Fructose 1,6-Bisphosphatase Expressed In E. Coli
87	BAE28940	74146344	unnamed protein product [Mus musculus]
88	CAG05216	47228396	unnamed protein product [Tetraodon nigroviridis]
89	NP_956236	41053949	fructose-1,6-bisphosphatase 1, like [Danio rerio]
90	Q07204	585118	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
91	BAF11578	113548135	Os03g0267300 [Oryza sativa (japonica cultivar-group)]
92	2FIXL	90109451	Chain L, Structure Of Human Liver Fbpase Complexed With Potent Benzoxazole Allosteric Inhibitiors
93	2FHYL	90109424	Chain L, Structure Of Human Liver Fpbase Complexed With A Novel Benzoxazole As Allosteric Inhibitor
94	XP_001...	109112377	PREDICTED: fructose-1,6-bisphosphatase 1 isoform 2 [Macaca mulatta]
95	1FTAD	1311149	Chain D, Fructose-1,6-Bisphosphatase(D-Fructose-1,6-Bisphosphate, 1-Phosphohydrolase) (E.C.3.1.3.11) Complexed With The Allosteric Inhibitor Amp
96	CAH72692	55662224	fructose-1,6-bisphosphatase 1 [Homo sapiens]
97	CAG08190	47221528	unnamed protein product [Tetraodon nigroviridis]
98	XP_533504	73946534	PREDICTED: similar to Fructose-1,6-bisphosphatase isozyme

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			2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) [Canis familiaris]
99	AAC25774	3293553	fructose-1,6-bisphosphatase [Homo sapiens]
100	AAA35817	182311	fructose-1,6-bisphosphatase
101	AAD12243	4218951	fructose-1,6-bisphosphatase precursor [Brassica napus]
102	NP_001...	114051459	hypothetical protein LOC514066 [Bos taurus]
103	P09195	119745	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
104	NP_001...	57524507	hypothetical protein LOC445505 [Danio rerio]
105	NP_001...	114051287	fructose-1,6-bisphosphatase [Bombyx mori]
106	NP_001...	73853862	hypothetical protein LOC613108 [Xenopus tropicalis]
107	AAD25541	4585576	fructose-1,6-bisphosphatase precursor [Solanum tuberosum]
108	Q9N0J6	75067927	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2)
109	AAN31884	23397203	putative fructose-bisphosphatase precursor [Arabidopsis thaliana]
110	AAH81229	51703601	Unknown (protein for MGC:85456) [Xenopus laevis]
111	P22418	3915687	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
112	CAA41154	11242	fructose-bisphosphatase [Arabidopsis thaliana]
113	XP_001...	109112375	PREDICTED: fructose-1,6-bisphosphatase 1 isoform 1 [Macaca mulatta]
114	P70695	76363514	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2) (RAE-30)
115	CAG08189	47221527	unnamed protein product [Tetraodon nigroviridis]
116	AAI13633	109731177	Fructose-1,6-bisphosphatase 2 [Homo sapiens]
117	1SPID	999624	Chain D, Fructose-1,6-Bisphosphatase (D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase) (E.C.3.1.3.11)
118	AAF72973	8118281	fructose-1,6-bisphosphatase [Zaocys dhumnades]
119	AAH12720	15215255	Fbp2 protein [Mus musculus]
120	O00757	76789651	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2)
121	XP_827196	71745132	fructose-1,6-bisphosphate cytosolic [Trypanosoma brucei TREU927]
122	Q9Z1N1	76364186	Fructose-1,6-bisphosphatase isozyme 2 (D-fructose-1,6-bisphosphate 1-phosphohydrolase 2) (FBPase 2)
123	BAE40306	74212301	unnamed protein product [Mus musculus]
124	CAC70747	15718373	fructose-1,6-bisphosphatase [Trypanosoma brucei]
125	NP_032020	6679761	fructose bisphosphatase 2 [Mus musculus]
126	AAP79192	32307574	fructose-1,6 bisphosphatase [Bigelowiella natans]
127	ZP_010...	86130901	fructose-1,6-bisphosphatase [Cellulophaga sp. MED134]
128	YP_422024	83311760	Fructose-1,6-bisphosphatase [Magnetospirillum magneticum AMB-1]
129	YP_679484	110639275	fructose-1,6-bisphosphatase [Cytophaga hutchinsonii ATCC 33406]
130	ZP_000...	23014308	COG0158: Fructose-1,6-bisphosphatase [Magnetospirillum magnetotacticum MS-1]
131	XP_888627	76363832	Leishmania major strain Friedlin cytosolic fructose-1,6-bisphosphatase [Leishmania major strain Friedlin]
132	ZP_009...	83855881	fructose-1,6-bisphosphatase [Croceibacter atlanticus HTCC2559]
133	YP_437516	83649081	Fructose-1,6-bisphosphatase [Hahella chejuensis KCTC 2396]
134	ZP_011...	88711300	fructose-1,6-bisphosphatase [Flavobacteriales bacterium

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			HTCC2170]
135	CAC82800	16519317	fructose 1,6-bisphosphatase [Galdieria sulphuraria]
136	ZP_012...	91215105	fructose-1,6-bisphosphatase [Psychroflexus torquis ATCC 700755]
137	ZP_012...	90591576	Inositol phosphatase/fructose-1,6-bisphosphatase [Flavobacterium johnsoniae UW101]
138	XP_793452	72046390	PREDICTED: similar to fructose-1,6-bisphosphatase 1, like [Strongylocentrotus purpuratus]
139	CAJ72223	91202584	strongly similar to fructose-1,6-bisphosphatase [Candidatus Kuenenia stuttgartiensis]
140	ZP_011...	88804197	fructose-1,6-bisphosphatase [Robiginitalea biformata HTCC2501]
141	YP_445598	83815956	fructose-1,6-bisphosphatase [Salinibacter ruber DSM 13855]
142	ZP_007...	75815977	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae V52]
143	ZP_011...	88802508	fructose-1,6-bisphosphatase [Polaribacter irgensii 23-P]
144	ZP_007...	75827798	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae O395]
145	ZP_011...	88797163	Fructose-1,6-bisphosphatase [Reinekea sp. MED297]
146	ZP_005...	68553442	Inositol phosphatase/fructose-1,6-bisphosphatase [Prosthecochloris aestuarii DSM 271]
147	ZP_007...	75830525	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae MO10]
148	Q42796	2494415	Fructose-1,6-bisphosphatase, chloroplast precursor (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase)
149	ZP_007...	75822783	COG0158: Fructose-1,6-bisphosphatase [Vibrio cholerae RC385]
150	NP_933227	37678618	fructose-1,6-bisphosphatase [Vibrio vulnificus YJ016]
151	XP_812636	71423971	fructose-1,6-bisphosphatase, cytosolic [Trypanosoma cruzi strain CL Brener]
152	ZP_006...	71480926	Inositol phosphatase/fructose-1,6-bisphosphatase [Prosthecochloris vibrioformis DSM 265]
153	ZP_007...	75854570	COG0158: Fructose-1,6-bisphosphatase [Vibrio sp. Ex25]
154	NP_931714	37528369	fructose-1,6-bisphosphatase [Photorhabdus luminescens subsp. laumondii TTO1]
155	XP_805839	71406635	fructose-1,6-bisphosphatase, cytosolic [Trypanosoma cruzi strain CL Brener]
156	YP_374392	78186349	fructose-1,6-bisphosphatase [Pelodictyon luteolum DSM 273]
157	NP_902097	34497882	fructose-1,6-bisphosphatase [Chromobacterium violaceum ATCC 12472]
158	XP_646323	66825937	D-fructose-1,6-bisphosphate 1-phosphohydrolase [Dictyostelium discoideum AX4]
159	ZP_010...	86147594	fructose-1,6-bisphosphatase [Vibrio sp. MED222]
160	NP_796691	28897086	fructose-1,6-bisphosphatase [Vibrio parahaemolyticus RIMD 2210633]
161	YP_052014	50122847	fructose-1,6-bisphosphatase [Erwinia carotovora subsp. atroseptica SCRI1043]
162	ZP_007...	77634762	COG0158: Fructose-1,6-bisphosphatase [Yersinia pestis Angola]
163	ZP_012...	90406722	fructose-1,6-bisphosphatase [Psychromonas sp. CNPT3]
164	ZP_006...	71549000	Inositol phosphatase/fructose-1,6-bisphosphatase [Nitrosomonas eutropha C71]
165	ZP_013...	106882698	Inositol phosphatase/fructose-1,6-bisphosphatase [Psychromonas ingrahamii 37]

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166	ZP_008...	77973994	COG0158: Fructose-1,6-bisphosphatase [Yersinia frederiksenii ATCC 33641]
167	ZP_012...	90411963	fructose-1,6-bisphosphatase [Photobacterium profundum 3TCK]
168	ZP_005...	67938188	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobium phaeobacteroides BS1]
169	NP_991956	45440417	fructose-1,6-bisphosphatase [Yersinia pestis biovar Microtus str. 91001]
170	NP_840606	30248536	fructose-1,6-bisphosphatase [Nitrosomonas europaea ATCC 19718]
171	YP_649191	108813424	fructose-1,6-bisphosphatase [Yersinia pestis Nepal516]
172	ZP_010...	86134593	fructose-1,6-bisphosphatase [Tenacibaculum sp. MED152]
173	ZP_012...	94268582	Inositol phosphatase/fructose-1,6-bisphosphatase [delta proteobacterium MLMS-1]
174	ZP_012...	94264279	Inositol phosphatase/fructose-1,6-bisphosphatase [delta proteobacterium MLMS-1]
175	ZP_005...	67919158	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobium limicola DSM 245]
176	NP_661262	21673197	fructose-1,6-bisphosphatase [Chlorobium tepidum TLS]
177	YP_128618	54307598	fructose-1,6-bisphosphatase [Photobacterium profundum SS9]
178	YP_378918	78188580	fructose-1,6-bisphosphatase [Chlorobium chlorochromatii CaD3]
179	ZP_005...	68551142	Inositol phosphatase/fructose-1,6-bisphosphatase [Pelodictyon phaeoclathratiforme BU-1]
180	YP_445968	83814754	fructose-1,6-bisphosphatase [Salinibacter ruber DSM 13855]
181	ZP_012...	90580816	fructose-1,6-bisphosphatase [Vibrio angustum S14]
182	ZP_011...	89075542	fructose-1,6-bisphosphatase [Photobacterium sp. SKA34]
183	YP_342093	77163568	fructose-1,6-bisphosphatase [Nitrosococcus oceani ATCC 19707]
184	ZP_009...	84387793	fructose-1,6-bisphosphatase [Vibrio splendidus 12B01]
185	ZP_010...	86141292	fructose-1,6-bisphosphatase [Flavobacterium sp. MED217]
186	ZP_005...	67937321	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobium phaeobacteroides DSM 266]
187	ZP_012...	91228829	fructose-1,6-bisphosphatase [Vibrio alginolyticus 12G01]
188	ZP_008...	77961846	COG0158: Fructose-1,6-bisphosphatase [Yersinia mollaretii ATCC 43969]
189	ZP_008...	77977605	COG0158: Fructose-1,6-bisphosphatase [Yersinia intermedia ATCC 29909]
190	YP_203647	59710871	fructose-1,6-bisphosphatase [Vibrio fischeri ES114]
191	ZP_013...	110596824	Inositol phosphatase/fructose-1,6-bisphosphatase [Chlorobium ferrooxidans DSM 13031]
192	YP_454036	85058334	fructose-1,6-bisphosphatase [Sodalis glossinidius str. 'morsitans']
193	ZP_001...	32035025	COG0158: Fructose-1,6-bisphosphatase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]
194	YP_011058	46580250	fructose-1,6-bisphosphatase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]
195	YP_219276	62182859	fructose-1,6-bisphosphatase [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
196	YP_560077	91784871	Inositolphosphatase/fructose-1,6-bisphosphatase [Burkholderia xenovorans LB400]
197	YP_316335	74318595	fructose-1,6-bisphosphatase [Thiobacillus denitrificans ATCC 25259]

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198	YP_388561	78357112	fructose-1,6-bisphosphatase [Desulfovibrio desulfuricans G20]
199	NP_313236	15834463	fructose-1,6-bisphosphatase [Escherichia coli O157:H7 str. Sakai]
200	YP_313128	74314709	fructose-bisphosphatase [Shigella sonnei Ss046]
201	ZP_011...	88801533	fructose-1,6-bisphosphatase [Polaribacter irgensii 23-P]

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Table 53. Examples of squalene epoxidase polypeptides

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	XP_503994	50553168	hypothetical protein [Yarrowia lipolytica].
2	EAS30670	90301039	hypothetical protein CIMG_06149 [Coccidioides immitis RS]
3	XP_753858	70998268	squalene monooxygenase Erg1 [Aspergillus fumigatus Af293]
4	XP_711894	68488538	squalene epoxidase [Candida albicans SC5314]
5	ABD48706	88697124	squalene epoxidase [Emericella nidulans]
6	XP_681020	67901528	hypothetical protein AN7751.2 [Aspergillus nidulans FGSC A4]
7	AAQ18215	33415411	squalene epoxidase [Trichophyton rubrum]
8	BAE62359	83772229	unnamed protein product [Aspergillus oryzae]
9	AAQ18216	61807216	squalene epoxidase [Trichophyton rubrum]
10	AAZ08563	70797544	squalene epoxidase [Trichophyton rubrum]
11	CAJ18281	90185988	squalene epoxidase [Hypocrea lixii]
12	XP_462160	50427105	hypothetical protein DEHA0G15202g [Debaryomyces hansenii CBS767]
13	NP_011691	6321614	Squalene epoxidase, catalyzes the epoxidation of squalene to 2,3-oxidosqualene; plays an essential role in the ergosterol-biosynthesis pathway and is the specific target of the antifungal drug terbinafine; Erg1p [Saccharomyces cerevisiae]
14	AAA34592	171471	squalene epoxidase
15	O13306	51704232	Squalene monooxygenase (Squalene epoxidase) (SE)
16	XP_455763	50311477	unnamed protein product [Kluyveromyces lactis]
17	XP_386391	46123675	hypothetical protein FG06215.1 [Gibberella zeae PH-1]
18	EAQ88139	88180671	hypothetical protein CHGG_04758 [Chaetomium globosum CBS 148.51]
19	XP_961806	85104779	hypothetical protein [Neurospora crassa OR74A]
20	XP_758545	71012984	hypothetical protein UM02398.1 [Ustilago maydis 521]
21	XP_369325	39975869	hypothetical protein MG06139.4 [Magnaporthe grisea 70-15]
22	XP_570092	58265872	squalene monooxygenase [Cryptococcus neoformans var. neoformans JEC21]
23	Q9C1W3	51701448	Probable squalene monooxygenase (Squalene epoxidase) (SE)
24	EAT79729	110586009	hypothetical protein SNOG_12929 [Phaeosphaeria nodorum SN15]
25	CAG38355	108743007	squalene epoxidase [Aspergillus niger]
26	BAE73094	84579321	hypothetical protein [Macaca fascicularis]
27	EAU31524	114189824	hypothetical protein ATEG_08351 [Aspergillus terreus NIH2624]
28	NP_003120	62865635	squalene monooxygenase [Homo sapiens]
29	CAI46076	57997512	hypothetical protein [Homo sapiens]
30	BAE37374	74200967	unnamed protein product [Mus musculus]
31	XP_850640	73974448	PREDICTED: similar to squalene monooxygenase isoform 1 [Canis familiaris]
32	Q75F69	51701415	Squalene monooxygenase (Squalene epoxidase) (SE)
33	AAS60234	45388098	squalene epoxidase 1 [Aspergillus fumigatus]
34	Q14534	12644414	Squalene monooxygenase (Squalene epoxidase) (SE)
35	XP_001...	109087424	PREDICTED: similar to squalene monooxygenase [Macaca mulatta]
36	AAH97330	66911977	Sqle protein [Rattus norvegicus]
37	EAU30782	114189082	hypothetical protein ATEG_08650 [Aspergillus terreus NIH2624]

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38	CAF98057	47218525	unnamed protein product [Tetraodon nigroviridis]
39	XP_861944	73974450	PREDICTED: similar to squalene monooxygenase isoform 2 [Canis familiaris]
40	ABF94794	108706999	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
41	BAF11377	113547934	Os03g0231800 [Oryza sativa (japonica cultivar-group)]
42	XP_470614	50920507	Putative Squalene monooxygenase [Oryza sativa (japonica cultivar-group)]
43	ABF94791	108706996	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
44	AAM61384	21537043	squalene epoxidase-like protein [Arabidopsis thaliana]
45	BAE98940	110742002	hypothetical protein [Arabidopsis thaliana]
46	ABE84801	92877833	Helix-turn-helix, AraC type; NAD-binding site; Fumarate lyase [Medicago truncatula]
47	BAE36598	74183459	unnamed protein product [Mus musculus]
48	XP_693698	68403773	PREDICTED: similar to squalene monooxygenase [Danio rerio]
49	CAB80441	7270759	squalene epoxidase-like protein [Arabidopsis thaliana]
50	O48651	6685403	Squalene monooxygenase (Squalene epoxidase) (SE)
51	AAY22200	62945915	squalene monooxygenase [Datura innoxia]
52	BAD15330	46359651	squalene epoxidase [Panax ginseng]
53	CAD23248	27475610	squalene monooxygenase 2 [Medicago truncatula]
54	ABC94943	86371770	squalene epoxidase [Medicago sativa]
55	CAD23249	27475612	squalene monooxygenase 1 [Medicago truncatula]
56	AAN15558	23198062	squalene monooxygenase, putative [Arabidopsis thaliana]
57	NP_179868	15227757	oxidoreductase [Arabidopsis thaliana]
58	AAG50645	12321049	squalene monooxygenase, putative [Arabidopsis thaliana]
59	XP_629022	66800193	hypothetical protein DDBDRAFT_0192021 [Dictyostelium discoideum AX4]
60	CAK11466	94733753	novel protein similar to vertebrate squalene epoxidase (SQLE) [Danio rerio]
61	AAQ13595	33337947	putative squalene epoxidase [Lycopersicon esculentum]
62	ABF94792	108706997	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
63	XP_604908	76660360	PREDICTED: similar to squalene monooxygenase [Bos taurus]
64	BAA11209	1483186	squalene epoxidase [Homo sapiens]
65	NP_197803	15237902	SQP1 [Arabidopsis thaliana]
66	NP_001...	79328611	SQP1 [Arabidopsis thaliana]
67	CAA06772	3123331	squalene epoxidase homologue [Arabidopsis thaliana]
68	O65726	6685410	Squalene monooxygenase 1,2 (Squalene epoxidase 1,2) (SE 1,2)
69	O65727	6685411	Squalene monooxygenase 1,1 (Squalene epoxidase 1,1) (SE 1,1)
70	NP_197804	15237903	oxidoreductase [Arabidopsis thaliana]
71	CAJ03182	68125205	squalene monooxygenase-like protein [Leishmania major]
72	NP_197802	15237900	SQP2; oxidoreductase [Arabidopsis thaliana]
73	XP_828409	71754989	squalene monooxygenase [Trypanosoma brucei TREU927]
74	XP_808343	71412304	squalene monooxygenase [Trypanosoma cruzi strain CL Brener]
75	XP_789059	72038634	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
76	XP_796297	72133073	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
77	AAB69189	2352528	squalene epoxidase [Candida glabrata]

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78	XP_813434	71649420	squalene monooxygenase [Trypanosoma cruzi strain CL Brener]
79	XP_796261	72133071	PREDICTED: similar to squalene monooxygenase [Strongylocentrotus purpuratus]
80	XP_793783	72114550	PREDICTED: similar to squalene monooxygenase, partial [Strongylocentrotus purpuratus]
81	XP_789028	72038632	PREDICTED: similar to squalene xygenase [Strongylocentrotus purpuratus]
82	AAT97087	51105054	squalene epoxidase-like protein [Lymnaea stagnalis]
83	XP_804343	71402993	squalene monooxygenase [Trypanosoma cruzi strain CL Brener]
84	YP_115265	53803024	monooxygenase family protein [Methylococcus capsulatus str. Bath]
85	AAM91177	22136198	unknown protein [Arabidopsis thaliana]
86	XP_799134	72026766	PREDICTED: similar to Squalene monooxygenase (Squalene epoxidase) (SE), partial [Strongylocentrotus purpuratus]

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Table 54. Examples of ERG1 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAA34592	171471	squalene epoxidase
2	O13306	51704232	Squalene monooxygenase (Squalene epoxidase) (SE)
3	XP_455763	50311477	unnamed protein product [Kluyveromyces lactis]
4	Q75F69	51701415	Squalene monooxygenase (Squalene epoxidase) (SE)
5	XP_462160	50427105	hypothetical protein DEHA0G15202g [Debaryomyces hansenii CBS767]
6	XP_711894	68488538	squalene epoxidase [Candida albicans SC5314]
7	XP_503994	50553168	hypothetical protein [Yarrowia lipolytica]
8	AAB69189	2352528	squalene epoxidase [Candida glabrata]
9	AAQ18215	33415411	squalene epoxidase [Trichophyton rubrum]
10	AAQ18216	61807216	squalene epoxidase [Trichophyton rubrum]
11	AAZ08563	70797544	squalene epoxidase [Trichophyton rubrum]
12	EAS30670	90301039	hypothetical protein CIMG_06149 [Coccidioides immitis RS]
13	Q9C1W3	51701448	Probable squalene monooxygenase (Squalene epoxidase) (SE)
14	XP_758545	71012984	hypothetical protein UM02398.1 [Ustilago maydis 521]
15	XP_681020	67901528	hypothetical protein AN7751.2 [Aspergillus nidulans FGSC A4]
16	ABD48706	88697124	squalene epoxidase [Emericella nidulans]
17	BAE62359	83772229	unnamed protein product [Aspergillus oryzae]
18	XP_753858	70998268	squalene monooxygenase Erg1 [Aspergillus fumigatus Af293]
19	XP_961806	85104779	hypothetical protein [Neurospora crassa OR74A]
20	XP_386391	46123675	hypothetical protein FG06215.1 [Gibberella zeae PH-1]
21	CAJ18281	90185988	squalene epoxidase [Hypocrea lixii]
22	BAE73094	84579321	hypothetical protein [Macaca fascicularis]
23	BAE37374	74200967	unnamed protein product [Mus musculus]
24	XP_570092	58265872	squalene monooxygenase [Cryptococcus neoformans var. neoformans JEC21]
25	NP_003120	62865635	squalene monooxygenase [Homo sapiens]
26	EAT79729	111058609	hypothetical protein SNOG_12929 [Phaeosphaeria nodorum SN15]
27	AAH97330	66911977	Sqle protein [Rattus norvegicus]
28	CAI46076	57997512	hypothetical protein [Homo sapiens]
29	CAF98057	47218525	unnamed protein product [Tetraodon nigroviridis]
30	XP_850640	73974448	PREDICTED: similar to squalene monooxygenase isoform 1 [Canis familiaris]
31	XP_369325	39975869	hypothetical protein MG06139.4 [Magnaporthe grisea 70-15]
32	Q14534	12644414	Squalene monooxygenase (Squalene epoxidase) (SE)
33	XP_001...	109087424	PREDICTED: similar to squalene monooxygenase [Macaca mulatta]
34	EAQ88139	88180671	hypothetical protein CHGG_04758 [Chaetomium globosum CBS 148.51]
35	XP_693698	68403773	PREDICTED: similar to squalene monooxygenase [Danio rerio]
36	CAG38355	108743007	squalene epoxidase [Aspergillus niger]
37	XP_861944	73974450	PREDICTED: similar to squalene monooxygenase isoform 2 [Canis familiaris]
38	XP_519950	55631226	PREDICTED: similar to squalene epoxidase [Pan troglodytes]
39	AAS60234	45388098	squalene epoxidase 1 [Aspergillus fumigatus]
40	XP_629022	66800193	hypothetical protein DDBDRAFT_0192021 [Dictyostelium discoideum AX4]
41	CAK11466	94733753	novel protein similar to vertebrate squalene epoxidase (SQLE) [Danio rerio]
42	BAE98940	110742002	hypothetical protein [Arabidopsis thaliana]
43	AAM61384	21537043	squalene epoxidase-like protein [Arabidopsis thaliana]
44	ABC94943	86371770	squalene epoxidase [Medicago sativa]
45	CAB80441	7270759	squalene epoxidase-like protein [Arabidopsis thaliana]
46	CAD23248	27475610	squalene monooxygenase 2 [Medicago truncatula]

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47	BAE36598	74183459	unnamed protein product [Mus musculus]
48	AAQ13595	33337947	putative squalene epoxidase [Lycopersicon esculentum]
49	AAY22200	62945915	squalene monooxygenase [Datura innoxia]
50	ABF94791	108706996	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
51	AAN15558	23198062	squalene monooxygenase, putative [Arabidopsis thaliana]
52	ABF94794	108706999	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
53	XP_470614	50920507	Putative Squalene monooxygenase [Oryza sativa (japonica cultivar-group)]
54	BAF11377	113547934	Os03g0231800 [Oryza sativa (japonica cultivar-group)]
55	CAD23249	27475612	squalene monooxygenase 1 [Medicago truncatula]
56	AAG50645	12321049	squalene monooxygenase, putative [Arabidopsis thaliana]
57	NP_179868	15227757	oxidoreductase [Arabidopsis thaliana]
58	ABE84801	92877833	Helix-turn-helix, AraC type; NAD-binding site; Fumarate lyase [Medicago truncatula]
59	ABF94792	108706997	Squalene monooxygenase, putative, expressed [Oryza sativa (japonica cultivar-group)]
60	BAA11209	1483186	squalene epoxidase [Homo sapiens]
61	XP_604908	76660360	PREDICTED: similar to squalene monooxygenase [Bos taurus]
62	XP_828409	71754989	squalene monooxygenase [Trypanosoma brucei TREU927]
63	XP_808343	71412304	squalene monooxygenase [Trypanosoma cruzi strain CL Brener]
64	CAJ03182	68125205	squalene monooxygenase-like protein [Leishmania major]
65	O65726	6685410	Squalene monooxygenase 1,2 (Squalene epoxidase 1,2) (SE 1,2)
66	NP_197804	15237903	oxidoreductase [Arabidopsis thaliana]
67	O65727	6685411	Squalene monooxygenase 1,1 (Squalene epoxidase 1,1) (SE 1,1)
68	CAA06772	3123331	squalene epoxidase homologue [Arabidopsis thaliana]
69	NP_001...	79328611	SQP1 [Arabidopsis thaliana]
70	NP_197803	15237902	SQP1 [Arabidopsis thaliana]
71	NP_197802	15237900	SQP2; oxidoreductase [Arabidopsis thaliana]

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Table 55. Examples of ERG7 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAT93062	51013537	YHR072W [Saccharomyces cerevisiae]
2	AAA16975	465105	lanosterol synthase
3	XP_448182	50291499	unnamed protein product [Candida glabrata]
4	XP_451982	50304065	unnamed protein product [Kluyveromyces lactis]
5	NP_987017	45201447	AGR351Wp [Eremothecium gossypii]
6	XP_457937	50418833	hypothetical protein DEHA0C06501g [Debaryomyces hansenii CBS767]
7	XP_722471	68467112	2,3-oxidosqualene-lanosterol cyclase [Candida albicans SC5314]
8	XP_722612	68466833	2,3-oxidosqualene-lanosterol cyclase [Candida albicans SC5314]
9	1903190A	383419	oxidosqualene cyclase
10	XP_504990	50555163	hypothetical protein [Yarrowia lipolytica]
11	AAB08472	1549343	inactive oxidosqualene-lansoterol cyclase [Saccharomyces cerevisiae]
12	Q96WJ0	30913110	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)
13	XP_747936	70984860	oxidosqualene:lanosterol cyclase [Aspergillus fumigatus Af293]
14	BAE61626	83771494	unnamed protein product [Aspergillus oryzae]
15	NP_593702	63054562	lanosterol synthase activity [Schizosaccharomyces pombe 972h-]
16	XP_758387	71010409	hypothetical protein UM02240.1 [Ustilago maydis 521]
17	XP_681529	67902546	hypothetical protein AN8260.2 [Aspergillus nidulans FGSC A4]
18	EAS37438	90307807	hypothetical protein CIMG_02792 [Coccidioides immitis RS]
19	XP_961026	85100788	lanosterol synthase related protein [MIPS] [Neurospora crassa OR74A]
20	XP_751627	70993560	oxidosqualene:lanosterol cyclase [Aspergillus fumigatus Af293]
21	EAQ86439	88178971	hypothetical protein CHGG_07692 [Chaetomium globosum CBS 148.51]
22	XP_386126	46123145	hypothetical protein FG05950.1 [Gibberella zeae PH-1]
23	BAE63415	83773288	unnamed protein product [Aspergillus oryzae]
24	EAS31167	90301536	hypothetical protein CIMG_06646 [Coccidioides immitis RS]
25	EAT81661	111060541	hypothetical protein SNOG_11162 [Phaeosphaeria nodorum SN15]
26	XP_570450	58266588	lanosterol synthase [Cryptococcus neoformans var. neoformans JEC21]
27	AAL56020	18028346	oxidosqualene:lanosterol cyclase [Cephalosporium caerulens]
28	BAC37102	26346907	unnamed protein product [Mus musculus]
29	Q8BLN5	62286881	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)
30	XP_001...	109065021	PREDICTED: lanosterol synthase isoform 2 [Macaca mulatta]
31	1W6KA	56966682	Chain A, Structure Of Human Osc In Complex With Lanosterol
32	BAC31739	26336108	unnamed protein product [Mus musculus]
33	XP_646246	66825783	hypothetical protein DDB_0191311 [Dictyostelium discoideum AX4]
34	AAF80384	8886139	cycloartenol synthase [Dictyostelium discoideum]
35	CAB42828	4808278	lanosterol synthase [Homo sapiens]
36	1W6JA	56966681	Chain A, Structure Of Human Osc In Complex With Ro 48-8071
37	BAA08208	639865	2,3-oxidosqualene:lanosterol cyclase [Rattus norvegicus]
38	NP_112311	13591981	lanosterol synthase [Rattus norvegicus]
39	NP_001...	114053041	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) [Bos taurus]
40	P48450	62296496	Lanosterol synthase (Oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC)
41	NP_001...	57529773	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) [Gallus gallus]
42	XP_751356	70993016	oxidosqualene cyclase [Aspergillus fumigatus Af293]
43	CAG08284	47222029	unnamed protein product [Tetraodon nigroviridis]
44	BAB83085	18147590	cycloartenol synthase [Betula platyphylla]
45	BAA76902	4589852	cycloartenol synthase [Glycyrrhiza glabra]
46	BAE61719	83771588	unnamed protein product [Aspergillus oryzae]
47	BAA33460	3688598	Cycloartenol Synthase [Panax ginseng]
48	XP_001...	109065023	PREDICTED: lanosterol synthase isoform 1 [Macaca mulatta]

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49	BAD34644	50896401	cycloartenol synthase [Cucurbita pepo]
50	BAA85266	6045133	cycloartenol synthase [Luffa aegyptiaca]
51	BAB83253	18147771	cycloartenol synthase [Costus speciosus]
52	ABB76767	82468805	cycloartenol synthase [Ricinus communis]
53	BAA23533	2627181	cycloartenol synthase [Pisum sativum]
54	BAD34645	50896403	cucurbitadienol synthase [Cucurbita pepo]
55	BAE53431	83016479	cycloartenol synthase [Lotus japonicus]
56	AAS83469	46242746	cycloartenol synthase [Bupleurum kaoi]
57	A49398	541855	cycloartenol synthase (EC 5.4.99.8) - Arabidopsis thaliana
58	AAN64509	24796994	At2g07050/T4E14.16 [Arabidopsis thaliana]
59	BAD34646	50896405	putative oxidosqualene cyclase [Cucurbita pepo]
60	AAC04931	452446	cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]
61	BAE95408	108743265	lanosterol synthase [Arabidopsis thaliana]
62	AAG44096	12004573	cycloartenol synthase [Abies magnifica]
63	AAS01524	41387168	cycloartenol synthase [Centella asiatica]
64	BAB83086	18147592	cycloartenol synthase [Betula platyphylla]
65	AAF03375	6090879	putative cycloartenol synthase [Oryza sativa]
66	BAF07762	113535379	Os02g0139700 [Oryza sativa (japonica cultivar-group)]
67	BAE95410	108743269	lanosterol synthase [Lotus japonicus]
68	AAK82995	15076959	lanosterol synthase [Trypanosoma cruzi]
69	XP_820967	71668047	lanosterol synthase [Trypanosoma cruzi strain CL Brener]
70	BAA85267	6045135	oxidosqualene cyclase [Luffa aegyptiaca]
71	NP_190099	42565553	catalytic/ lyase [Arabidopsis thaliana]
72	AAT38889	47834383	cycloartenol synthase [Avena longiglumis]
73	BAA86933	6456469	oxidosqualene cyclase [Taraxacum officinale]
74	AAT38891	47834387	cycloartenol synthase [Avena strigosa]
75	CAC84559	15866702	cycloartenol synthase [Avena strigosa]
76	AAT38890	47834385	cycloartenol synthase [Avena prostrata]
77	AAT38888	47834381	cycloartenol synthase [Avena longiglumis]
78	AAT38887	47834379	cycloartenol synthase [Avena clauda]
79	AAT38892	47834389	cycloartenol synthase [Avena ventricosa]
80	XP_819758	71665580	lanosterol synthase [Trypanosoma cruzi strain CL Brener]
81	BAA86930	6456434	lupeol synthase [Olea europaea]
82	CAA61078	984145	lanosterol synthase [Homo sapiens]
83	BAA33462	3688602	Oxidosqualene Cyclase [Panax ginseng]
84	AAG26328	11023151	lanosterol synthase [Trypanosoma brucei brucei]
85	XP_825673	71752517	lanosterol synthase [Trypanosoma brucei TREU927]
86	BAA86932	6456467	lupeol synthase [Taraxacum officinale]
87	CAD23247	27475608	beta-amyrin synthase [Medicago truncatula]
88	BAA97558	8918271	beta-amyrin synthase [Pisum sativum]
89	BAA86931	6456465	cycloartenol synthase [Olea europaea]
90	BAD08587	41687978	lupeol synthase [Glycyrrhiza glabra]
91	BAA84603	5922599	oxidosqualene cyclase [Allium macrostemon]
92	AAO33578	28194504	beta-amyrin synthase [Medicago truncatula]
93	BAB83087	18147594	lupeol synthase [Betula platyphylla]
94	BAB83254	18147773	multifunctional triterpene synthase [Costus speciosus]
95	BAA89815	6730969	beta-amyrin synthase [Glycyrrhiza glabra]
96	BAE53429	83016474	beta-amyrin synthase [Lotus japonicus]
97	AAO33579	28194506	putative beta-amyrin synthase [Lotus japonicus]
98	BAA33461	3688600	beta-Amyrin Synthase [Panax ginseng]
99	CAB72151	6911851	oxidosqualene cyclase-like protein [Arabidopsis thaliana]

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100	CAJ02110	68124127	lanosterol synthase, putative [Leishmania major]
101	BAA33722	3721856	beta-Amyrin Synthase [Panax ginseng]
102	AAX14716	60203059	beta-amyrin synthase [Aster sedifolius]
103	BAE53430	83016477	lupeol synthase [Lotus japonicus]
104	ABE91090	92892072	Prenyltransferase/squalene oxidase [Medicago truncatula]
105	XP_681518	67902524	hypothetical protein AN8249.2 [Aspergillus nidulans FGSC A4]
106	AAC17080	3152599	Strong similarity to lupeol synthase gb|U49919 and cycloartenol synthase gb|U02555 from A. thaliana (the third gene with similar homology). [Arabidopsis thaliana]
107	BAF28067	113644926	Os11g0286800 [Oryza sativa (japonica cultivar-group)]
108	NP_683508	22330736	beta-amyrin synthase [Arabidopsis thaliana]
109	AAS83468	46242744	beta-armyrin synthase [Bupleurum kaoi]
110	AAO33580	28194508	multifunctional beta-amyrin synthase [Lotus japonicus]
111	BAE43642	73991374	beta-amyrin synthase [Euphorbia tirucalli]
112	BAB83088	18147596	beta-amyrin synthase [Betula platyphylla]
113	ABB76766	82468803	lupeol synthase [Ricinus communis]
114	ABG22399	108864084	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultivar-group)]
115	BAF28063	113644922	Os11g0285000 [Oryza sativa (japonica cultivar-group)]
116	ABG22398	108864083	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultivar-group)]
117	NP_849903	30699380	LUP1 (LUPEOL SYNTHASE 1); lupeol synthase [Arabidopsis thaliana]
118	AAB94341	2738027	2,3-oxidosqualene-triterpenoid cyclase [Arabidopsis thaliana]
119	AAN77001	25991999	2,3-oxidosqualene-triterpene cyclase [Arabidopsis thaliana]
120	AAT38893	47834391	beta-amyrin synthase [Avena clauda]
121	AAD05032	1762150	lupeol synthase [Arabidopsis thaliana]
122	NP_178017	30699377	ATLUP2; lupeol synthase [Arabidopsis thaliana]
123	ABE88599	92887080	squalene/oxidosqualene cyclases [Medicago truncatula]
124	ABG22449	108864253	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultivar-group)]
125	BAB68529	15787841	isomultiflorenol synthase [Luffa aegyptiaca]
126	AAT38898	47834401	beta-amyrin synthase [Avena ventricosa]
127	AAT38894	47834393	beta-amyrin synthase [Avena longiglumis]
128	AAT38897	47834399	beta-amyrin synthase [Avena strigosa]
129	NP_178016	22330734	catalytic/ lyase [Arabidopsis thaliana]
130	AAT38895	47834395	beta-amyrin synthase [Avena longiglumis]
131	AAT38896	47834397	beta-amyrin synthase [Avena prostrata]
132	BAA97559	8918273	mixed-amyrin synthase [Pisum sativum]
133	AAC98864	4090722	pentacyclic triterpene synthase [Arabidopsis thaliana]
134	BAF28466	113645325	Os11g0562100 [Oryza sativa (japonica cultivar-group)]
135	AAG41762	11934652	pentacyclic triterpene synthase [synthetic construct]
136	XP_480759	50942463	putative Cycloartenol Synthase [Oryza sativa (japonica cultivar-group)]
137	BAE43643	73991380	putative oxidosqulene cyclase [Euphorbia tirucalli]
138	AAC17070	3152589	Strong similarity to lupeol synthase gb|U49919 from A. thaliana (second gene in a series of three with similar homologies). [Arabidopsis thaliana]
139	BAD15332	46359655	beta-amyrin synthase [Panax ginseng]
140	AAM23264	23428800	beta-amyrin synthase [Glycine max]
141	ABC33922	83638481	beta-amyrin synthase [Gypsophila paniculata]
142	AAS01523	41387158	putative beta-amyrin synthase [Centella asiatica]
143	BAE99758	110743847	cycloartenol synthase [Arabidopsis thaliana]
144	BAB11065	10177752	cycloartenol synthase [Arabidopsis thaliana]
145	NP_177971	15218390	catalytic [Arabidopsis thaliana]
146	CAD39196	32526539	cycloartenol synthase [Stigmatella aurantiaca]

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147	ABG22450	108864254	Cycloartenol synthase, putative, expressed [Oryza sativa (japonica cultivar-group)]
148	CAA93571	1204221	erg7 [Schizosaccharomyces pombe]
149	NP_567462	18414430	ATPEN1; catalytic/ lyase [Arabidopsis thaliana]
150	NP_199612	42568386	catalytic [Arabidopsis thaliana]
151	NP_193272	15233798	catalytic/ lyase [Arabidopsis thaliana]
152	ABE88610	92887091	squalene/oxidosqualene cyclases [Medicago truncatula]
153	AAW30034	56790234	At5g42600 [Arabidopsis thaliana]
154	BAF01935	110740066	putative lupeol synthase [Arabidopsis thaliana]
155	NP_198464	15239312	ATPEN3; catalytic [Arabidopsis thaliana]
156	BAB83089	18147598	putative oxidosqualene cyclase [Betula platyphylla]
157	YP_115266	53803023	squalene cyclase family protein [Methylococcus capsulatus str. Bath]
158	CAB78579	7268284	lupeol synthase like protein [Arabidopsis thaliana]
159	CAB78576	7268281	lupeol synthase like protein [Arabidopsis thaliana]

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Table 56. Examples of ERG6 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	CAA89944	854482	Erg6p [Saccharomyces cerevisiae]
2	P25087	462024	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
3	CAA52308	396515	S-adenosyl-methionine:delta-24-sterol-C- methyltransferase [Saccharomyces cerevisiae]
4	AAB31378	619251	putative S-adenosylmethionine-dependent methyltransferase [Saccharomyces cerevisiae]
5	Q6FRZ7	62900214	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
6	AAX73200	62178560	C24 sterol methyltransferase [Candida glabrata]
7	P_446997	50289135	unnamed protein product [Candida glabrata]
8	CAG59930	49526306	unnamed protein product [Candida glabrata CBS138]
9	AAX73199	62178558	C24 sterol methyltransferase [Candida glabrata]
10	Q6CYB3	62900210	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
11	P_451076	50302283	unnamed protein product [Kluyveromyces lactis]
12	CAH02664	49640207	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
13	Q759S7	62900245	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
14	P_984292	45188069	ADR196Wp [Eremothecium gossypii]
15	AAS52116	44982886	ADR196Wp [Ashbya gossypii ATCC 10895]
16	CAA37826	4122	unnamed protein product [Saccharomyces cerevisiae]
17	Q875K1	62900279	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
18	AAO21936	27803704	S-adenosylmethionine:D24-methyltransferase [Clavispora lusitaniae]
19	Q6BRB7	62900203	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
20	P_459253	50421405	hypothetical protein DEHA0D19151g [Debaryomyces hansenii CBS767]
21	CAG87427	49654920	unnamed protein product [Debaryomyces hansenii CBS767]
22	P_721588	68468538	SAM:delta 24-methyltransferase [Candida albicans SC5314]
23	P_721708	68468297	SAM:delta 24-methyltransferase [Candida albicans SC5314]
24	EAL02920	46443640	hypothetical protein CaO19.1631 [Candida albicans SC5314]
25	EAL02792	46443511	hypothetical protein CaO19.9199 [Candida albicans SC5314]
26	O74198	6015114	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
27	AAC26626	3323500	sterol transmethylase [Candida albicans]
28	Q6C2D9	62900205	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
29	P_505173	50555530	hypothetical protein [Yarrowia lipolytica]
30	CAG77980	49651043	unnamed protein product [Yarrowia lipolytica CLIB122]
31	P_595787	19112579	hypothetical protein SPBC16E9.05 [Schizosaccharomyces pombe 972h-]
32	O14321	6166151	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
33	CAB16897	2467267	SPBC16E9.05 [Schizosaccharomyces pombe]
34	EAT84719	111063599	hypothetical protein SNOG_08443 [Phaeosphaeria nodorum SN15]
35	EAS29698	90300067	hypothetical protein CIMG_08444 [Coccidioides immitis RS]
36	EAQ70709	86196071	hypothetical protein MGG_ch7g116 [Magnaporthe grisea 70-15]
37	P_366350	39969919	hypothetical protein MG10568.4 [Magnaporthe grisea 70-15]

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38	P_746550	70982043	sterol 24-c-methyltransferase [Aspergillus fumigatus Af293]
39	EAL84512	66844173	sterol 24-c-methyltransferase, putative [Aspergillus fumigatus Af293]
40	BAE64809	83774686	unnamed protein product [Aspergillus oryzae]
41	P_965392	85118140	probable DELTA(24)-STEROL C-METHYLTRANSFERASE [MIPS] [Neurospora crassa OR74A]
42	Q9P3R1	62900336	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
43	EAA36156	28927200	probable DELTA(24)-STEROL C-METHYLTRANSFERASE [MIPS] [Neurospora crassa]
44	CAB97289	9367272	probable DELTA(24)-STEROL C-METHYLTRANSFERASE (ERG6) [Neurospora crassa]
45	P_664750	67541965	hypothetical protein AN7146.2 [Aspergillus nidulans FGSC A4]
46	EAA61398	40742208	hypothetical protein AN7146.2 [Aspergillus nidulans FGSC A4]
47	P_382959	46111803	hypothetical protein FG02783.1 [Gibberella zeae PH-1]
48	EAA70778	42547935	hypothetical protein FG02783.1 [Gibberella zeae PH-1]
49	Q96WX4	62900323	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
50	AAK54439	14192727	S-adenosyl methionine:sterol methyl transferase [Pneumocystis carinii]
51	EAQ89522	88182054	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
52	BAA13793	41688402	unnamed protein product [Schizosaccharomyces pombe]
53	P_385916	46122725	hypothetical protein FG05740.1 [Gibberella zeae PH-1]
54	EAA75815	42552972	hypothetical protein FG05740.1 [Gibberella zeae PH-1]
55	P_361872	39944670	hypothetical protein MG04346.4 [Magnaporthe grisea 70-15]
56	Q5EN22	62900141	Sterol 24-C-methyltransferase (Delta(24)-sterol C-methyltransferase)
57	AAX07631	59802827	sterol 24-C-methyltransferase-like protein [Magnaporthe grisea]
58	BAE61033	83770900	unnamed protein product [Aspergillus oryzae]
59	P_759329	71018197	hypothetical protein UM03182.1 [Ustilago maydis 521]
60	EAK84412	46099179	hypothetical protein UM03182.1 [Ustilago maydis 521]
61	AAK00294	12642580	sterol methyl transferase [Pneumocystis carinii f. sp. carinii]
62	P_360548	39942022	hypothetical protein MG10860.4 [Magnaporthe grisea 70-15]
63	P_568887	58262954	sterol 24-C-methyltransferase [Cryptococcus neoformans var. neoformans JEC21]
64	AAW41580	57223537	sterol 24-C-methyltransferase, putative [Cryptococcus neoformans var. neoformans JEC21]
65	EAL22628	50259962	hypothetical protein CNBB2600 [Cryptococcus neoformans var. neoformans B-3501A]
66	AAC34951	3560474	S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
67	AAC04265	2909846	(S)-adenosyl-L-methionine:delta 24-sterol methyltransferase [Zea mays]
68	AAB49338	1872473	delta-24-sterol methyltransferase [Triticum aestivum]
69	Q9LM02	62901053	Cycloartenol-C-24-methyltransferase (24-sterol C-methyltransferase 1) (Sterol C-methyltransferase 1) (Protein STEROL METHYLTRANSFERASE 1) (Protein CEPHALOPOD)
70	AAN15377	23197700	24-sterol C-methyltransferase [Arabidopsis thaliana]
71	AAM53274	21539443	24-sterol C-methyltransferase [Arabidopsis thaliana]
72	P_196875	15240691	SMT1 (STEROL METHYLTRANSFERASE 1) [Arabidopsis thaliana]
73	AAG28462	11066105	sterol methyltransferase SMT1 [Arabidopsis thaliana]

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74	BAB08698	9758037	24-sterol C-methyltransferase [Arabidopsis thaliana]
75	AAF78847	8745241	SAM:cycloartenol-C24-methyltransferase [Arabidopsis thaliana]
76	AAM53553	21434843	cephalopod [Arabidopsis thaliana]
77	AAB70886	1899060	endosperm C-24 sterol methyltransferase [Zea mays]
78	AAB37769	1706965	delta-24-sterol methyltransferase [Triticum aestivum]
79	BAF21068	113610690	Os07g0206700 [Oryza sativa (japonica cultivar-group)]
80	Q6ZIX2	68566037	Cycloartenol-C-24-methyltransferase 1 (24-sterol C-methyltransferase 1) (Sterol C-methyltransferase 1)
81	P_477078	50935101	cycloartenol-C24-methyltransferase [Oryza sativa (japonica cultivar-group)]
82	BAC83238	34393309	cycloartenol-C24-methyltransferase [Oryza sativa (japonica cultivar-group)]
83	AAB04057	1399380	S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase
84	AAB62812	2246458	S-adenosyl-methionine-sterol-C- methyltransferase [Ricinus communis]
85	AAC35787	3603295	S-adenosyl-methionine cycloartenol-C24-methyltransferase [Nicotiana tabacum]
86	AAC34988	3560531	cycloartenol-C24-methyltransferase [Oryza sativa subsp. japonica]
87	AAZ83345	73761691	24-sterol C-methyltransferase [Gossypium hirsutum]
88	EAS30660	90301029	hypothetical protein CIMG_06139 [Coccidioides immitis RS]
89	P_470035	50919277	putative endosperm C-24 sterol methyltransferase [Oryza sativa (japonica cultivar-group)]
90	AAP21419	30103006	putative endosperm C-24 sterol methyltransferase [Oryza sativa (japonica cultivar-group)]
91	AAR92099	40806291	S-adenosyl-L-methionine-C-24-delta-sterol-methyltransferase B [Leishmania donovani]
92	AAR92098	40806289	S-adenosyl-L-methionine-C-24-delta-sterol-methyltransferase A [Leishmania donovani]
93	CAJ09197	68129891	sterol 24-c-methyltransferase, putative [Leishmania major]
94	CAJ09196	68129890	sterol 24-c-methyltransferase, putative [Leishmania major]
95	P_802864	71399753	sterol 24-c-methyltransferase [Trypanosoma cruzi strain CL Brener]
96	EAN81418	70865128	sterol 24-c-methyltransferase, putative [Trypanosoma cruzi]
97	P_802716	71399140	sterol 24-c-methyltransferase [Trypanosoma cruzi strain CL Brener]
98	EAN81270	70864663	sterol 24-c-methyltransferase, putative [Trypanosoma cruzi]
99	P_822930	71747750	sterol 24-c-methyltransferase [Trypanosoma brucei TREU927]
100	AAZ40214	71738257	sterol methyltransferase [Trypanosoma brucei brucei]
101	CAJ16958	70908212	s-adenosyl-L-methionine-c-24-delta-sterol-methy lt ransferase a, putative [Trypanosoma brucei]
102	EAN78102	70832598	sterol 24-c-methyltransferase, putative [Trypanosoma brucei]
103	P_636481	66805519	hypothetical protein DDBDRAFT_0188166 [Dictyostelium discoideum AX4]
104	EAL62977	60464861	hypothetical protein DDBDRAFT_0188166 [Dictyostelium discoideum AX4]
105	ABF99454	108711659	Cyclopropane-fatty-acyl-phospholipid synthase family protein, expressed [Oryza sativa (japonica cultivar-group)]
106	P_802811	71399535	sterol 24-c-methyltransferase [Trypanosoma cruzi strain CL Brener]
107	EAN81365	70864963	sterol 24-c-methyltransferase, putative [Trypanosoma cruzi]
108	ABB90541	82780739	c24-sterol methyltransferase [Paracoccidioides brasiliensis]
109	AAB62807	2246452	S-adenosyl-methionine-sterol-C-methyltransferase homolog [Nicotiana tabacum]
110	Q39227	62900893	24-methylenesterol C-methyltransferase 2 (24-sterol C-methyltransferase 2) (Sterol-C-methyltransferase 2)
111	AAM45009	21281107	putative sterol-C-methyltransferase [Arabidopsis thaliana]

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112	P_173458	15217917	SMT2 (STEROL METHYLTRANSFERASE 2) [Arabidopsis thaliana]
113	AAK76716	15028255	putative sterol-C-methyltransferase [Arabidopsis thaliana]
114	AAG48780	12083242	putative sterol-C-methyltransferase [Arabidopsis thaliana]
115	AAF88156	9558593	Identical to 24-sterol C-methyltransferase from Arabidopsis thaliana gi|2129517 and is a member of the ubiE/COQ5 methyltransferase family PF|01209. ESTs gb|T42228, gb|T46520, gb|T41746, gb|N38458, gb|AI993515, gb|AA389843, gb|AI099890, gb|AI099653 come f
116	2207220A	1587694	sterol C-methyltransferase
117	CAA61966	1061040	sterol-C-methyltransferase [Arabidopsis thaliana]
118	AAN72104	25083682	24-sterol C-methyltransferase [Arabidopsis thaliana]
119	AAM91592	22136020	24-sterol C-methyltransferase [Arabidopsis thaliana]
120	Q94JS4	67472706	24-methylenesterol C-methyltransferase 3 (24-sterol C-methyltransferase 3) (Sterol-C-methyltransferase 3)
121	AAM47339	21360447	At1g76090/T23E18_40 [Arabidopsis thaliana]
122	P_177736	15222955	SMT3; S-adenosylmethionine-dependent methyltransferase [Arabidopsis thaliana]
123	AAK52981	14030613	At1g76090/T23E18_40 [Arabidopsis thaliana]
124	AAN31890	23397216	putative sterol-C-methyltransferase [Arabidopsis thaliana]
125	AAB62809	2246456	S-adenosyl-methionine-sterol-C-methyltransferase [Arabidopsis thaliana]
126	AAB62808	2246454	S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
127	AAM63753	21555010	sterol-C-methyltransferase [Arabidopsis thaliana]
128	BAF10805	113547362	Os03g0136200 [Oryza sativa (japonica cultivar-group)]
129	ABF93854	108706059	24-methylenesterol C-methyltransferase 2, putative, expressed [Oryza sativa (japonica cultivar-group)]
130	O82427	68566013	24-methylenesterol C-methyltransferase 2 (24-sterol C-methyltransferase 2) (Sterol-C-methyltransferase 2)

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Table 57. Examples of ERG5 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	P54781	1706693	Cytochrome P450 61 (C-22 sterol desaturase)
2	AAB06217	1235991	cytochrome P450
3	CAA89116	798924	unknown [Saccharomyces cerevisiae]
4	AAU09769	51830482	YMR015C [Saccharomyces cerevisiae]
5	AAX73198	62178556	C22 sterol desaturase [Candida glabrata]
6	AAX73197	62178554	C22 sterol desaturase [Candida glabrata]
7	P_449681	50294540	hypothetical protein CAGL0M07656g [Candida glabrata CBS138]
8	CAG62657	49528995	unnamed protein product [Candida glabrata CBS138]
9	P_453562	50307167	unnamed protein product [Kluyveromyces lactis]
10	CAH00658	49642696	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
11	P_982999	45185282	ABR053Cp [Eremothecium gossypii]
12	AAS50823	44980940	ABR053Cp [Ashbya gossypii ATCC 10895]
13	P_458727	50420383	hypothetical protein DEHA0D06842g [Debaryomyces hansenii CBS767]
14	CAG86871	49654394	unnamed protein product [Debaryomyces hansenii CBS767]
15	P_888893	77022898	hypothetical protein CaJ7.0323 [Candida albicans SC5314]
16	BAE44790	76573706	hypothetical protein [Candida albicans]
17	P_716933	68478128	cytochrome P450 [Candida albicans SC5314]
18	P_717000	68477993	hypothetical protein CaO19.5178 [Candida albicans SC5314]
19	EAK98020	46438693	hypothetical protein CaO19.5178 [Candida albicans SC5314]
20	EAK97950	46438622	hypothetical protein CaO19.12645 [Candida albicans SC5314]
21	CAA21953	3850153	cytochrome P450 [Candida albicans]
22	P_500188	50545301	hypothetical protein [Yarrowia lipolytica]
23	CAG84120	49646053	unnamed protein product [Yarrowia lipolytica CLIB122]
24	BAC01142	21624361	sterol C-22 desaturase [Symbiotaphrina buchneri]
25	BAC01140	21624354	sterol C-22 desaturase [Symbiotaphrina buchneri]
26	BAC01141	21624359	sterol C-22 desaturase [Symbiotaphrina kochii]
27	BAC01139	21624352	sterol C22 desaturase [Symbiotaphrina kochii]
28	EAQ88206	88180738	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
29	P_961915	85105220	hypothetical protein [Neurospora crassa OR74A]
30	EAA32679	28923500	hypothetical protein [Neurospora crassa]
31	EAS33985	90304354	hypothetical protein CIMG_05009 [Coccidioides immitis RS]
32	P_750145	70990592	cytochrome P450 sterol C-22 desaturase [Aspergillus fumigatus Af293]
33	EAL88107	66847777	cytochrome P450 sterol C-22 desaturase, putative [Aspergillus fumigatus Af293]
34	EAT87119	111065999	hypothetical protein SNOG_06055 [Phaeosphaeria nodorum SN15]
35	BAE58068	83767929	unnamed protein product [Aspergillus oryzae]
36	P_382135	46110154	hypothetical protein FG01959.1 [Gibberella zeae PH-1]
37	EAA68855	42546012	hypothetical protein FG01959.1 [Gibberella zeae PH-1]
38	P_661646	67527317	hypothetical protein AN4042.2 [Aspergillus nidulans FGSC A4]
39	EAA59513	40740323	hypothetical protein AN4042.2 [Aspergillus nidulans FGSC A4]
40	P_383862	46115688	hypothetical protein FG03686.1 [Gibberella zeae PH-1]
41	EAA71499	42548656	hypothetical protein FG03686.1 [Gibberella zeae PH-1]
42	P_369417	39976053	hypothetical protein MG06047.4 [Magnaporthe grisea 70-15]
43	BAE57461	83767322	unnamed protein product [Aspergillus oryzae]
44	P_593788	19114700	hypothetical protein SPAC19A8.04 [Schizosaccharomyces pombe 972h-]
45	CAB11640	7007345	SPAC19A8.04 [Schizosaccharomyces pombe]

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46	P_756497	71003662	hypothetical protein UM00350.1 [Ustilago maydis 521]
47	EAK81168	46095935	hypothetical protein UM00350.1 [Ustilago maydis 521]
48	P_571445	58268578	C-22 sterol desaturase [Cryptococcus neoformans var. neoformans JEC21]
49	AAW44138	57227680	C-22 sterol desaturase, putative [Cryptococcus neoformans var. neoformans JEC21]
50	EAL20298	50257593	hypothetical protein CNBF1100 [Cryptococcus neoformans var. neoformans B-3501A]
51	EAQ86140	88178672	hypothetical protein CHGG_07393 [Chaetomium globosum CBS 148.51]
52	AAO48601	28864257	ERG5 [Clavispora lusitaniae]
53	P_647018	66827327	cytochrome P450 family protein [Dictyostelium discoideum AX4]
54	EAL73097	60475161	cytochrome P450 family protein [Dictyostelium discoideum AX4]
55	BAF04287	113531904	Os01g0211200 [Oryza sativa (japonica cultivar-group)]
56	P_913287	34903880	unnamed protein product [Oryza sativa (japonica cultivar-group)]
57	BAA96196	8096624	putative sterol C-22 desaturase [Oryza sativa (japonica cultivar-group)]
58	BAA96154	8096581	putative sterol C-22 desaturase [Oryza sativa (japonica cultivar-group)]
59	ABC59097	84514177	cytochrome P450 monooxygenase CYP710A15 [Medicago truncatula]
60	P_180452	15226976	CYP710A4; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
61	AAC79590	3927833	putative cytochrome P450 [Arabidopsis thaliana]
62	P_913285	34903876	unnamed protein product [Oryza sativa (japonica cultivar-group)]
63	BAA96194	8096622	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-group)]
64	BAA96152	8096579	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-group)]
65	P_913291	34903888	unnamed protein product [Oryza sativa (japonica cultivar-group)]
66	BAA96200	8096628	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-group)]
67	BAA96158	8096585	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-group)]
68	BAF04286	113531903	Os01g0210900 [Oryza sativa (japonica cultivar-group)]
69	P_913284	34903874	unnamed protein product [Oryza sativa (japonica cultivar-group)]
70	BAA96193	8096621	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-group)]
71	BAA96151	8096578	sterol C-22 desaturase -like [Oryza sativa (japonica cultivar-group)]
72	BAE71351	84468537	CYP710 [Arabidopsis thaliana]
73	AAQ65177	34365731	At2g34500 [Arabidopsis thaliana]
74	AAN72080	25083451	putative cytochrome P450 [Arabidopsis thaliana]
75	AAM14944	20197156	putative cytochrome P450 [Arabidopsis thaliana]
76	P_180997	15226758	CYP710A1; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
77	AAC26690	3128210	putative cytochrome P450 [Arabidopsis thaliana]
78	P_180451	15226974	CYP710A3; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
79	AAC79589	3927832	putative cytochrome P450 [Arabidopsis thaliana]
80	BAE80316	89111285	CYP710 protein [Arabidopsis thaliana]
81	AAM26664	20856398	At2g34490/T31E10.17 [Arabidopsis thaliana]
82	AAM14945	20197157	putative cytochrome P450 [Arabidopsis thaliana]
83	AAL75888	18650637	At2g34490/T31E10.17 [Arabidopsis thaliana]
84	P_180996	15226756	CYP710A2; heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]
85	AAC26691	3128211	putative cytochrome P450 [Arabidopsis thaliana]
86	AAM62799	21553706	putative cytochrome P450 [Arabidopsis thaliana]
87	BAE93156	91204699	sterol 22-desaturase [Lycopersicon esculentum]

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Table 58. Examples of ERG3 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAT93015	51013443	YLR056W [Saccharomyces cerevisiae]
2	NP_013157	6323085	C-5 sterol desaturase, catalyzes the introduction of a C-5(6)
3	BAA20292	2143190	C-5 sterol desaturase [Saccharomyces cerevisiae]
4	CAA64303	1181277	C-5 sterol desaturase [Saccharomyces cerevisiae]
5	P32353	416963	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
6	AAB39844	233331	C-5 sterol desaturase [Saccharomyces cerevisiae]
7	AAA34595	171477	C-5 sterol desaturase
8	AAA34594	171475	C-5 sterol desaturase
9	XP_446050	50287241	unnamed protein product [Candida glabrata]
10	CAG58974	49525357	unnamed protein product [Candida glabrata CBS138]
11	P50860	1706691	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
12	AAB02330	755695	ERG3
13	Q754B9	51701406	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
14	NP_985698	45198669	AFR151Cp [Eremothecium gossypii]
15	AAS53522	44984679	AFR151Cp [Ashbya gossypii ATCC 10895]
16	XP_455482	50310919	unnamed protein product [Kluyveromyces lactis]
17	CAG98190	49644618	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
18	Q8NJ57	51701432	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
19	CAD13131	22022945	ergosterol delta 5,6 desaturase [Candida dubliniensis]
20	XP_713577	68485022	hypothetical protein CaO19.767 [Candida albicans SC5314]
21	XP_713612	68484947	hypothetical protein CaO19.8387 [Candida albicans SC5314]
22	EAK94507	46435118	hypothetical protein CaO19.8387 [Candida albicans SC5314]
23	EAK94472	46435082	hypothetical protein CaO19.767 [Candida albicans SC5314]
24	O93875	51701379	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
25	AAC99343	4091929	C5,6 desaturase [Candida albicans]
26	XP_460747	50424321	hypothetical protein DEHA0F09757g [Debaryomyces hansenii CBS76
27	CAG89088	49656416	unnamed protein product [Debaryomyces hansenii CBS767]
28	XP_503090	50551233	hypothetical protein [Yarrowia lipolytica]
29	CAG81282	49648958	unnamed protein product [Yarrowia lipolytica CLIB122]
30	XP_664110	67540672	hypothetical protein AN6506.2 [Aspergillus nidulans FGSC A4]
31	EAA57846	40738656	hypothetical protein AN6506.2 [Aspergillus nidulans FGSC A4]
32	BAE61784	83771654	unnamed protein product [Aspergillus oryzae]
33	XP_747563	70984086	sterol delta 5,6-desaturase ERG3 [Aspergillus fumigatus Af293]
34	EAL85525	66845190	sterol delta 5,6-desaturase ERG3 [Aspergillus fumigatus Af293]
35	AAU82098	52548218	C-5 sterol desaturase B-like [Aspergillus fumigatus]
36	BAE56076	83765933	unnamed protein product [Aspergillus oryzae]
37	XP_962923	85109451	hypothetical protein [Neurospora crassa OR74A]
38	Q7SBB6	51701418	Probable C-5 sterol desaturase (Sterol-C5-desaturase) (Ergoste
39	EAA33687	28924567	hypothetical protein [Neurospora crassa]
40	EAS37256	90307625	C-5 sterol desaturase [Coccidioides immitis RS]
41	Q8J207	51701428	C-5 sterol desaturase (Sterol-C5-desaturase) (Ergosterol delta
42	AAN27998	23476431	sterol delta 5,6-desaturase ERG3 [Leptosphaeria maculans]
43	XP_363987	39953467	hypothetical protein MG08832.4 [Magnaporthe grisea 70-15]
44	EAT83541	111062421	hypothetical protein SNOG_09349 [Phaeosphaeria nodorum SN15]
45	O94457	51701380	Probable C-5 sterol desaturase 1 (Sterol-C5-desaturase 1) (Erg
46	NP_593135	19114047	hypothetical protein SPAC1687.16c [Schizosaccharomyces pombe 9
47	CAA22610	4106670	SPAC1687.16c [Schizosaccharomyces pombe]
48	XP_382678	46111241	hypothetical protein FG02502.1 [Gibberella zeae PH-1]
49	EAA67236	42544393	hypothetical protein FG02502.1 [Gibberella zeae PH-1]

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50	BAE65607	83775487	unnamed protein product [Aspergillus oryzae]
51	O13666	6015113	Probable C-5 sterol desaturase 2 (Sterol-C5-desaturase 2) (Erg
52	CAA16898	2853109	SPBC27B12.03c [Schizosaccharomyces pombe]
53	BAA21457	2257565	C-5 STEROL DESATURASE [Schizosaccharomyces pombe]

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Table 59. Examples of ERG2 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAS56448	45270134	YMR202W [Saccharomyces cerevisiae]
2	CAA88643	736299	Erg2p [Saccharomyces cerevisiae]
3	P32352	416962	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
4	AAA34593	171473	C-8 sterol isomerase
5	P_985369	45198340	AFL181Cp [Eremothecium gossypii]
6	AAS53193	44984227	AFL181Cp [Ashbya gossypii ATCC 10895]
7	P_449233	50293643	unnamed protein product [Candida glabrata]
8	CAG62207	49528546	unnamed protein product [Candida glabrata CBS138]
9	P_455367	50310691	unnamed protein product [Kluyveromyces lactis]
10	CAG98075	49644503	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
11	P_458891	50420709	hypothetical protein DEHA0D10714g [Debaryomyces hansenii CBS767]
12	CAG87043	49654558	unnamed protein product [Debaryomyces hansenii CBS767]
13	P_718886	68473979	sterol C8-C7 isomerase [Candida albicans SC5314]
14	P_718988	68473770	sterol C8-C7 isomerase [Candida albicans SC5314]
15	EAL00087	46440785	hypothetical protein CaO19.6026 [Candida albicans SC5314]
16	EAK99982	46440679	hypothetical protein CaO19.13447 [Candida albicans SC5314]
17	P_504668	50554519	hypothetical protein [Yarrowia lipolytica]
18	CAG80272	49650537	unnamed protein product [Yarrowia lipolytica CLIB122]
19	P_501006	50547073	hypothetical protein [Yarrowia lipolytica]
20	CAG83259	49646872	unnamed protein product [Yarrowia lipolytica CLIB122]
21	Q92254	67476925	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
22	CAC28749	12718205	C-8 sterol isomerase erg-1 [Neurospora crassa]
23	AAB09470	1575320	C-8 sterol isomerase
24	P_658055	67516339	hypothetical protein AN0451.2 [Aspergillus nidulans FGSC A4]
25	EAA66550	40747394	hypothetical protein AN0451.2 [Aspergillus nidulans FGSC A4]
26	P_593324	19114236	hypothetical protein SPAC20G8.07c [Schizosaccharomyces pombe 972h-]
27	P87113	3219796	Probable C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
28	CAB08601	2094862	SPAC20G8.07c [Schizosaccharomyces pombe]
29	P_363040	39947737	hypothetical protein MG08624.4 [Magnaporthe grisea 70-15]
30	P33281	462023	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
31	CAA80454	311322	C-8 sterol isomerase [Magnaporthe grisea]
32	EAQ85888	88178420	hypothetical protein CHGG_07141 [Chaetomium globosum CBS 148.51]
33	P_961312	85102300	C-8 STEROL ISOMERASE (DELTA-8--DELTA-7 STEROL ISOMERASE) [Neurospora crassa OR74A]
34	EAA32076	28922855	C-8 STEROL ISOMERASE (DELTA-8--DELTA-7 STEROL ISOMERASE) [Neurospora crassa]
35	P_844057	72387265	C-8 sterol isomerase, putative [Trypanosoma brucei]
36	P_826540	71905267	C-8 sterol isomerase, putative [Trypanosoma brucei]
37	AAZ10498	70800589	C-8 sterol isomerase, putative [Trypanosoma brucei]
38	AAX80634	62360216	C-8 sterol isomerase, putative [Trypanosoma brucei]
39	P_758081	71006989	C-8 sterol isomerase [Ustilago maydis 521]
40	EAK82388	46097155	ERG2_USTMA C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase) [Ustilago maydis 521]
41	P32360	416961	C-8 sterol isomerase (Delta-8--delta-7 sterol isomerase)
42	CAA78959	2967	C-8 sterol isomerase [Ustilago maydis]
43	P_567070	58259315	C-8 sterol isomerase [Cryptococcus neoformans var. neoformans JEC21]
44	AAW41251	57223207	C-8 sterol isomerase, putative [Cryptococcus neoformans var.

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			neoformans JEC21]
45	EAL23045	50260386	hypothetical protein CNBA8120 [Cryptococcus neoformans var. neoformans B-3501A]
46	P_821186	71658920	C-8 sterol isomerase [Trypanosoma cruzi strain CL Brener]
47	EAN99335	70886558	C-8 sterol isomerase, putative [Trypanosoma cruzi]
48	AAQ18796	33439494	C-8 sterol isomerase [Trypanosoma cruzi]
49	P_847879	73536920	C-8 sterol isomerase-like protein [Leishmania major strain Friedlin]
50	AAZ09671	70799755	C-8 sterol isomerase-like protein [Leishmania major strain Friedlin]

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Table 60. Examples of ERG3-like polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	BAA33730	3721884	sterol-C5-desaturase [Mus musculus]
2	BAE32506	74178504	unnamed protein product [Mus musculus]
3	AAH24132	18848246	Sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae) [Mus musculus]
4	NP_766357	27777693	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Mus musculus]
5	BAC36944	26346591	unnamed protein product [Mus musculus]
6	BAC31666	26335931	unnamed protein product [Mus musculus]
7	AAH81704	51859106	Sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae) [Rattus norvegicus
8	NP_446094	25742651	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Rattus norvegicus]
9	BAB19798	11990472	sterol C5-desaturase [Rattus norvegicus]
10	XP_853004	73955000	PREDICTED: similar to sterol-C5-desaturase-like [Canis familiaris]
11	XP_508825	55637121	PREDICTED: similar to delta7-sterol-C5-desaturase [Pan troglodytes]
12	NP_001...	68160945	sterol-C5-desaturase-like [Homo sapiens]
13	NP_008849	68160941	sterol-C5-desaturase-like [Homo sapiens]
14	BAD96861	62897843	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like variant [Homo sapiens]
15	BAD96406	62896931	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like variant [Homo sapiens]
16	AAH50427	30046554	Sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like [Homo sapiens]
17	AAH12333	15147389	Sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like [Homo sapiens]
18	AAF00544	6003685	delta7-sterol-C5-desaturase [Homo sapiens]
19	BAB68218	15637108	sterol C5 desaturase [Homo sapiens]
20	O75845	6174975	Lathosterol oxidase (Lathosterol 5-desaturase) (Delta-7-sterol 5-desaturase) (C-5 sterol desatur
21	BAA33729	3721882	sterol-C5-desaturase [Homo sapiens]
22	XP_001...	1.09E+08	PREDICTED: sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like isoform 2 [Macaca
23	AAH78055	50416254	Sc5d-prov protein [Xenopus laevis]
24	NP_001...	52219112	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Danio rerio]
25	AAH81395	51859008	Sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae) [Danio rerio]
26	BAA18970	1906796	fungal sterol-C5-desaturase homolog [Homo sapiens]
27	XP_001...	1.09E+08	PREDICTED: sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like isoform 1 [Macaca
28	XP_793331	72159211	PREDICTED: similar to sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog [Strongyloc
29	NP_001...	78369462	hypothetical protein LOC525154 [Bos taurus]
30	AAI03339	74353920	Similar to sterol-C5-desaturase-like [Bos taurus]
31	CAF90498	47207599	unnamed protein product [Tetraodon nigroviridis]

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Table 61. Examples of ERG27 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	Q12452	60392263	3-keto-steroid reductase
2	CAA97664	1360483	unnamed protein product [Saccharomyces cerevisiae]
3	AAB67544	1256850	Ylr100wp [Saccharomyces cerevisiae]
4	Q6FIV3	62286920	3-keto-steroid reductase
5	P_449841	50294860	hypothetical protein CAGL0M11506g [Candida glabrata CBS138]
6	CAG62821	49529155	unnamed protein product [Candida glabrata CBS138]
7	Q6CJC2	62286919	3-keto-steroid reductase
8	P_455967	50311871	unnamed protein product [Kluyveromyces lactis]
9	CAG98675	49645103	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
10	Q74ZZ0	62286926	3-keto-steroid reductase
11	P_986733	45201163	AGR068Wp [Eremothecium gossypii]
12	AAS54557	44985946	AGR068Wp [Ashbya gossypii ATCC 10895]
13	Q6BNP0	62286917	3-keto-steroid reductase
14	P_460180	50423199	hypothetical protein DEHA0E21263g [Debaryomyces hansenii CBS
15	CAG88453	49655848	unnamed protein product [Debaryomyces hansenii CBS767]
16	Q874K0	62286935	3-keto-steroid reductase
17	AAN28009	29465858	3-keto reductase [Candida albicans]
18	P_717865	68476112	3-keto sterol reductase [Candida albicans SC5314]
19	P_717931	68475981	3-keto sterol reductase [Candida albicans SC5314]
20	EAK98982	46439667	hypothetical protein CaO19.3240 [Candida albicans SC5314]
21	EAK98915	46439599	hypothetical protein CaO19.10750 [Candida albicans SC5314]
22	Q6CE88	62286918	3-keto-steroid reductase
23	P_501024	50547109	hypothetical protein [Yarrowia lipolytica]
24	CAG83277	49646890	unnamed protein product [Yarrowia lipolytica CLIB122]
25	P_595440	19112232	3-keto sterol reductase [Schizosaccharomyces pombe 972h-]
26	CAA21246	3738145	SPBC1709.07 [Schizosaccharomyces pombe]
27	BAA13878	1749642	unnamed protein product [Schizosaccharomyces pombe]
28	P_751680	70993666	3-ketosteroid reductase [Aspergillus fumigatus Af293]
29	EAL89642	66849314	3-ketosteroid reductase [Aspergillus fumigatus Af293]
30	P_958799	85091228	hypothetical protein [Neurospora crassa OR74A]
31	EAA29563	28920185	hypothetical protein [Neurospora crassa]
32	BAE58171	83768032	unnamed protein product [Aspergillus oryzae]
33	EAQ85086	88177618	hypothetical protein CHGG_09100 [Chaetomium globosum CBS 148
34	EAT86025	111064905	hypothetical protein SNOG_06194 [Phaeosphaeria nodorum SN15]
35	P_663189	67538830	hypothetical protein AN5585.2 [Aspergillus nidulans FGSC A4]
36	EAA62228	40743038	hypothetical protein AN5585.2 [Aspergillus nidulans FGSC A4]
37	EAS36221	90306590	hypothetical protein CIMG_01575 [Coccidioides immitis RS]
38	AAO64345	29150686	3-ketosteroid reductase [Botryotinia fuckeliana]
39	P_796770	72131681	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
40	P_793145	72086766	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
41	P_570518	58266724	3-keto sterol reductase [Cryptococcus neoformans var. neofor
42	AAW43211	57226751	3-keto sterol reductase, putative [Cryptococcus neoformans v
43	EAL21279	50258592	hypothetical protein CNBD3330 [Cryptococcus neoformans var.
44	AAI00220	71681260	Unknown (protein for MGC:114978) [Xenopus laevis]
45	BAE06843	70720928	hypothetical protein [Epichloe festucae]
46	P_001...	62859081	hydroxysteroid (17-beta) dehydrogenase 7 [Xenopus tropicalis
47	P_851698	74006237	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
48	CAC88119	18077845	17beta-hydroxysteroid dehydrogenase type 7 [Mus musculus]
49	AAH11464	15079256	Hsd17b7 protein [Mus musculus]

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50	P_034606	87162470	hydroxysteroid (17-beta) dehydrogenase 7 [Mus musculus]
51	BAC25918	26390565	unnamed protein product [Mus musculus]
52	BAC34124	26340924	unnamed protein product [Mus musculus]
53	O88736	8134403	3-keto-steroid reductase (Estradiol 17-beta-dehydrogenase 7)
54	CAA75742	3319971	17-beta-hydroxysteroid dehydrogenase type 7 [Mus musculus]
55	P_695820	68440091	PREDICTED: similar to Hydroxysteroid (17-beta) dehydrogenase
56	P_058931	8393576	hydroxysteroid (17-beta) dehydrogenase 7 [Rattus norvegicus]
57	Q62904	8134405	3-keto-steroid reductase (Estradiol 17-beta-dehydrogenase 7)
58	AAC52623	1397235	ovarian-specific protein
59	BAC37061	26346825	unnamed protein product [Mus musculus]
60	AAM21211	20385196	17-beta-hydroxysteroid dehydrogenase type 7 [Mus musculus]
61	P_363377	39951321	hypothetical protein MG01303.4 [Magnaporthe grisea 70-15]
62	P_581467	76611932	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase
63	CAC88111	18077843	17beta hydroxysteroid dehydrogenase [Homo sapiens]
64	AAX42032	61361334	hydroxysteroid (17-beta) dehydrogenase 7 [synthetic construc
65	AAX42031	61361326	hydroxysteroid (17-beta) dehydrogenase 7 [synthetic construc
66	CAI13457	55959848	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
67	CAI15947	55959770	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
68	AAH65246	40807207	Hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
69	AAQ89321	37183042	HSD17B7 [Homo sapiens]
70	AAP35738	30582989	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
71	AAH07068	13937918	Hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
72	CAC20418	12053691	17beta-hydroxysteroid dehydrogenase type 7 [Homo sapiens]
73	P56937	8134404	3-keto-steroid reductase (Estradiol 17-beta-dehydrogenase 7)
74	P_057455	7705421	hydroxysteroid (17-beta) dehydrogenase 7 [Homo sapiens]
75	AAF09266	6721095	17 beta-hydroxysteroid dehydrogenase type VII [Homo sapiens]
76	ABB72853	82400271	17-beta hydroxysteroid dehydrogenase 7 [Macaca fascicularis]
77	AAX29487	60653587	hydroxysteroid (17-beta) dehydrogenase 7 [synthetic construc
78	AAP36180	30583863	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 7 [synth
79	AAF14537	6502988	17beta-hydroxysteroid dehydrogenase type 7 [Homo sapiens]
80	AAK20950	13383374	17-beta-hydroxysteroid dehydrogenase type 7 [Oryctolagus cun
81	AAP97275	33150794	ovarian-specific protein; OSP [Homo sapiens]
82	P_422210	50750970	PREDICTED: similar to Estradiol 17 beta-dehydrogenase 7 (17-

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Table 62. Examples of ERG26 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAT93045	51013503	YGL001C [Saccharomyces cerevisiae]
2	P53199	1723793	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
3	CAA96701	1322447	unnamed protein product [Saccharomyces cerevisiae]
4	P_446390	50287923	unnamed protein product [Candida glabrata]
5	CAG59317	49525698	unnamed protein product [Candida glabrata CBS138]
6	P_453025	50306127	unnamed protein product [Kluyveromyces lactis]
7	CAH01876	49642158	unnamed protein product [Kluyveromyces lactis NRRL Y-1140]
8	CAC38016	13940379	putative C-3 sterol dehydrogenase [Zygosaccharomyces rouxii]
9	P_985548	45198519	AFR001Wp [Eremothecium gossypii]
10	AAS53372	44984470	AFR001Wp [Ashbya gossypii ATCC 10895]
11	P_458178	50419307	hypothetical protein DEHA0C12463g [Debaryomyces hansenii CBS767]
12	CAG86252	49653844	unnamed protein product [Debaryomyces hansenii CBS767]
13	P_715564	68481045	C-3 sterol dehydrogenase/C-4 decarboxylase [Candida albicans SC53
14	P_715620	68480934	C-3 sterol dehydrogenase/C-4 decarboxylase [Candida albicans SC53
15	EAK96601	46437251	hypothetical protein CaO19.10427 [Candida albicans SC5314]
16	EAK96542	46437191	hypothetical protein CaO19.2909 [Candida albicans SC5314]
17	AAK69617	14582743	C-3 sterol dehydrogenase/C-4 decarboxylase [Candida albicans]
18	P_502124	50549307	hypothetical protein [Yarrowia lipolytica]
19	CAG82444	49647991	unnamed protein product [Yarrowia lipolytica CLIB122]
20	P_596741	19113533	hypothetical protein SPBC3F6.02c [Schizosaccharomyces pombe 972h-
21	CAA17691	2924499	SPBC3F6.02c [Schizosaccharomyces pombe]
22	AAQ88129	37039511	C-3 sterol dehydrogenase [Cryptococcus neoformans var. grubii H99
23	P_381379	46108642	hypothetical protein FG01203.1 [Gibberella zeae PH-1]
24	EAA67667	42544824	hypothetical protein FG01203.1 [Gibberella zeae PH-1]
25	EAQ90884	88183416	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
26	P_640712	66813066	3beta-hydroxysteroid dehydrogenase [Dictyostelium discoideum AX4]
27	EAL66725	60468723	3beta-hydroxysteroid dehydrogenase [Dictyostelium discoideum AX4]
28	EAT77489	111056369	hypothetical protein SNOG_15264 [Phaeosphaeria nodorum SN15]
29	P_965466	85118539	hypothetical protein [Neurospora crassa OR74A]
30	CAE76518	38567226	related to C-3 sterol dehydrogenase (C-4 decarboxylase) [Neurospo
31	EAA36230	28927275	hypothetical protein [Neurospora crassa]
32	P_420279	50745878	PREDICTED: similar to NAD(P) dependent steroid dehydrogenase-like
33	P_001...	78369400	hypothetical protein LOC616694 [Bos taurus]
34	AAI03390	73586574	Similar to NAD(P) dependent steroid dehydrogenase-like [Bos tauru
35	P_001...	62859757	hypothetical protein LOC550044 [Xenopus tropicalis]
36	AAH88699	56788986	LOC496236 protein [Xenopus laevis]
37	P_538199	74008671	PREDICTED: similar to NAD(P) dependent steroid dehydrogenase-like
38	P_853073	74008673	PREDICTED: similar to NAD(P) dependent steroid dehydrogenase-like
39	AAH52834	31127258	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]
40	P_001...	109132673	PREDICTED: similar to NAD(P) dependent steroid dehydrogenase-like
41	P_001...	109132671	PREDICTED: similar to NAD(P) dependent steroid dehydrogenase-

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			like
42	P_001...	57164113	NAD(P) dependent steroid dehydrogenase-like [Rattus norvegicus]
43	AAH87626	56388600	NAD(P) dependent steroid dehydrogenase-like [Rattus norvegicus]
44	BAE24522	74187675	unnamed protein product [Mus musculus]
45	P_035071	31982437	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]
46	Q9R1J0	8473695	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating
47	CAA15948	7619723	NAD(P)H steroid dehydrogenase [Mus musculus]
48	AAD38448	5052206	putative NAD(P)H steroid dehydrogenase [Mus musculus]
49	AAH19945	18043286	NAD(P) dependent steroid dehydrogenase-like [Mus musculus]
50	AAH07816	14043700	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]
51	AAH00245	12652969	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]
52	Q15738	8488997	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating (H105
53	P_057006	8393516	NAD(P) dependent steroid dehydrogenase-like [Homo sapiens]
54	AAC50558	4457237	H105e3 [Homo sapiens]
55	CAF99107	47222951	unnamed protein product [Tetraodon nigroviridis]
56	P_756075	71002788	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumigatus
57	EAL94037	66853713	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumigatus
58	P_567299	58259773	C-3 sterol dehydrogenase (C-4 sterol decarboxylase) [Cryptococcus
59	AAW45782	57229349	C-3 sterol dehydrogenase (C-4 sterol decarboxylase), putative [Cr
60	EAL18383	50255650	hypothetical protein CNBJ3060 [Cryptococcus neoformans var. neofo
61	P_001...	62955325	hypothetical protein LOC550369 [Danio rerio]
62	AAH93332	62204675	Zgc:112474 [Danio rerio]
63	EAS37011	90307380	hypothetical protein CIMG_02365 [Coccidioides immitis RS]
64	P_755836	71002310	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumigatus
65	EAL93798	66853474	C-3 sterol dehydrogenase/C-4 decarboxylase [Aspergillus fumigatus
66	CAH90815	55728130	hypothetical protein [Pongo pygmaeus]
67	P_760274	71020087	hypothetical protein UM04127.1 [Ustilago maydis 521]
68	EAK85155	46099922	hypothetical protein UM04127.1 [Ustilago maydis 521]
69	P_680844	67901176	hypothetical protein AN7575.2 [Aspergillus nidulans FGSC A4]
70	EAA62155	40742965	hypothetical protein AN7575.2 [Aspergillus nidulans FGSC A4]
71	AAZ14936	70906332	putative sterol dehydrogenase [Coprinellus disseminatus]

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Table 63. Examples of ERG25 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAS56153	45269545	YGR060W [Saccharomyces cerevisiae]
2	XP_448420	50291975	unnamed protein product [Candida glabrata]
3	XP_451890	50303885	unnamed protein product [Kluyveromyces lactis]
4	NP_986119	45199090	AFR572Wp [Eremothecium gossypii]
5	XP_456861	50409318	hypothetical protein DEHA0A12661g [Debaryomyces hansenii CBS767]
6	XP_713420	68485318	C-4 sterol methyl oxidase [Candida albicans SC5314]
7	XP_461658	50426123	hypothetical protein DEHA0G03124g [Debaryomyces hansenii CBS767]
8	XP_505281	50555746	hypothetical protein [Yarrowia lipolytica]
9	XP_722703	68466442	putative C-4 sterol methyl oxidase [Candida albicans SC5314]
10	XP_722849	68466149	putative C-4 sterol methyl oxidase [Candida albicans SC5314]
11	ABF84061	107785180	C-4 sterol methyl oxidase [Chaetomium globosum]
12	Q9UUH4	28558117	C-4 methylsterol oxidase (Methylsterol monooxygenase)
13	XP_962240	85106720	hypothetical protein [Neurospora crassa OR74A]
14	EAT84680	111063560	hypothetical protein SNOG_08404 [Phaeosphaeria nodorum SN15]
15	XP_746668	70982279	hypothetical protein Afu4g04820 [Aspergillus fumigatus Af293]
16	XP_390006	46136629	hypothetical protein FG09830.1 [Gibberella zeae PH-1]
17	BAE65381	83775259	unnamed protein product [Aspergillus oryzae]
18	XP_360827	39942580	hypothetical protein MG03370.4 [Magnaporthe grisea 70-15]
19	ABA70590	77377695	hypothetical protein [Penicillium chrysogenum]
20	XP_369331	39975881	hypothetical protein MG06133.4 [Magnaporthe grisea 70-15]
21	EAS29762	90300131	hypothetical protein CIMG_08508 [Coccidioides immitis RS]
22	XP_762027	71023595	hypothetical protein UM05880.1 [Ustilago maydis 521]
23	XP_569526	58264740	C-4 methyl sterol oxidase [Cryptococcus neoformans var. neoformans JEC21]
24	EAQ88125	88180657	hypothetical protein CHGG_04744 [Chaetomium globosum CBS 148.51].
25	BAE66491	83776372	unnamed protein product [Aspergillus oryzae]
26	XP_746962	70982869	c-4 methyl sterol oxidase [Aspergillus fumigatus Af293]
27	XP_682176	67903840	hypothetical protein AN8907.2 [Aspergillus nidulans FGSC A4]
28	XP_664577	67541619	hypothetical protein AN6973.2 [Aspergillus nidulans FGSC A4]
29	XP_646277	66825845	hypothetical protein DDBDRAFT_0190553 [Dictyostelium discoideum AX4]
30	NP_998917	47523336	sterol-C4-methyl oxidase-like protein [Sus scrofa]
31	AAI07880	79160074	Sterol-C4-methyl oxidase-like [Homo sapiens]
32	BAE01921	67971158	unnamed protein product [Macaca fascicularis]
33	XP_001...	109076099	PREDICTED: sterol-C4-methyl oxidase-like isoform 3 [Macaca mulatta]
34	XP_580615	61871492	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) isoform 1 [Bos taurus]
35	CAC24471	12311696	hypothetical protein [Candida albicans]
36	BAE30143	74185334	unnamed protein product [Mus musculus]
37	XP_532714	57096891	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) isoform 1 [Canis familiaris]
38	CAF92153	47211304	unnamed protein product [Tetraodon nigroviridis]
39	AAH63155	38649308	Sterol-C4-methyl oxidase-like [Rattus norvegicus]
40	NP_001...	57530155	sterol-C4-methyl oxidase-like [Gallus gallus]
41	NP_998518	47087009	sterol-C4-methyl oxidase-like [Danio rerio]
42	NP_563789	18390767	SMO2-2; C-4 methylsterol oxidase [Arabidopsis thaliana]
43	AAI21457	111309060	Unknown (protein for MGC:146461) [Xenopus tropicalis]

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44	AAM64821	21592871	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
45	AAF79571	8778563	F22G5.23 [Arabidopsis thaliana]
46	AAO13795	27448145	putative sterol 4-alpha-methyl-oxidase [Gossypium arboreum]
47	AAO48604	28864263	ERG25 [Clavispora lusitaniae]
48	AAQ83692	34978966	C-4 sterol methyl oxidase 2 [Nicotiana benthamiana]
49	ABD97153	90658509	C-4 methyl sterol oxidase [Cryptococcus neoformans var. neoformans]
50	ABD97146	90658495	C-4 methyl sterol oxidase [Cryptococcus neoformans var. grubii]
51	ABD97147	90658497	C-4 methyl sterol oxidase [Cryptococcus neoformans var. grubii]
52	ABD97134	90658471	C-4 methyl sterol oxidase [Cryptococcus neoformans var. neoformans]
53	AAL82576	27447203	putative sterol 4-alpha-methyl-oxidase [Zea mays]
54	NP_850133	30684225	SMO2-1; C-4 methylsterol oxidase [Arabidopsis thaliana]
55	NP_973559	42570971	SMO2-1; C-4 methylsterol oxidase [Arabidopsis thaliana]
56	AAL32287	16973432	sterol 4-alpha-methyl-oxidase [Arabidopsis thaliana]
57	ABE83226	92875070	Sterol desaturase [Medicago truncatula]
58	BAF28920	113645779	Os11g0707600 [Oryza sativa (japonica cultivar-group)]
59	BAF20592	113610214	Os07g0101500 [Oryza sativa (japonica cultivar-group)]
60	XP_787442	72077919	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) [Strongylocentrotus purpuratus]
61	AAM64359	21592408	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
62	NP_973777	42571373	SMO2-2; C-4 methylsterol oxidase [Arabidopsis thaliana]
63	NP_001...	62865628	sterol-C4-methyl oxidase-like isoform 2 [Homo sapiens]
64	AAX95419	62733302	4-alpha-methyl-sterol C4-methyl-oxidase [Oryza sativa (japonica cultivar-group)]
65	XP_883875	76638226	PREDICTED: similar to C-4 methylsterol oxidase (Methylsterol monooxygenase) isoform 3 [Bos taurus]
66	ABE87434	92884635	Sterol desaturase [Medicago truncatula]
67	XP_641553	66814748	hypothetical protein DDBDRAFT_0205936 [Dictyostelium discoideum AX4]
68	AAM65428	21593461	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
69	NP_567669	18416002	SMO1-3 (STEROL 4-ALPHA METHYL OXIDASE); catalytic [Arabidopsis thaliana]
70	AAM64961	21593012	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
71	AAN18115	23308291	At4g12110/F16J13_180 [Arabidopsis thaliana]
72	AAK61361	27446631	putative sterol 4-alpha-methyl-oxidase [Arabidopsis thaliana]
73	BAF01201	110738551	hypothetical protein [Arabidopsis thaliana]
74	AAQ13424	33337546	sterol-4-methyl-oxidase [Arabidopsis thaliana]
75	BAF27120	113639815	Os10g0545200 [Oryza sativa (japonica cultivar-group)]
76	CAB78254	7267912	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]
77	AAQ94118	37591406	sterol-4-alpha methyl oxidase [Arabidopsis thaliana]
78	AAQ83691	34978964	C-4 sterol methyl oxidase 1 [Nicotiana benthamiana]
79	ABD65536	89266491	sterol-C4-methyl oxidase-like [Ictalurus punctatus]
80	BAC57961	28804511	putative C-4 sterol methyl oxidase [Aster tripolium]

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Table 64. Examples of ERG24 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAB30203	545906	sterol delta 14 reductase; Erg24p [Saccharomyces cerevisiae]
2	XP_447380	50289897	hypothetical protein CAGL0I02970g [Candida glabrata CBS138]
3	XP_452744	50305569	unnamed protein product [Kluyveromyces lactis]
4	NP_985893	45198864	AFR346Wp [Eremothecium gossypii]
5	XP_710670	68491033	sterol C-14 reductase [Candida albicans SC5314]
6	XP_458371	50419687	hypothetical protein DEHA0C16984g [Debaryomyces hansenii CBS767]
7	XP_501260	50547581	hypothetical protein [Yarrowia lipolytica]
8	XP_566548	58258271	C-14 sterol reductase [Cryptococcus neoformans var. neoformans JEC21]
9	NP_596767	19113559	hypothetical protein SPBC16G5.18 [Schizosaccharomyces pombe 972h-]
10	EAL23454	50260804	hypothetical protein CNBA1040 [Cryptococcus neoformans var. neoformans B-3501A]
11	XP_759786	71019111	hypothetical protein UM03639.1 [Ustilago maydis 521]
12	XP_386782	46124457	ER24_FUSSO Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase) [Gibberella zeae PH-1]
13	P78575	6015106	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase)
14	Q01447	3929349	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase)

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Table 65. Examples of ERG11 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAA34546	171354	lanosterol 14-demethylase cytochrome P450
2	AAA34547	171356	lanosterol 14-demethylase cytochrome P450
3	AAY59417	66967944	14alpha-demethylase [Candida glabrata]
4	XP_454109	50308217	unnamed protein product [Kluyveromyces lactis]
5	Q759W0	51701328	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
6	AAB32679	912807	cytochrome P-450 lanosterol-alpha-demethylase; P450-L1A1 [Candida glabrata]
7	AAX39316	61189834	lanosterol 14 alpha demethylase [Candida tropicalis]
8	AAF00598	6006769	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
9	XP_716761	68478280	lanosterol 14-alpha-demethylase [Candida albicans SC5314]
10	XP_460143	50423125	hypothetical protein DEHA0E20383g [Debaryomyces hansenii CBS767]
11	ABC41921	83728463	cytochrome P450 lanosterol 14 alpha demethylase [Candida albicans]
12	AAX39315	61189832	lanosterol 14 alpha demethylase [Candida tropicalis]
13	O4CK51	65689	lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 51 - yeast (Candida albicans)
14	XP_716822	68478161	lanosterol 14-alpha-demethylase [Candida albicans SC5314]
15	AAF00603	6006774	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
16	AAF00600	6006771	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
17	BAB03401	9558446	CYP51 variant 3 [Candida albicans]
18	AAK57519	14280372	lanosterol 14-alpha demethylase Erg11p [Candida dubliniensis]
19	AAF00602	6006773	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
20	AAF00601	6006772	cytochrome P450 lanosterol 14-alpha demethylase [Candida albicans]
21	BAB03400	9558444	CYP51 variant 2 [Candida albicans]
22	AAO83898	29378393	cytochrome P-450 lanosterol-alpha-demethylase [Issatchenkia orientalis]
23	AAW50593	57341382	Erg11p [Candida albicans]
24	AAW50592	57341380	Erg11p [Candida albicans]
25	XP_500518	50545962	hypothetical protein [Yarrowia lipolytica]
26	BAC16517	23263326	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
27	BAC16520	23263332	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
28	BAC16518	23263328	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
29	BAC16519	23263330	cytochrome P-450 lanosterol 14alpha-demethylase [Candida albicans]
30	Q02315	2493385	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
31	AAO38776	28395121	lanosterol 14 alpha demethylase; ERG11 [Pneumocystis carinii]
32	ABG91757	110816094	sterol 14alpha-demethylase [Pneumocystis carinii]
33	BAE60239	83770104	unnamed protein product [Aspergillus oryzae]
34	XP_749134	70987441	14-alpha sterol demethylase Cyp51B [Aspergillus fumigatus Af293]
35	XP_659505	67522889	hypothetical protein AN1901.2 [Aspergillus nidulans FGSC A4]

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36	XP_681552	67902592	hypothetical protein AN8283.2 [Aspergillus nidulans FGSC A4]
37	AAK73659	14861413	14-alpha sterol demethylase [Aspergillus fumigatus]
38	XP_752137	70994720	14-alpha sterol demethylase Cyp51A [Aspergillus fumigatus Af293]
39	BAE57417	83767278	unnamed protein product [Aspergillus oryzae]
40	AAF79204	8778097	cytochrome P450 sterol 14 alpha-demethylase [Emericella nidulans]
41	CAE18091	33300264	eburicol 14 alpha demethylase [Blumeria graminis]
42	EAS28723	90299092	cytochrome P450 51 [Coccidioides immitis RS]
43	CAE18094	33300270	eburicol 14 alpha demethylase [Blumeria graminis]
44	CAC85624	33300256	eburicol 14alpha demethylase [Blumeria graminis f. sp. tritici]
45	CAE18095	33300272	eburicol 14 alpha demethylase [Blumeria graminis]
46	CAE17515	33284834	eburicol 14 alpha demethylase [Blumeria graminis f. sp. tritici]
47	AAU43734	52352491	eburicol 14 alpha-demethylase [Mycosphaerella graminicola]
48	EAS35219	90305588	cytochrome P450 51 [Coccidioides immitis RS]
49	CAE18102	33300286	eburicol 14 alpha demethylase [Blumeria graminis]
50	CAE18103	33300288	eburicol 14 alpha demethylase [Blumeria graminis]
51	CAE18105	33300292	eburicol 14 alpha demethylase [Blumeria graminis]
52	NP_592990	19113902	hypothetical protein SPAC13A11.02c [Schizosaccharomyces pombe 972h-]
53	CAE18100	33300282	eburicol 14 alpha demethylase [Blumeria graminis]
54	AAP79601	32330152	eburicol 14alpha-demethylase [Mycosphaerella graminicola]
55	AAC97606	4049645	eburicol 14alpha demethylase; CYP51; cytochrome P450 sterol 14-demethylase [Blumeria graminis f. sp. hordei]
56	CAE18099	33300280	eburicol 14 alpha demethylase [Blumeria graminis]
57	BAE63554	83773427	unnamed protein product [Aspergillus oryzae]
58	XP_381176	46108236	hypothetical protein FG01000.1 [Gibberella zeae PH-1]
59	AAF85983	9230788	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
60	AAP81934	32441730	eburicol 14 alpha-demethylase [Mycosphaerella graminicola]
61	XP_362183	39945292	hypothetical protein MG04628.4 [Magnaporthe grisea 70-15]
62	AAP12370	30314338	lanosterol 14 alpha-demethylase; 14 alpha lanosterol demethylase [Cryptococcus neoformans var. grubii]
63	AAF74756	8347731	eburicol 14-alpha demethylase [Mycosphaerella graminicola]
64	AAF76464	8570176	14 alpha-demethylase [Venturia inaequalis]
65	XP_566464	58258103	sterol 14-demethylase [Cryptococcus neoformans var. neoformans JEC21]
66	EAQ93417	88185949	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
67	AAL79180	18766932	eburicol 14 alpha-demethylase [Monilinia fructicola]
68	AAU01157	51341094	lanosterol 14-alpha-demethylase [Coccidioides posadasii]
69	CAD27793	19572745	cytochrome P-450 14DM [Penicillium digitatum]
70	XP_384268	46116500	hypothetical protein FG04092.1 [Gibberella zeae PH-1]
71	AAG18433	10505323	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
72	AAK26391	13445823	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
73	AAG18431	10505318	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
74	AAK26386	13445813	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
75	AAD55135	5881952	eburicol 14-alpha demethylase; cytochrome P450 sterol 14-alpha demethylase; Erg11 [Uncinula necator]
76	AAK26389	13445819	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
77	CAC85409	15864613	euburicol 14 alpha-demethylase [Venturia nashicola]
78	BAB03659	9664027	cytochrome P-450 14DM [Penicillium digitatum]
79	AAG18435	10505329	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
80	AAG18434	10505326	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
81	AAU01158	51341096	lanosterol 14-alpha-demethylase [Ajellomyces capsulatus]

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82	AAK26387	13445815	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
83	AAG18432	10505321	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
84	AAK26388	13445817	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
85	XP_391200	46139019	hypothetical protein FG11024.1 [Gibberella zeae PH-1]
86	AAK26390	13445821	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
87	O14442	14916976	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Eburicol 14-alpha-demethylase) (P450-14DM)
88	AAG18438	10505336	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
89	XP_759809	71019157	sterol 14-alpha demethylase [Ustilago maydis 521]
90	AAF18468	6581118	eburicol 14 alpha-demethylase [Tapesia acuformis]
91	AAG18436	10505331	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
92	AAC49801	5733843	eburicol 14-alpha demethylase [Uncinula necator]
93	ABE01107	90823211	14alpha demethylase [Blumeriella jaapii]
94	AAG18437	10505334	eburicol 14 alpha-demethylase [Botryotinia fuckeliana]
95	CAD27792	19572743	cytochrome P-450 14DM [Penicillium digitatum]
96	XP_964049	85111674	hypothetical protein [Neurospora crassa OR74A]
97	AAF18469	11178694	eburicol 14 alpha-demethylase [Tapesia yallundae]
98	Q12664	2493386	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Eburicol 14-alpha-demethylase) (P450-14DM)
99	AAG44832	12006321	eburicol 14-alpha demethylase [Tapesia yallundae]
100	AAG44831	12006319	eburicol 14-alpha demethylase [Tapesia yallundae]
101	AAN28927	23505745	sterol 14 alpha-demethylase ERG11 [Leptosphaeria maculans]
102	XP_361987	39944900	hypothetical protein MG04432.4 [Magnaporthe grisea 70-15]
103	EAT88907	111067787	hypothetical protein SNOG_03702 [Phaeosphaeria nodorum SN15]
104	AAU01160	51341100	lanosterol 14-alpha-demethylase [Phanerochaete chrysosporium]
105	AAC23550	3220152	cytochrome P450 L1A1 demethylase [Pichia anomala]
106	AAU01159	51341098	lanosterol 14-alpha-demethylase [Coprinopsis cinerea]
107	Q9UVC3	12229768	Cytochrome P450 51 (CYPLI) (P450-LIA1) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
108	AAQ88128	37039509	cytochrome P450 lanosterol 14a-demethylase [Cryptococcus neoformans var. grubii H99]
109	NP_064394	71061451	cytochrome P450, family 51 [Mus musculus]
110	EAL24154	51094909	cytochrome P450, family 51, subfamily A, polypeptide 1 [Homo sapiens]
111	Q16850	3915660	Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
112	NP_999597	47523914	cytochrome P450 51 [Sus scrofa]
113	BAC27231	26326975	unnamed protein product [Mus musculus]
114	Q5RE72	83287777	Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
115	Q4PJW3	75075066	Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
116	AAF74562	8347236	lanosterol 14-alpha-demethylase [Mus musculus]
117	AAC50951	1698484	lanosterol 14-alpha demethylase [Homo sapiens]
118	XP_532457	57095976	PREDICTED: similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM) isoform 1 [Canis familiaris]
119	AAF73986	8215679	lanosterol 14-alpha-demethylase [Mus musculus]
120	AAH81210	51703589	MGC84806 protein [Xenopus laevis]
121	AAA87074	699396	lanosterol 14-alpha-demethylase

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122	XP_418650	50732469	PREDICTED: similar to lanosterol 14-demethylase [Gallus gallus]
123	BAE01508	67970330	unnamed protein product [Macaca fascicularis]
124	AAR89624	40748287	14-alpha demethylase [Fundulus heteroclitus]
125	NP_001...	50053648	cytochrome P450, family 51 [Strongylocentrotus purpuratus]
126	AAR89625	40748289	14-alpha demethylase [Danio rerio]
127	NP_001...	99028936	cytochrome P450, family 51 [Danio rerio]
128	CAJ81841	89268132	cytochrome P450, family 51, subfamily A, polypeptide 1 [Xenopus tropicalis]
129	AAR89626	40748291	14-alpha demethylase [Abudefduf saxatilis]

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Table 66. Examples of ERG4 polypeptides.

Row	ACCESSION	GI	PROTEIN DESCRIPTION
1	AAD13895	4261595	Unknown [Saccharomyces cerevisiae]
2	AAT93224	51013861	YGL012W [Saccharomyces cerevisiae]
3	AAY42962	66270055	C24 sterol reductase [Candida glabrata]
4	XP_451223	50302575	unnamed protein product [Kluyveromyces lactis]
5	NP_986579	45201009	AGL087Cp [Eremothecium gossypii]
6	XP_456709	50407411	hypothetical protein DEHA0A08888g [Debaryomyces hansenii CBS767]
7	XP_717662	68476402	sterol C-24 (28) reductase [Candida albicans SC5314]
8	XP_503021	50551095	hypothetical protein [Yarrowia lipolytica]
9	EAU37607	114195907	Delta(24(24(1)))-sterol reductase [Aspergillus terreus NIH2624]
10	BAE61064	83770931	unnamed protein product [Aspergillus oryzae]
11	NP_594742	19115654	hypothetical protein SPAC20G4.07c [Schizosaccharomyces pombe 972h-]
12	CAA45113	5109	sts1+ [Schizosaccharomyces pombe]
13	XP_662788	67538028	hypothetical protein AN5184.2 [Aspergillus nidulans FGSC A4]
14	XP_750461	70991224	c-24(28) sterol reductase [Aspergillus fumigatus Af293]
15	EAS37114	90307483	hypothetical protein CIMG_02468 [Coccidioides immitis RS]
16	XP_365763	39968745	hypothetical protein MG02465.4 [Magnaporthe grisea 70-15]
17	CAC18223	16944336	probable sterol C-24 reductase [Neurospora crassa]
18	XP_961419	85102913	probable sterol C-24 reductase [MIPS] [Neurospora crassa OR74A]
19	XP_660288	67524453	hypothetical protein AN2684.2 [Aspergillus nidulans FGSC A4]
20	EAU33849	114192149	Delta(24(24(1)))-sterol reductase [Aspergillus terreus NIH2624]
21	XP_753221	70996933	c-24(28) sterolreductase [Aspergillus fumigatus Af293]
22	BAE59624	83769489	unnamed protein product [Aspergillus oryzae]
23	EAT92432	111071312	predicted protein [Phaeosphaeria nodorum SN15]
24	XP_390179	46136975	hypothetical protein FG10003.1 [Gibberella zeae PH-1]
25	XP_757645	71005958	hypothetical protein UM01498.1 [Ustilago maydis 521]
26	EAS37449	90307818	hypothetical protein CIMG_02803 [Coccidioides immitis RS]
27	NP_820201	29654509	c-24(28) sterol reductase, putative [Coxiella burnetii RSA 493]
28	ZP_012...	94491050	hypothetical protein CburD_01001859 [Coxiella burnetii Dugway 7E9-12]
29	AAQ88130	37039513	sterol C-24 reductase [Cryptococcus neoformans var. grubii H99]
30	XP_569697	58265082	delta24(24-1) sterol reductase [Cryptococcus neoformans var. neoformans JEC21]
31	EAQ90721	88183253	hypothetical protein CHGG_02656 [Chaetomium globosum CBS 148.51]
32	BAE55606	83765463	unnamed protein product [Aspergillus oryzae]
33	CAJ06078	68128884	sterol C-24 reductase, putative [Leishmania major]
34	ABD46555	88601114	sterol C-24 reductase-like protein [Acanthamoeba castellanii]
35	XP_638613	66809779	ERG4/ERG24 ergosterol biosynthesis protein family protein [Dictyostelium discoideum AX4]

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Table 67. Examples of beta-carotene 15,15'-monooxygenase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAG15381	10242318	beta, beta-carotene 15,15'-dioxygenase [Mus musculus]
EDL92648	149038288	beta-carotene 15,15'-monooxygenase [Rattus norvegicus]
Q91XT5	46397349	Beta,beta-carotene 15,15'-monooxygenase (Beta-carotene dioxygenase 1)
XP_546815	57087275	PREDICTED: similar to Beta,beta-carotene 15,15-monooxygenase (Beta-carotene dioxygenase 1) [Canis familiaris]
XP_001...	149699876	PREDICTED: similar to beta, beta-carotene 15,15- dioxygenase [Equus caballus]
EAW95537	119615943	beta-carotene 15,15'-monooxygenase 1, isoform CRA_a [Homo sapiens]
Q9HAY6	41688803	Beta,beta-carotene 15,15'-monooxygenase (Beta-carotene dioxygenase 1)
BAA91776	7022941	unnamed protein product [Homo sapiens]
BAC35679	26344045	unnamed protein product [Mus musculus]
NP_001...	66792910	beta-carotene 15, 15'-monooxygenase 1 [Bos taurus]
XP_001...	126303742	PREDICTED: similar to beta, beta-carotene 15,15- dioxygenase [Monodelphis domestica]
XP_523435	114663815	PREDICTED: beta-carotene 15, 15'-monooxygenase 1 [Pan troglodytes]
XP_414163	50753878	PREDICTED: beta-carotene 15,15'-monooxygenase 1 [Gallus gallus]
EAW95538	119615944	beta-carotene 15,15'-monooxygenase 1, isoform CRA_b [Homo sapiens]
AAH56789	34784018	Zgc:63614 [Danio rerio]
NP_571873	42476258	beta-carotene 15,15'-monooxygenase 1 [Danio rerio]
CAC37566	13872740	putative b,b-carotene-15,15'-dioxygenase [Danio rerio]
CAF95764	47214429	unnamed protein product [Tetraodon nigroviridis]
CAF92469	47212035	unnamed protein product [Tetraodon nigroviridis]
ABQ09267	146186430	beta-carotene 15,15'-monooxygenase 1 [Oryzias latipes]
CAM14044	122890964	beta-carotene 15, 15-dioxygenase 2 [Danio rerio]
AAI33726	126631776	Bcdo2 protein [Rattus norvegicus]
CAC37567	13872742	putative b,b-carotene-9',10'-dioxygenase [Danio rerio]
AAI07007	76825286	Beta-carotene 9', 10'-dioxygenase 2 [Mus musculus]
AAI35025	141795614	Bcdo2l protein [Danio rerio]
NP_001...	55741954	beta-carotene dioxygenase 2 [Xenopus tropicalis]
XP_417929	118102019	PREDICTED: similar to carotene-9,10-monooxygenase [Gallus gallus]
Q5RF16	75042584	Beta,beta-carotene 9',10'-dioxygenase (Beta-carotene dioxygenase 2) (B-diox-II)
XP_001...	109108669	PREDICTED: beta-carotene dioxygenase 2 [Macaca mulatta]
BAC41782	26449309	hypothetical protein [Macaca fascicularis]
Q8HXG8	47117670	Beta,beta-carotene 9',10'-dioxygenase (Beta-carotene dioxygenase 2) (B-diox-II)
AAI15260	92098295	Beta-carotene 15, 15-dioxygenase 2 [Danio rerio]
AAS20392	42560440	carotene-9',10'-monooxygenase [Mustela putorius furo]
CAG03680	47217728	unnamed protein product [Tetraodon nigroviridis]
XP_536572	73955144	PREDICTED: similar to Beta,beta-carotene 9,10-dioxygenase (Beta-carotene dioxygenase 2) (B-diox-II) [Canis familiaris]
XP_001...	126327024	PREDICTED: similar to carotene-9,10-monooxygenase [Monodelphis domestica]
XP_001...	114640348	PREDICTED: beta-carotene dioxygenase 2 isoform 3 [Pan troglodytes]
XP_001...	114640346	PREDICTED: beta-carotene dioxygenase 2 isoform 4 [Pan troglodytes]
AAK69433	14582265	putative carotene dioxygenase [Homo sapiens]

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Q9BYV7	41688802	Beta,beta-carotene 9',10'-dioxygenase (Beta-carotene dioxygenase 2) (B-diox-II)
EAW67194	119587598	beta-carotene dioxygenase 2, isoform CRA_f [Homo sapiens]
EAW67189	119587593	beta-carotene dioxygenase 2, isoform CRA_a [Homo sapiens]
XP_001...	149716895	PREDICTED: similar to carotene-9,10-monooxygenase [Equus caballus]
NP_001...	82617628	beta-carotene dioxygenase 2 isoform b [Homo sapiens]
NP_114144	82617624	beta-carotene dioxygenase 2 isoform a [Homo sapiens]
CAC27994	12666531	putative b,b-carotene-9',10'-dioxygenase [Homo sapiens]
XP_508757	114640350	PREDICTED: hypothetical protein isoform 5 [Pan troglodytes]
BAB55379	14042749	unnamed protein product [Homo sapiens]
EAW67193	119587597	beta-carotene dioxygenase 2, isoform CRA_e [Homo sapiens]
NP_001...	147906096	hypothetical protein LOC791719 [Danio rerio]
XP_001...	125824393	PREDICTED: similar to retinal pigment epithelium 65b [Danio rerio]
AAH59559	37748750	Zgc:73213 [Danio rerio]
AAC14586	675485	retinal pigment epithelium-specific 61 kDa protein [Homo sapiens]
XP_001...	109008381	PREDICTED: retinal pigment epithelium-specific protein 65kDa [Macaca mulatta]
NP_001...	71480121	retinal pigment epithelium 65b [Danio rerio]
NP_084263	147902089	retinal pigment epithelium 65 [Mus musculus]
AAD42042	5326773	retinal pigment epithelium-specific protein RPE65 [Cercopithecus aethiops]
AAL01119	15488446	RPE65 [Mus musculus]
CAA46988	564	membrane receptor p63 [Bos taurus]
AAC37306	163657	retinal pigment epithelium-specific 65kD protein
EDL82582	149026339	retinal pigment epithelium 65 [Rattus norvegicus]
NP_446014	16758332	retinal pigment epithelium 65 [Rattus norvegicus]
NP_001...	148228575	retinal pigment epithelium-specific protein 65kDa [Xenopus laevis]
AAC72356	3851555	retinal pigment epithelium-specific protein RPE65 [Canis familiaris]
CAF98473	47220374	unnamed protein product [Tetraodon nigroviridis]
NP_001...	50978910	retinal pigment epithelium-specific protein 65kDa [Canis lupus familiaris]
AAD12758	4001821	RPE65 protein; retinal pigment epithelium 65-protein [Ambystoma tigrinum]
XP_001...	126305965	PREDICTED: similar to membrane receptor p63 [Monodelphis domestica]
NP_001...	156120623	hypothetical protein LOC514135 [Bos taurus]
Q9YGX2	48475042	Retinal pigment epithelium-specific 65 kDa protein
NP_001...	147906384	MGC85437 protein [Xenopus laevis]
NP_001...	118344140	beta-carotene-15,15'-monooxygenase [Ciona intestinalis]
BAC41351	26005798	retinal pigment epithelium abundant protein [Cynops pyrrhogaster]
XP_001...	114557125	PREDICTED: retinal pigment epithelium-specific protein 65kDa [Pan troglodytes]
NP_001...	148230104	beta-carotene dioxygenase 2 [Xenopus laevis]
XP_001...	114640352	PREDICTED: beta-carotene dioxygenase 2 isoform 2 [Pan troglodytes]
XP_001...	115928922	PREDICTED: similar to beta-carotene 15,15-dioxygenase [Strongylocentrotus purpuratus]
AAL39096	17432605	RPE65 [Mus musculus]
XP_001...	125816256	PREDICTED: similar to Beta-carotene 15, 15-dioxygenase 2 [Danio rerio]
XP_001...	156342819	hypothetical protein NEMVEDRAFT_v1g222532 [Nematostella vectensis]
XP_001...	125824367	PREDICTED: similar to retinal pigment epithelium 65b [Danio rerio]

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XP_001...	156393603	predicted protein [Nematostella vectensis]
XP_001...	156371447	predicted protein [Nematostella vectensis]
AAH67696	45767835	Bcdo2l protein [Danio rerio]
CAD45010	22657452	retinal pigment epithelium-specific protein [Canis familiaris]
NP_001...	118344130	RPE65 homolog [Ciona intestinalis]
XP_317319	118789286	ENSANGP00000006854 [Anopheles gambiae str. PEST]
EAA12399	157014990	AGAP008143-PA [Anopheles gambiae str. PEST]
AAY85350	68132170	carotenoid 9',10' monoxygenase II [Rattus norvegicus]
XP_001...	115969938	PREDICTED: similar to beta-carotene 15,15-dioxygenase, partial [Strongylocentrotus purpuratus]
XP_001...	157135394	beta-carotene dioxygenase [Aedes aegypti]
XP_967460	91093114	PREDICTED: similar to CG9347-PA [Tribolium castaneum]
NP_496729	71998242	Y46G5A.24 [Caenorhabditis elegans]
XP_001...	156398339	predicted protein [Nematostella vectensis]
XP_394000	66523635	PREDICTED: similar to neither inactivation nor afterpotential B CG9347-PA isoform 1 [Apis mellifera]
F88115	25395537	protein F53C3.12 [imported] - Caenorhabditis elegans
AAC67462	26251528	Hypothetical protein F53C3.12 [Caenorhabditis elegans]
XP_001...	149709742	PREDICTED: similar to retinal pigment epithelium abundant protein RPE65 [Equus caballus]
CAE71494	39582162	Hypothetical protein CBG18419 [Caenorhabditis briggsae]
CAE71509	39582177	Hypothetical protein CBG18441 [Caenorhabditis briggsae]
XP_001...	156555525	PREDICTED: similar to beta-carotene dioxygenase [Nasonia vitripennis]
XP_001...	125824371	PREDICTED: similar to retinal pigment epithelium 65b [Danio rerio]
CAF91639	47209442	unnamed protein product [Tetraodon nigroviridis]
CAG02881	47222516	unnamed protein product [Tetraodon nigroviridis]
CAG06487	47224917	unnamed protein product [Tetraodon nigroviridis]
EDL95460	149041619	beta-carotene 9', 10'-dioxygenase 2 [Rattus norvegicus]
YP_001...	154707125	putative dioxygenase [Coxiella burnetii Dugway 7E9-12]
NP_650307	24646669	neither inactivation nor afterpotential B CG9347-PA [Drosophila melanogaster]
BAA94508	7593040	DRPE65 [Drosophila melanogaster]
ZP_019...	153206838	dioxygenase, putative [Coxiella burnetii 'MSU Goat Q177']
AAH92162	62132948	Zgc:110538 [Danio rerio]
YP_444280	83814867	15,15' beta carotene dioxygenase [Salinibacter ruber DSM 13855]
BAB32248	12861637	unnamed protein product [Mus musculus]
EAW67192	119587596	beta-carotene dioxygenase 2, isoform CRA_d [Homo sapiens]
XP_001...	114640354	PREDICTED: hypothetical protein isoform 1 [Pan troglodytes]
BAC03747	21750237	unnamed protein product [Homo sapiens]
EAW67190	119587594	beta-carotene dioxygenase 2, isoform CRA_b [Homo sapiens]
XP_001...	125774315	GA21719-PA [Drosophila pseudoobscura]
YP_001...	134096631	lignostilbene-alpha/beta-dioxygenase [Saccharopolyspora erythraea NRRL 2338]
EAW67191	119587595	beta-carotene dioxygenase 2, isoform CRA_c [Homo sapiens]
XP_001...	149486496	PREDICTED: similar to b,b-carotene-9,10-dioxygenase, partial [Ornithorhynchus anatinus]
AAO90531	29541592	dioxygenase, putative [Coxiella burnetii RSA 493]
XP_001...	109129384	PREDICTED: similar to Beta,beta-carotene 15,15-monooxygenase (Beta-carotene dioxygenase 1) [Macaca mulatta]
CAJ53109	109626642	beta,beta-carotene 9',10'-dioxygenase 2 [Haloquadratum walsbyi DSM 16790]
XP_001...	109129778	PREDICTED: similar to Beta,beta-carotene 15,15-monooxygenase

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		(Beta-carotene dioxygenase 1), partial [Macaca mulatta]
XP_001...	118109416	PREDICTED: similar to beta-carotene 15,15-dioxygenase, partial [Gallus gallus]
ABF70124	102139989	dioxygenase-related protein [Musa balbisiana]
AAW59435	57918684	decreased apical dominance protein [Petunia x hybrida]
EAY74583	125526469	hypothetical protein OsI_002430 [Oryza sativa (indica cultivar-group)]
AAL66961	18377622	unknown protein [Arabidopsis thaliana]
EAY74584	125526470	hypothetical protein OsI_002431 [Oryza sativa (indica cultivar-group)]
BAC05598	21902049	putative dioxygenase [Oryza sativa (japonica cultivar-group)]
AAW33596	57116144	Dad1/CCD8 [Petunia x hybrida]
NP_001...	115439899	Os01g0746400 [Oryza sativa (japonica cultivar-group)]
EAY75798	125527684	hypothetical protein OsI_003645 [Oryza sativa (indica cultivar-group)]
EAZ13518	125572003	hypothetical protein OsJ_003343 [Oryza sativa (japonica cultivar-group)]
ABQ08577	146160696	beta-carotene 15,15'-monooxygenase 2 [Oryzias latipes]
BAB63485	15289786	retinal pigment epithelium 65-like [Oryza sativa (japonica cultivar-group)]
AAS66906	45504725	dioxygenase RAMOSUS1 [Pisum sativum]
ZP_013...	95927318	hypothetical protein CburR_01000925 [Coxiella burnetii RSA 331]
YP_658115	110668304	beta,beta-carotene 15,15'-monooxygenase; beta-carotene dioxygenase 1 [Haloquadratum walsbyi DSM 16790]
CAL90971	121495644	torulene oxygenase [Gibberella fujikuroi]
YP_134677	55376826	retinal pigment epithelial membrane protein [Haloarcula marismortui ATCC 43049]
CAL90970	121495642	torulene oxygenase [Gibberella fujikuroi]
XP_382801	46111487	hypothetical protein FG02625.1 [Gibberella zeae PH-1]
XP_001...	149480289	PREDICTED: similar to carotene-9,10-monooxygenase, partial [Ornithorhynchus anatinus]
ABQ76053	148508268	beta,beta-carotene 9',10'-dioxygenase 2 [uncultured haloarchaeon]
YP_657779	110667968	beta,beta-carotene 9',10'-dioxygenase 2 [Haloquadratum walsbyi DSM 16790]
XP_001...	109149184	PREDICTED: similar to Beta,beta-carotene 15,15-monooxygenase (Beta-carotene dioxygenase 1), partial [Macaca mulatta]
AAP92577	33086530	Ab2-079 [Rattus norvegicus]
ABN50352	125662819	carotenoid cleavage dioxygenase 1 [Hypocrea jecorina]
EAL93736	66853412	dioxygenase, putative [Aspergillus fumigatus Af293]
XP_001...	125876361	PREDICTED: hypothetical protein, partial [Danio rerio]
XP_001...	119481741	dioxygenase, putative [Neosartorya fischeri NRRL 181]
XP_001...	119494253	retinal pigment epithelial membrane family protein [Neosartorya fischeri NRRL 181]
XP_958452	85090512	hypothetical protein [Neurospora crassa OR74A]
EDO64867	157069539	predicted protein [Neurospora crassa OR74A]
XP_001...	121716178	dioxygenase, putative [Aspergillus clavatus NRRL 1]
CAL64769	148353839	putative carotene oxygenase [Blakeslea trispora]
BAD79505	56686283	lignostilbene-alpha beta-dioxygenase [Synechococcus elongatus PCC 6301]
ZP_016...	119509407	Retinal pigment epithelial membrane protein [Nodularia spumigena CCY9414]
BAE56886	83766746	unnamed protein product [Aspergillus oryzae]
BAE59247	83769110	unnamed protein product [Aspergillus oryzae]
ECC98172	139038333	hypothetical protein GOS_5249294 [marine metagenome]
ZP_017...	126656631	Beta-carotene 15,15'-dioxygenase [Cyanothece sp. CCY0110]
BAC91630	35214261	gll3689 [Gloeobacter violaceus PCC 7421]

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EAT90277	111069157	hypothetical protein SNOG_02065 [Phaeosphaeria nodorum SN15]
CAB79998	7270228	putative protein [Arabidopsis thaliana]
CAL49287	117557505	putative carotene-dioxygenase [Rhizopus oryzae]
XP_659308	67522495	hypothetical protein AN1704.2 [Aspergillus nidulans FGSC A4]
XP_001...	125824373	PREDICTED: similar to retinal pigment epithelium 65b [Danio rerio]
XP_001...	119185939	hypothetical protein CIMG_03017 [Coccidioides immitis RS]
2BIWB	66361521	Chain B, Crystal Structure Of Apocarotenoid Cleavage Oxygenase From Synechocystis, Native Enzyme
ABA20860	75701184	Retinal pigment epithelial membrane protein [Anabaena variabilis ATCC 29413]
XP_001...	116207620	hypothetical protein CHGG_03103 [Chaetomium globosum CBS 148.51]
XP_001...	145257182	hypothetical protein An04g02710 [Aspergillus niger]
BAB75983	17133419	lignostilbene-alpha,beta-dioxygenase [Nostoc sp. PCC 7120]
XP_501958	50548975	hypothetical protein [Yarrowia lipolytica]
XP_001...	109129782	PREDICTED: similar to Beta,beta-carotene 15,15-monooxygenase (Beta-carotene dioxygenase 1), partial [Macaca mulatta]
ZP_016...	119484919	Retinal pigment epithelial membrane protein [Lyngbya sp. PCC 8106]
ZP_017...	126656882	Retinal pigment epithelial membrane protein [Cyanothece sp. CCY0110]
XP_001...	109149035	PREDICTED: similar to Beta,beta-carotene 15,15-monooxygenase (Beta-carotene dioxygenase 1), partial [Macaca mulatta]
CAL49288	117557507	putative carotene-dioxygenase [Rhizopus oryzae]
ZP_001...	23130610	COG3670: Lignostilbene-alpha,beta-dioxygenase and related enzymes [Nostoc punctiforme PCC 73102]
XP_362433	39945792	hypothetical protein MGG_08016 [Magnaporthe grisea 70-15]
XP_001...	115951205	PREDICTED: hypothetical protein [Strongylocentrotus purpuratus]
AAC12875	3033545	lignostilbene-alpha,beta-dioxygenase [Synechococcus sp. PCC 7942]
XP_001...	154282379	conserved hypothetical protein [Ajellomyces capsulatus NAm1]
ABG52331	110167791	Carotenoid oxygenase [Trichodesmium erythraeum IMS101]
ABC99263	86554305	putative lignostilbene-alpha,beta-dioxygenase [Synechococcus sp. JA-3-3Ab]
NP_931511	37528166	hypothetical protein plu4336 [Photorhabdus luminescens subsp. laumondii TTO1]
EDD33453	143171893	hypothetical protein GOS_1320815 [marine metagenome]
XP_001...	115387251	predicted protein [Aspergillus terreus NIH2624]
YP_885943	118467371	lignostilbene-alpha,beta-dioxygenase [Mycobacterium smegmatis str. MC2 155]

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Table 68. Examples of beta-carotene retinol dehydrogenase polypeptides.

ACCESSION	GI	PROTEIN DESCRIPTION
AAX33670	60678607	epithelial retinol dehydrogenase [Mus musculus]
BAC34110	26340896	unnamed protein product [Mus musculus]
XP_001...	149730699	PREDICTED: similar to short-chain dehydrogenase/reductase RETSDR8 [Equus caballus]
XP_545513	74004823	PREDICTED: similar to NADP-dependent retinol dehydrogenase/reductase [Canis familiaris]
Q8HYR6	75064969	Dehydrogenase/reductase SDR family member 9 precursor (3-alpha hydroxysteroid dehydrogenase) (3alpha-HSD) (Short-chain dehydrogenase/reductase retSDR8)
XP_001...	114581559	PREDICTED: NADP-dependent retinol dehydrogenase/reductase isoform 3 [Pan troglodytes]
XP_001...	109099963	PREDICTED: similar to NADP-dependent retinol dehydrogenase/reductase isoform 3 [Macaca mulatta]
AAL37037	17224600	short-chain dehydrogenase/reductase RETSDR8 [Homo sapiens]
AAD32458	4894382	retinol dehydrogenase homolog [Homo sapiens]
XP_001...	126326289	PREDICTED: similar to short-chain dehydrogenase/reductase RETSDR8 [Monodelphis domestica]
XP_001...	149639643	PREDICTED: similar to short-chain dehydrogenase/reductase RETSDR8 [Ornithorhynchus anatinus]
XP_001...	114581568	PREDICTED: NADP-dependent retinol dehydrogenase/reductase isoform 1 [Pan troglodytes]
AAF82748	9082139	retinol dehydrogenase homolog isoform-1 [Homo sapiens]
XP_001...	109099969	PREDICTED: similar to NADP-dependent retinol dehydrogenase/reductase isoform 1 [Macaca mulatta]
AAY24306	62988919	unknown [Homo sapiens]
XP_422015	118093666	PREDICTED: similar to short-chain dehydrogenase/reductase RETSDR8 [Gallus gallus]
XP_001...	114581566	PREDICTED: NADP-dependent retinol dehydrogenase/reductase isoform 2 [Pan troglodytes]
NP_001...	147905288	NADP-dependent retinol dehydrogenase/reductase [Xenopus laevis]
AAH67304	45501367	Dehydrogenase/reductase (SDR family) member 9 [Xenopus tropicalis]
EDM16447	149066574	rCG60176, isoform CRA_a [Rattus norvegicus]
AAH62000	38303814	Rdh2 protein [Rattus norvegicus]
AAC52316	1072046	retinol dehydrogenase type II
NP_001...	148227174	hypothetical protein LOC398882 [Xenopus laevis]
NP_033066	6677697	retinol dehydrogenase 16 [Mus musculus]
NP_001...	147900576	hypothetical protein LOC432178 [Xenopus laevis]
NP_694773	23680945	retinol dehydrogenase 9 [Mus musculus]
NP_003716	19743808	hydroxysteroid (17-beta) dehydrogenase 6 [Homo sapiens]
BAE21017	74205129	unnamed protein product [Mus musculus]
EDL24523	148692576	mCG140848 [Mus musculus]
AAL14860	22651436	cis-retinol/3alpha hydroxysterol short-chain dehydrogenase-like protein [Mus musculus]
P55006	1710631	Retinol dehydrogenase 7 (Retinol dehydrogenase type III) (RODH III)
AAH82896	52354822	LOC494781 protein [Xenopus laevis]
XP_001...	109097334	PREDICTED: similar to 3-hydroxysteroid epimerase [Macaca mulatta]
AAI35515	134023801	LOC100124842 protein [Xenopus tropicalis]
P50169	1710629	Retinol dehydrogenase 3 (Retinol dehydrogenase type I) (RODH I)
BAC98304	37360649	cis-retinol/androgen dehydrogenase type 3 [Mus musculus]
NP_663399	21703846	cis-retinol/3alpha hydroxysterol short-chain dehydrogenase-like [Mus musculus]

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AAB07997	841197	retinol dehydrogenase type I
XP_001...	126343946	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 [Monodelphis domestica]
NP_775427	27545384	hydroxysteroid (17-beta) dehydrogenase 6 [Rattus norvegicus]
EDL24527	148692580	mCG134493 [Mus musculus]
XP_531641	73968454	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 isoform 1 [Canis familiaris]
AAH24603	19354049	Retinol dehydrogenase 7 [Mus musculus]
AAL02134	22074192	retinol dehydrogenase similar protein 2 [Mus musculus]
NP_536684	20147789	retinol dehydrogenase 1 (all trans) [Mus musculus]
AAH88104	56789874	Hydroxysteroid (17-beta) dehydrogenase 6 [Rattus norvegicus]
EDL24532	148692585	hydroxysteroid (17-beta) dehydrogenase 9, isoform CRA_a [Mus musculus]
ABG81445	110665598	microsomal NAD+-dependent retinol dehydrogenase 4 [Bos taurus]
EDL24533	148692586	hydroxysteroid (17-beta) dehydrogenase 9, isoform CRA_b [Mus musculus]
XP_538239	73968448	PREDICTED: similar to 3-hydroxysteroid epimerase isoform 3 [Canis familiaris]
CAJ81333	89272084	novel retinol dehydrogenase protein [Xenopus tropicalis]
AAH46694	28302191	Rodh-A-prov protein [Xenopus laevis]
XP_001...	149715148	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 [Equus caballus]
XP_001...	109097338	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 isoform 2 [Macaca mulatta]
XP_001...	109097336	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 isoform 3 [Macaca mulatta]
XP_858182	73968456	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 isoform 2 [Canis familiaris]
AAI02627	74354657	Similar to 3-hydroxysteroid epimerase [Bos taurus]
XP_858059	73968446	PREDICTED: similar to 3-hydroxysteroid epimerase isoform 4 [Canis familiaris]
AAC39922	3372592	sterol/retinol dehydrogenase [Homo sapiens]
AAY44823	66354281	retinol dehydrogenase 5 [Danio rerio]
XP_522604	55639443	PREDICTED: retinol dehydrogenase 16 [Pan troglodytes]
AAH97151	66911361	Retinol dehydrogenase 5 (11-cis/9-cis) [Danio rerio]
CAK05049	94732559	novel protein similar to vertebrate retinol dehydrogenase family [Danio rerio]
NP_990044	45382649	11-cis retinol dehydrogenase [Gallus gallus]
EAW96968	119617374	retinol dehydrogenase 16 (all-trans and 13-cis) [Homo sapiens]
NP_001...	148233310	hypothetical protein LOC398939 [Xenopus laevis]
CAG04959	47218630	unnamed protein product [Tetraodon nigroviridis]
AAH88014	56789076	Hypothetical LOC496749 [Xenopus tropicalis]
AAI23192	114107846	Rdh9 protein [Xenopus laevis]
AAC72923	3859946	retinol dehydrogenase [Homo sapiens]
AAF82747	9082137	retinol dehydrogenase homolog isoform-2 [Homo sapiens]
AAH75455	49522586	MGC89248 protein [Xenopus tropicalis]
AAH59614	37590384	Retinol dehydrogenase 1, like [Danio rerio]
AAB88252	2661211	oxidative 3 alpha hydroxysteroid dehydrogenase [Homo sapiens]
EDL24633	148692686	retinol dehydrogenase 5, isoform CRA_b [Mus musculus]
BAE22435	74149341	unnamed protein product [Mus musculus]
XP_538220	73968269	PREDICTED: similar to 11-cis retinol dehydrogenase (11-cis RDH) [Canis familiaris]
NP_001...	147899633	MGC84134 protein [Xenopus laevis]

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XP_001...	109097121	PREDICTED: retinol dehydrogenase 5 (11-cis and 9-cis) [Macaca mulatta]
NP_001...	147905378	MGC84099 protein [Xenopus laevis]
CAF92451	47210426	unnamed protein product [Tetraodon nigroviridis]
XP_522429	55638373	PREDICTED: similar to 11-cis retinol dehydrogenase isoform 2 [Pan troglodytes]
AAH88529	56788840	Hypothetical LOC496830 [Xenopus tropicalis]
NP_002896	50726952	retinol dehydrogenase 5 (11-cis and 9-cis) [Homo sapiens]
CAA57715	663171	11-cis retinol dehydrogenase [Bos taurus]
AAH28298	20271410	Retinol dehydrogenase 5 (11-cis/9-cis) [Homo sapiens]
NP_001...	148230094	hypothetical protein LOC399015 [Xenopus laevis]
AAA80694	1054531	11-cis-retinol dehydrogenase
NP_932335	37620196	retinol dehydrogenase 1 [Danio rerio]
XP_538240	73968424	PREDICTED: similar to orphan short-chain dehydrogenase / reductase [Canis familiaris]
AAI34659	134024746	MGC151815 protein [Bos taurus]
AAH64820	40673988	Orphan short chain dehydrogenase/reductase [Mus musculus]
EDL24531	148692584	orphan short chain dehydrogenase/reductase [Mus musculus]
AAB93668	1916935	9-cis-retinol specific dehydrogenase [Homo sapiens]
XP_001...	149715290	PREDICTED: hypothetical protein [Equus caballus]
XP_001...	109482100	PREDICTED: similar to retinol dehydrogenase similar protein [Rattus norvegicus]
EAW96967	119617373	orphan short-chain dehydrogenase / reductase [Homo sapiens]
XP_522439	114644207	PREDICTED: orphan short-chain dehydrogenase / reductase [Pan troglodytes]
EDL24528	148692581	mCG134494, isoform CRA_a [Mus musculus]
ABQ09278	146186452	retinol dehydrogenase 1 [Oryzias latipes]
ABQ09279	146186454	retinol dehydrogenase 5 [Oryzias latipes]
XP_001...	109097340	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 isoform 1 [Macaca mulatta]
EDM16444	149066571	orphan short chain dehydrogenase/reductase [Rattus norvegicus]
AAG44849	12006418	microsomal retinol dehydrogenase [Branchiostoma lanceolatum]
BAE88760	90078160	unnamed protein product [Macaca fascicularis]
AAG44847	12006414	microsomal retinol dehydrogenase 1 [Branchiostoma floridae]
XP_782726	115665382	PREDICTED: similar to retinol dehydrogenase type 1, partial [Strongylocentrotus purpuratus]
XP_001...	115939186	PREDICTED: similar to retinol dehydrogenase type 1 [Strongylocentrotus purpuratus]
XP_001...	118093664	PREDICTED: similar to MGC83505 protein [Gallus gallus]
XP_781379	115654644	PREDICTED: similar to retinol dehydrogenase type 1, partial [Strongylocentrotus purpuratus]
XP_001...	115958895	PREDICTED: similar to retinol dehydrogenase type 1 [Strongylocentrotus purpuratus]
AAG44848	12006416	microsomal retinol dehydrogenase 2 [Branchiostoma floridae]
XP_001...	115960451	PREDICTED: similar to retinol dehydrogenase type III [Strongylocentrotus purpuratus]
EDL84786	149029615	rCG42422, isoform CRA_a [Rattus norvegicus]
AAL14861	22651438	cis-retinol/3alpha hydroxysterol short-chain dehydrogenase-like protein isoform [Mus musculus]
XP_001...	156386264	predicted protein [Nematostella vectensis]
XP_001...	156389613	predicted protein [Nematostella vectensis]
XP_001...	156368581	predicted protein [Nematostella vectensis]
XP_001...	156362183	predicted protein [Nematostella vectensis]

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BAC28142	26328807	unnamed protein product [Mus musculus]
XP_001...	156367012	predicted protein [Nematostella vectensis]
XP_001...	156367010	predicted protein [Nematostella vectensis]
CAG14527	47203967	unnamed protein product [Tetraodon nigroviridis]
XP_001...	156367016	predicted protein [Nematostella vectensis]
XP_001...	156401057	predicted protein [Nematostella vectensis]
AAB69884	2384782	Dehydrogenases, short chain protein 16 [Caenorhabditis elegans]
XP_001...	156367014	predicted protein [Nematostella vectensis]
XP_001...	156367008	predicted protein [Nematostella vectensis]
NP_871815	32563809	DeHydrogenases, Short chain family member (dhs-2) [Caenorhabditis elegans]
NP_491575	17507613	DeHydrogenases, Short chain family member (dhs-2) [Caenorhabditis elegans]
NP_505941	115534660	DeHydrogenases, Short chain family member (dhs-20) [Caenorhabditis elegans]
CAE74886	39583813	Hypothetical protein CBG22749 [Caenorhabditis briggsae]
XP_001...	156408325	predicted protein [Nematostella vectensis]
XP_001...	126343453	PREDICTED: similar to 3-hydroxybutyrate dehydrogenase, type 1 [Monodelphis domestica]
CAE64533	39593064	Hypothetical protein CBG09275 [Caenorhabditis briggsae]
XP_001...	149571441	PREDICTED: similar to retinol dehydrogenase similar protein, partial [Ornithorhynchus anatinus]
NP_955017	49227085	truncated cis-retinol/3alpha-hydroxysterol short-chain dehydrogenase [Mus musculus]
XP_001...	156363786	predicted protein [Nematostella vectensis]
XP_001...	109097342	PREDICTED: similar to microsomal NAD+-dependent retinol dehydrogenase 4 [Macaca mulatta]
NP_001...	147899736	hypothetical protein LOC100037356 [Danio rerio]
XP_001...	156366980	predicted protein [Nematostella vectensis]
XP_001...	125853068	PREDICTED: hypothetical protein [Danio rerio]
AAH11964	15080429	3-hydroxybutyrate dehydrogenase, type 1 [Homo sapiens]
XP_345771	109480152	PREDICTED: similar to retinol dehydrogenase 5 [Rattus norvegicus]
XP_001...	149731507	PREDICTED: similar to 3-hydroxybutyrate dehydrogenase, type 1 [Equus caballus]
NP_976059	44680136	3-hydroxybutyrate dehydrogenase precursor [Homo sapiens]
XP_001...	149633623	PREDICTED: similar to 3-hydroxybutyrate dehydrogenase, type 1 [Ornithorhynchus anatinus]
AAH89597	58476255	BC089597 protein [Mus musculus]
XP_001...	114591350	PREDICTED: 3-hydroxybutyrate dehydrogenase isoform 1 [Pan troglodytes]
XP_516981	114591348	PREDICTED: 3-hydroxybutyrate dehydrogenase isoform 2 [Pan troglodytes]
XP_001...	156405501	predicted protein [Nematostella vectensis]
CAG04267	47223406	unnamed protein product [Tetraodon nigroviridis]
XP_545160	74002972	PREDICTED: similar to 3-hydroxybutyrate dehydrogenase precursor [Canis familiaris]
AAI03052	73587365	3-hydroxybutyrate dehydrogenase, type 1 [Bos taurus]
BAF35260	116267595	11beta-hydroxysteroid dehydrogenase short form [Anguilla japonica]
AAH65613	41350974	Hydroxysteroid 11-beta dehydrogenase 2 [Danio rerio]
AAB59684	203921	D-beta-hydroxybutyrate dehydrogenase
BAE27076	74226863	unnamed protein product [Mus musculus]
NP_446447	55742813	3-hydroxybutyrate dehydrogenase, type 1 [Rattus norvegicus]
P29147	68837285	D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor

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		(BDH) (3-hydroxybutyrate dehydrogenase)
EDK97750	148665334	3-hydroxybutyrate dehydrogenase, type 1 [Mus musculus]
CAE75331	39592111	Hypothetical protein CBG23309 [Caenorhabditis briggsae]
BAE23523	74206030	unnamed protein product [Mus musculus]
BAC36453	26345604	unnamed protein product [Mus musculus]
ABH02937	110931880	17-beta hydroxysteroid dehydrogenase 2 [Bos taurus]
NP_509415	17568189	F55E10.6 [Caenorhabditis elegans]
XP_546810	73957269	PREDICTED: similar to hydroxysteroid (17-beta) dehydrogenase 2 [Canis familiaris]
XP_001...	115925077	PREDICTED: similar to retinol dehydrogenase type 1 [Strongylocentrotus purpuratus]
AAA58352	177198	(R)-3-hydroxybutyrate dehydrogenase
XP_422703	50752249	PREDICTED: hypothetical protein [Gallus gallus]
XP_001...	149640222	PREDICTED: similar to 17-beta hydroxysteroid dehydrogenase 2 [Ornithorhynchus anatinus]
XP_511130	114663836	PREDICTED: hydroxysteroid (17-beta) dehydrogenase 2 [Pan troglodytes]
P37059	544152	Estradiol 17-beta-dehydrogenase 2 (17-beta-HSD 2) (Microsomal 17-beta-hydroxysteroid dehydrogenase) (20 alpha-hydroxysteroid dehydrogenase) (20-alpha-HSD) (E2DH)
AAV38556	54696368	hydroxysteroid (17-beta) dehydrogenase 2 [synthetic construct]
AAH90448	60649586	Hsd17b2 protein [Danio rerio]
XP_001...	118087716	PREDICTED: hypothetical protein [Gallus gallus]
NP_001...	93277072	hydroxysteroid (17-beta) dehydrogenase 2 [Danio rerio]
P51658	2507561	Estradiol 17-beta-dehydrogenase 2 (17-beta-HSD 2) (17-beta-hydroxysteroid dehydrogenase 2)
BAC76709	30844232	11-beta-hydroxysteroid dehydrogenase [Oncorhynchus mykiss]
AAY84567	67975199	17-beta hydroxysteroid dehydrogenase 2 [Macaca fascicularis]
BAD96721	62897563	hydroxysteroid (17-beta) dehydrogenase 2 variant [Homo sapiens]
XP_414168	118096516	PREDICTED: similar to 17 beta hydroxysteroid dehydrogenase type 2 [Gallus gallus]
CAE66933	39589698	Hypothetical protein CBG12325 [Caenorhabditis briggsae]
AAK95857	22074155	retinol dehydrogenase similar protein [Rattus norvegicus]
AAH74144	49257832	MGC81883 protein [Xenopus laevis]
XP_001...	125850087	PREDICTED: hypothetical protein [Danio rerio]
AAH90181	58701977	Zgc:113142 [Danio rerio]
AAA87007	755574	11-beta-hydroxylsteroid dehydrogenase type 2
Q62730	3334165	Estradiol 17-beta-dehydrogenase 2 (17-beta-HSD 2) (17-beta-hydroxysteroid dehydrogenase 2)
XP_001...	115956172	PREDICTED: similar to Retinol dehydrogenase 3 (Retinol dehydrogenase type I) (RODH I) [Strongylocentrotus purpuratus]
CAA64982	1200097	17-beta-hydroxysteroid dehydrogenase type II [Mus musculus]
EDL11587	148679640	hydroxysteroid (17-beta) dehydrogenase 2 [Mus musculus]
EDL92656	149038296	hydroxysteroid (17-beta) dehydrogenase 2 [Rattus norvegicus]
XP_001...	149626583	PREDICTED: similar to 11 beta-hydroxysteroid dehydrogenase type 2 [Ornithorhynchus anatinus]
XP_001...	109482098	PREDICTED: similar to Retinol dehydrogenase 2 (Retinol dehydrogenase type II) (RODH II) (29 k-protein) [Rattus norvegicus]
XP_001...	109128927	PREDICTED: similar to Corticosteroid 11-beta-dehydrogenase isozyme 2 (11-DH2) (11-beta-hydroxysteroid dehydrogenase type 2) (11-beta-HSD2) (NAD-dependent 11-beta-hydroxysteroid dehydrogenase) [Macaca mulatta]

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Table 69. Genes Comprising the SAGA Complex.

S. cerevisiae gene	*Y lipolytica* gene
SPT3	YALI0E21417g
SPT7	none identified
SPT8	YALI0E23804g
SPT20	YALI0C04070g
ADA2	YALI0F14443g
ADA3	none identified
GCN5	YALI0E02772g
ADA1	none identified
TRA1	YALI0C02057g

Equivalents

[00477] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. The scope of the present invention is not intended to be limited to the above Description, but rather is as set forth in the following claims:

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CLAIMS

1. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one carotenoid, and can accumulate the produced carotenoid to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, which parental fungus both is not oleaginous and does not accumulate the carotenoid to at least about 1% of its dry cell weight, the at least one modification being selected from the group consisting of carotenogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one carotenoid to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one carotenoid which the parental fungus does not produce.

2. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one carotenoid selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof, and can accumulate the produced carotenoid to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of carotenogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one carotenoid to a level at least about 1% of its dry cell weight, or confers to the

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recombinant fungus the ability to produce at least one carotenoid which the parental fungus does not naturally produce.

3. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one carotenoid, and can accumulate the produced carotenoid to at least about 1% of its dry cell weight;

wherein the recombinant fungus is a member of a genus selected from the group consisting of: *Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia)*, and *Yarrowia*

or is a species selected from the group consisting of:

Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), and *Yarrowia lipolytica*

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of carotenogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one carotenoid to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one carotenoid which the parental fungus does not naturally produce.

4. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one carotenoid selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-

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cryptoxanthin, α-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof, and can accumulate the produced carotenoid to at least about 1% of its dry cell weight;

wherein the recombinant fungus is a member of a genus selected from the group consisting of:

Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia), and *Yarrowia*

or is of a species selected from the group consisting of:

Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), and *Yarrowia lipolytica*

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of carotenogenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one carotenoid to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one carotenoid which the parental fungus does not naturally produce.

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5. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Saccharomyces, Xanthophyllomyces (Phaffia)*, and *Yarrowia*

6. The recombinant fungus of claim 5 wherein the recombinant fungus is a member of the genus *Saccharomyces* genus.

7. The recombinant fungus of claim 5 wherein the recombinant fungus is a member of the genus *Xanthophyllomyces (Phaffia)*.

8. The recombinant fungus of claim 5 wherein the recombinant fungus is a member of the genus *Yarrowia*.

9. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Candida utilis, Saccharomyces cerevisiae, Xanthophyllomyces dendrorhous (Phaffia rhodozyma)*, and *Yarrowia lipolytica*.

10. The recombinant fungus of claim 9 wherein the recombinant fungus of the species *Candida utilis*.

11. The recombinant fungus of claim 9 wherein the recombinant fungus of the species *Saccharomyces cerevisiae*.

12. The recombinant fungus of claim 9 wherein the recombinant fungus of the species *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)*.

13. The recombinant fungus of claim 9 wherein the recombinant fungus of the species *Yarrowia lipolytica*.

14. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Aspergillus, Candida, Cunninghamella, Kluyveromyces, Lipomyces, Mortierella, Pichia (Hansenula), Rhodosporidium, Rhodotorula, Trichoderma*, and *Trichosporon*.

15. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Cunninghamella echinulata, Cunninghamella elegans, Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Pichia pastoris, Rhodosporidium toruloides, Rhodotorula glutinis, Trichoderma reesei*, and *Trichosporon pullans*.

16. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Cercospora, Fusarium (Gibberella), Mucor, Neurospora, Penicillium, Phycomyces, Puccinia*, and *Pythium*.

17. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Cercospora nicotianae, Fusarium fujikuroi (Gibberella zeae), Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Puccinia distincta, Pythium*

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irregulare, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, and *Trichosporon cutaneum.*

18. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Botrytis, Cryptococcus,* and *Sclerotium*

19. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a species selected from the group consisting of: *Botrytis cinerea, Cryptococcus curvatus, Sclerotium rolfsii.*

20. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus grows as a single cell.

21. The recombinant fungus of any one of claims 1-4 wherein the recombinant fungus is a yeast.

22. The recombinant fungus of any one of claims 1, 3, or 5-21 wherein the carotenoid is carotenoid is selected from the group consisting of adonirubin, astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, phytoene, phytofluene, and combinations thereof.

23. The recombinant fungus of any one of claims 1-21 wherein the carotenoid is selected from the group consisting of adonirubin, astaxanthin, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, phytoene, phytofluene and combinations thereof.

24. The recombinant fungus of claim 22 wherein the carotenoid is β-carotene.

25. The recombinant fungus of claim 22 wherein the carotenoid is predominantly β-carotene.

26. The recombinant fungus of claim 22 or 23 wherein the carotenoid is selected from the group consisting of: canthaxanthin, echinenone, and β-cryptoxanthin.

27. The recombinant fungus of claim 22 or 23 wherein the carotenoid is zeaxanthin

28. The recombinant fungus of claim 22 or 23 wherein the carotenoid is lutein.

29. The recombinant fungus of claim 22 or 23 wherein the carotenoid is astaxanthin.

30. The recombinant fungus of claim 22 or 23 wherein the carotenoid is phytoene.

31. The recombinant fungus of claim 22 or 23 wherein the carotenoid is phytofluene.

32. The recombinant fungus of claim 22 or 23 wherein the carotenoid is adonirubin.

33. The recombinant fungus of claim 22 or 23 wherein the carotenoid is adonixanthin.

34. The recombinant fungus of any one of claims 1-33 wherein the parental fungus is oleaginous.

35. The recombinant fungus of 1-33 wherein the parental fungus is not oleaginous.

36. The recombinant fungus of any one of claims 1-35 wherein the parental fungus does not naturally produce the at least one carotenoid.

37. The recombinant fungus of any one of claims 1-35 wherein the parental fungus naturally produces the at least one carotenoid.

38. The recombinant fungus of any one of claims 1-37 wherein the parental fungus does not naturally produce at least one carotenoid.

39. The recombinant fungus of any one of claims 1-37 wherein the parental fungus naturally produces at least one carotenoid.

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40. The recombinant fungus of any one of claims 1-39 wherein the recombinant fungus grows as a single cell.

41. The recombinant fungus of any one of claims 1-39 wherein the recombinant fungus is a yeast.

42. The recombinant fungus of any one of claims 1-41 wherein the recombinant fungus contains at least one oleaginic modification.

43. The recombinant fungus of claim 42 wherein the at least one oleaginic modification confers oleaginy upon the fungus.

44. The fungus of claim 42 wherein the at least one oleaginic modification alters oleaginicity of the fungus.

45. The recombinant fungus of claim 42 wherein the recombinant fungus further comprises at least one carotenogenic modification wherein the carotenogenic modification confers to the recombinant fungus the ability to produce the at least one carotenoid to a level at least about 1% of its dry cell weight or confers to the recombinant fungus the ability to produce at least one carotenoid which the parental fungus does not naturally produce.

46. The recombinant fungus of any one of claims 42-45 wherein the at least one oleaginic modification increases expression or activity of at least one oleaginic polypeptide.

47. The recombinant fungus of any one of claims 42-45 wherein the at least one oleaginic modification decreases expression or activity of at least one oleaginic polypeptide.

48. The recombinant fungus of any one of claims 42-45 wherein the at least one oleaginic modification increases expression or activity of at least one oleaginic polypeptide and decreases expression or activity of at least one other oleaginic polypeptide.

49. The recombinant fungus of claim 46 or 47, wherein the at least one oleaginic polypeptide is selected from the group consisting of acetyl-CoA carboxylase polypeptide, pyruvate decarboxylase polypeptide, isocitrate dehydrogenase polypeptide, ATP-citrate lyase polypeptide, malic enzyme polypeptide, AMP deaminase polypeptide, malate dehydrogenase polypeptide, glucose-6 -phosphate dehydrogenase polypeptide, 6-phosphogluconate dehydrogenase polypeptide, fructose 1, 6 bisphosphatase polypeptide, NADH kinase polypeptide, transhydrogenase polypeptide, acyl-CoA:diacylglycerol acyltransferase polypeptide, phospholipid:diacylglycerol acyltransferase polypeptide, acyl-CoA:cholesterol acyltransferase polypeptide, triglyceride lipase polypeptide, acyl-coenzyme A oxidase polypeptide and combinations thereof.

50. The recombinant fungus of claim 46 or 47 wherein the least one oleaginic polypeptide is at least one polypeptide selected from the group consisting of a polypeptide in any one of Tables 1 through 6 or 31-47.

51. The recombinant fungus of any one of claims 46-48, wherein the at least one oleaginic modification comprises expression of at least one heterologous oleaginic polypeptide in the fungus.

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52. The recombinant fungus of claim 51, wherein the at least one oleaginic modification comprises expression of at least one heterologous gene encoding the at least one heterologous oleaginic polypeptide.

53. The recombinant fungus of claim 51, wherein the at least one heterologous oleaginic polypeptide comprises an animal polypeptide, a mammalian polypeptide, an insect polypeptide, a plant polypeptide, a fungal polypeptide, a yeast polypeptide, an algal polypeptide, a bacterial polypeptide, a cyanobacterial polypeptide, an archaebacterial polypeptide, or a protozoal polypeptide.

54. The recombinant fungus of claim 51, wherein the at least one heterologous oleaginic polypeptide comprises at least two heterologous oleaginic polypeptides.

55. The recombinant fungus of claim 54, wherein the at least two heterologous oleaginic polypeptides are from a single source organism.

56. The recombinant fungus of claim 54, wherein the at least two heterologous oleaginic polypeptides are from at least two different source organisms.

57. The recombinant fungus of any one of claims 1-41 wherein the fungus contains at least one carotenogenic modification.

58. The recombinant fungus of claim 57 wherein the at least one carotenogenic modification confers to the recombinant fungus the ability to produce the at least one carotenoid to a level at least about 1% of its dry cell weight.

59. The recombinant fungus of claim 57 wherein the at least one carotenogenic modification confers to the fungus the ability to produce at least one carotenoid which the parental fungus does not naturally produce.

60. The recombinant fungus of claim 57 wherein the recombinant fungus further comprises at least one oleaginic modification wherein the oleaginic modification alters oleaginicity of the recombinant fungus or confers to the recombinant fungus oleaginy.

61. The recombinant fungus of any one of claims 57-60, wherein the at least one carotenogenic modification confers the ability to the recombinant fungus to produce the at least one carotenoid to a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the dry cell weight of the recombinant fungus.

62. The recombinant fungus of any one of claims 57-60, wherein the at least one carotenogenic modification confers the ability to the recombinant fungus to produce the at least one carotenoid such that total carotenoid production by the recombinant fungus occurs at a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the dry cell weight of the recombinant fungus.

63. The recombinant fungus of any one of claims 57-62, wherein the at least one carotenogenic modification increases expression or activity of a carotenogenic polypeptide.

64. The recombinant fungus of any one of claims 57-62, wherein the at least one carotenogenic modification decreases expression or activity of a carotenogenic polypeptide.

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65. The recombinant fungus of any one of claims 57-62, wherein the at least one carotenogenic modification increases expression or activity of at least one carotenogenic polypeptide and decreases expression or activity of at least one other carotenogenic polypeptide.

66. The recombinant fungus of any one of claims 63-65, wherein the at least one carotenogenic modification comprises expression of at least one heterologous carotenogenic polypeptide.

67. The recombinant fungus of claim 66 wherein the at least one carotenogenic modification comprises expression of at least one heterologous gene encoding the at least one heterologous carotenogenic polypeptide.

68. The recombinant fungus of claim 63 or 64, wherein the carotenogenic polypeptide is selected from the group consisting of: isoprenoid biosynthesis polypeptides, carotenoid biosynthesis polypeptides, isoprenoid biosynthesis competitor polypeptides, and combinations thereof.

69. The recombinant fungus of claim 68 wherein the isoprenoid biosynthesis polypeptides are selected from the group consisting of: acetoacetyl-CoA thiolase polypeptide, HMG-CoA synthase polypeptide, HMG-CoA reductase polypeptide, mevalonate kinase polypeptide, phosphomevalonate kinase polypeptide, mevalonate pyrophosphate decarboxylase polypeptide, IPP isomerase polypeptide, FPP synthase polypeptide, and GGPP synthase polypeptide, and combinations thereof.

70. The recombinant fungus of claim 68, wherein the carotenoid biosynthesis polypeptides are selected from the group consisting of: phytoene synthase polypeptide, phytoene dehydrogenase polypeptide, lycopene cyclase polypeptide, carotenoid ketolase polypeptide, carotenoid hydroxylase polypeptide, astaxanthin synthase polypeptide, carotenoid epsilon hydroxylase polypeptide, carotenoid glucosyltransferase polypeptide, lycopene cyclase (beta and epsilon subunits) polypeptides, and acyl CoA:diacyglycerol acyltransferase polypeptide, and combinations thereof.

71. The recombinant fungus of claim 68, wherein the isoprenoid biosynthesis competitor polypeptides are selected from the group consisting of squalene synthase polypeptide, prenyldiphosphate synthase and PHB polyprenyltransferase, and combinations thereof.

72. The recombinant fungus of claim 68, wherein the carotenogenic polypeptide is selected from the group consisting of any of the polypeptides of any one of Tables 7-25, Table 29, and Table 30, and combinations thereof.

73. The recombinant fungus of claim 66, wherein the at least one heterologous carotenogenic polypeptide comprises an animal polypeptide, a mammalian polypeptide, an insect polypeptide, a plant polypeptide, a fungal polypeptide, a yeast polypeptide, an algal polypeptide, a bacterial polypeptide, cyanobacterial polypeptide, an archaebacterial polypeptide, or a protozoal polypeptide, and combinations thereof.

74. The recombinant fungus of claim 66, wherein the at least one heterologous carotenogenic polypeptide comprises at least two heterologous carotenogenic polypeptides.

75. The recombinant fungus of claim 74, wherein the at least two heterologous carotenogenic polypeptides are from a single source organism.

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76. The recombinant fungus of claim 74, wherein the at least two heterologous carotenogenic polypeptides are from at least two different source organisms.

77. A recombinant fungus according to any one of the preceding claims wherein the fungus accumulates the produced at least one carotenoid to a level selected from the group consisting of: above about 1%, above about 2%, above about 3%, above about 5%, and above about 10% of the dry cell weight of the recombinant fungus.

78. A recombinant fungus according to any one of the preceding claims characterized in that the fungus accumulates lipid in the form of cytoplasmic bodies.

79. The recombinant fungus of claim 78 wherein the at least one carotenoid accumulates in the cytoplasmic oil bodies.

80. A strain of *Yarrowia lipolytica* comprising one or more modifications selected from the group consisting of an oleaginic modification, a carotenogenic modification, and combinations thereof, such that the strain accumulates from 1% to 15% of its dry cell weight as at least one carotenoid.

81. The strain of claim 80 further characterized in that it accumulates from 20% to 50% of its dry cell weight as lipid.

82. The strain of claim 81, wherein the strain accumulates from 20% to 50% of its dry cell weight as lipid in the form of cytoplasmic oil bodies.

83. The strain of claim 80, wherein the strain comprises a carotenogenic modification selected from the group consisting of:

a. expression of a polypeptide selected from a group consisting of a truncated endogenous HMG CoA reductase polypeptide that lacks the N-terminal membrane spanning domain, acetoacetyl-CoA thiolase, HMG-CoA synthase, FPP synthase, and GGPP synthase;

b. expression of a heterologous polypeptide selected from the group consisting of phytoene synthase, phytoene desaturase, lycopene cyclase, and combinations thereof;

c. decreased expression or activity of an endogenous polypeptide selected from the group consisting of squalene synthase polypeptide prenyldiphosphate synthase polypeptide and PHB polyprenyltransferase polypeptide; and combinations thereof.

84. The strain of any one of claims 80-83, wherein the strain accumulates 1-15% of its dry cell weight as β-carotene.

85. The strain of claim 80, wherein the strain comprises a carotenogenic modification selected from the group consisting of:

a. expression of a polypeptide selected from a group consisting of a truncated endogenous HMG CoA reductase polypeptide that lacks the N-terminal membrane spanning domain, acetoacetyl-CoA thiolase, HMG-CoA synthase, FPP synthase, and GGPP synthase;

b. expression of a heterologous polypeptide selected from the group consisting of phytoene synthase, phytoene desaturase, lycopene cyclase, carotenoid ketolase, carotenoid hydroxylase,

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astaxanthin synthase, carotenoid epsilon hydroxylase, lycopene cyclase (beta and epsilon subunits), carotenoid glucosyltransferase, acyl CoA:diacyglycerol acyltransferase, and combinations thereof;

c. decreased expression or activity of an endogenous polypepetide selected from the group consisting of squalene synthase polypeptide prenyldiphosphate synthase polypeptide and PHB polyprenyltransferase polypeptide; and combinations thereof.

86. The strain of any one of claims 80-83 or 85, wherein the strain accumulates 1-15% of its dry cell weight as astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, phytoene, phytofluene and combinations thereof.

87. A method of producing a carotenoid, the method comprising steps of:

a. cultivating the fungus of any one of the preceding claims under conditions that allow production of the carotenoid;

b. and isolating the produced carotenoid.

88. The method of claim 87, wherein the step of cultivating comprising cultivating under conditions and for a time sufficient that the carotenoid accumulates to a level above at least about 1% of the dry cell weight of the fungus.

89. The method of claim 87 or 88, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus accumulates lipid bodies to a level above about 20% of its dry cell weight.

90. The method of any one of claims 87-89, wherein the carotenoid is selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

91. The method of any one of claims 87-90, wherein the step of cultivating comprises growing cells under conditions of excess carbon and limiting non-carbon nutrient.

92. The method of claim 91, wherein the limiting non-carbon nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, and combinations thereof.

93. The method of claim 91 wherein the limiting non-carbon nutrient comprises nitrogen.

94. The method of claim 93 wherein the carbon:nitrogen ratio is within the range selected from the group consisting of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 6-:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, and 10:1.v

95. The method of claim 93 wherein the carbon:nitrogen ratio is less than about 10:1.

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96. The method of any one of claims 87-95, wherein the step of cultivating comprises growing under conditions of controlled dissolved oxygen concentration.

97. The method of claim 96, wherein the step of cultivating comprises modulating feed rate to maintain a specific level of dissolved oxygen.

98. The method of any one of claims 87-97, wherein the step of cultivating comprises growing under conditions between a pH of 7.0 and 8.0.

99. The method of claim 98, wherein production of the carotenoid is increased relative to carotenoid production that would be observed if the fungus were grown under a pH below 7.0 or above 8.0.

100. The method of claim 98 or 99, wherein the produced carotenoid is hydroxylated, and wherein the carotenoid is hydoxylated to a greater extent than would be observed if the fungus were grown under at a pH below 7.0 or above 8.0.

101. The method of claim 98, wherein the step of cultivating comprises increasing the pH during the course of cultivation.

102. The method of 101, wherein the pH is increased at a rate of about 0.021 pH units/hour.

103. The method of 101, wherein the pH is increased at a rate of about 0.042 pH units/hour.

104. The method of any one of claims 101-103, wherein production of the carotenoid is increased relative to carotenoid production that would be observed if the fungus were grown under at a pH below 7.0 or above 8.0.

105. The method of any one of claims 101-103, wherein the produced carotenoid is hydroxylated, and wherein the carotenoid is hydroxylated to a greater extent than would be observed if the fungus were grown under at a pH below 7.0 or above 8.0.

106. The method of claim 100 or 105, wherein the produced carotenoid comprises beta-carotene and the hydroxylated carotenoid comprises zeaxanthin.

107. The method of claim 87, wherein the step of cultivating comprises a first phase of growing under conditions of excess carbon and limiting oxygen, followed by a second phase of growing under conditions of excess oxygen and limiting carbon.

108. The method of claim 87, wherein the step of isolating comprises homogenizing cells and subjecting them to extraction.

109. The method of claim 108, wherein the step of isolating comprises extracting with a solvent selected from the group consisting of acetone, supercritical fluids, propane, xenon, ethane, propylene, methane, ethylene, ethanol, carbon dioxide, chloroform, ethanol, ethyl acetate, heptane, hexane, isopropanol, methanol, methylene chloride, octane, tetrahydrofuran (THF), cyclohexane, isobutyl acetate, methyl ketone, ethyl ketone, toluene, cyclohexanone, benzene, propylene glycol, vegetable oils, and combinations thereof.

110. The method of claim 109, wherein the step of isolating comprises extracting with a supercritical fluid.

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111. The method of claim 110, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

112. The method of claim 111, wherein the supercritical fluid comprises carbon dioxide.

113. The method of claim 109, wherein the step of isolating comprises extracting with propylene glycol.

114. The method of claim 113, wherein the produced carotenoid is a xanthophyll.

115. The method of claim 114, wherein the xanthophyll comprises canthaxanthin, echinenone, or both.

116. The method of claim 109, wherein the step of isolating comprises extracting with one or more vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

117. The method of claim 109, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

118. The method of claim 109, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

119. The method of claim 118, wherein the step of isolating comprises extracting with a combination of an alcohol and hexane.

120. The method of claim 118, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

121. The method of any one of claims 119 or 120, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

122. The method of claim 108, wherein the step of isolating comprises disrupting the cells by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the cells to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

123. The method of claim 122, wherein the step of isolating comprises disrupting the cells by mechanical disruption.

124. The method of claim 123, wherein mechanical disruption is achieved by subjecting the cells to a bead mill/mashing at high pressure.

125. The method of claim 124, wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

126. The method of claim 87, wherein the carotenoid in the cell accumulates in lipid bodies.

127. The method of claim 126, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

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128. The method of claim 126, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

129. The method of claim 128, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

130. The method of claim 87, wherein the step of isolating comprises fractionating the cultivation medium to obtain at least one carotenoid-enriched fraction.

131. The method of claim 87, wherein the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the carotenoid in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

132. The method of claim 87, wherein the carotenoid is selected from the group consisting of adonirubin, adonixanthin, astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, phytoene, phytofluene and combinations thereof.

133. The method of claim 87, wherein the carotenoid comprises β-carotene.

134. The method of claim 87, wherein the carotenoid is selected from the group consisting of canthaxanthin, echinenone, β-cryptoxanthin, and combinations thereof.

135. The method of claim 87, wherein the carotenoid comprises zeaxanthin or lutein.

136. The method of claim 87, wherein the carotenoid comprises astaxanthin.

137. The method of claim 87, wherein the step of isolating comprises concentrating the carotenoid.

138. The method of claim 137, wherein the step of isolating comprises concentrating the carotenoid until it is at least about 5-fold more concentrated.

139. The method of any one of claims 87-138, further comprising a step of chemically modifying the carotenoid.

140. The method of claim 139, wherein the step of chemically modifying comprises esterifying or de-esterifying the carotenoid.

141. The method of any one of claims 87-138, further comprising a step of combining the carotenoid with one or more other agents in a composition.

142. The method of claim 141, wherein the step of combining comprises combining the carotenoid with one or more other agents selected from the group consisting of binders, fillers, and combinations thereof.

143. The method of claim 141, wherein the step of combining comprises combining the carotenoid with one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

144. An engineered *Y. lipolytica* strain that produces β -carotene, the strain containing one or more carotenogenic modifications selected from the group consisting of:

a. increased expression or activity of a *Y. lipolytica* GGPP synthase polypeptide;

b. increased expression or activity of a truncated HMG CoA reductase polypeptide;

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c. increased expression or activity of a phytoene dehydrogenase polypeptide
d. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide;
e. increased expression or activity of an FPP synthase polypeptide;
f. increased expression or activity of an IPP isomerase polypeptide;
g. increased expression or activity of an HMG synthase polypeptide;
h. increased expression or activity of a mevalonate kinase polypeptide;
i. increased expression or activity of a phosphomevalonate kinase polypeptide;
j. increased expression or activity of a mevalonate pyrophosphate decarboxylate polypeptide;
k. increased expression or activity of a malic enzyme polypeptide;
l. increased expression or activity of a malate dehydrogenase polypeptide;
m. increased expression or activity of an AMP deaminase polypeptide;
n. increased expression or activity of a glucose 6 phosphate dehydrogenase polypeptide;
o. increased expression or activity of a malate dehydrogenase homolog2 polypeptide;
p. increased expression or activity of a GND1-6-phosphogluconate dehydrogenase polypeptide;
q. increased expression or activity of a isocitrate dehydrogenase polypeptide;
r. increased expression or activity of a IDH2-isocitrate dehydrogenase polypeptide;
s. increased expression or activity of a fructose 1,6 bisphosphatase polypeptide;
t. increased expression or activity of a Erg10-acetoacetyl CoA thiolase polypeptide;
u. increased expression or activity of a ATP citrate lyase subunit 2 polypeptide;
v. increased expression or activity of a ATP citrate lyase subunit 1 polypeptide;
w. decreased expression or activity of a squalene synthase polypeptide;
x. decreased expression or activity of a prenyldiphosphate synthase polypeptide; or
y. decreased expression or activity of a PHB polyprenyltransferase polypeptide; and combinations thereof.

145. The engineered *Y. lipolytica* strain of claim 144, wherein the one or more carotenogenic modifications is selected from the group consisting of:
a. increased expression or activity of a *Y. lipolytica* GGPP synthase polypeptide;
b. increased expression or activity of an FPP synthase polypeptide;
c. increased expression or activity of an HMG CoA reductase polypeptide;
d. decreased expression or activity of a squalene synthase polypeptide;
e. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide;
f. increased expression or activity of a phytoene dehydrogenase polypeptide; and combinations thereof.

146. The engineered *Y. lipolytica* strain of any one of claims 144-145, wherein the GGPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

147. The engineered *Y. lipolytica* strain of any one of claims 144-146, wherein the FPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

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148. The engineered *Y. lipolytica* strain of claim 144, wherein the one or more carotenogenic modifications is selected from the group consisting of:

a. increased expression or activity of a phytoene dehydrogenase polypeptide,

b. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide, and combinations thereof.

149. The engineered *Y. lipolytica* strain of claim 144, wherein one of the one or more the carotenogenic modifications consists of increased expression or activity of a GGPP synthase polypeptide.

150. The engineered *Y. lipolytica* strain of claim 144, wherein one of the one or more the carotenogenic modifications consists of increased expression or activity of a truncated HMG CoA reductase polypeptide.

151. The engineered *Y. lipolytica* strain of claim 150, further comprising a second carotenogenic modification comprising increased expression or activity of a GGPP synthase polypeptide.

152. The engineered *Y. lipolytica* strain of any one of claims 144-151, wherein the truncated HMG CoA reductase polypeptide is a *Yarrowia* polypeptide.

153. The engineered *Y. lipolytica* strain of claim 152, wherein the truncated HMG CoA reductase polypeptide is a *Yarrowia lipolytica* polypeptide.

154. The engineered *Y. lipolytica* strain of any one of claims 144-151, wherein the GGPP synthase polypeptide is a *Yarrowia* polypeptide.

155. The engineered *Y. lipolytica* strain of claim 154, wherein the GGPP synthase polypeptide is a *Yarrowia lipolytica* polypeptide.

156. The engineered *Y. lipolytica* strain of claim 144, further comprising a second carotenogenic modification selected from the group consisting of:

a. increased expression or activity of a phytoene dehydrogenase polypeptide, or

b. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide, and combinations thereof.

157. The engineered *Y. lipolytica* strain of any one of claims 144-156, wherein the phytoene dehydrogenase polypeptide is a polypeptide from an organism of the genus *Mucor*.

158. The engineered *Y. lipolytica* strain of claim 157, wherein the phytoene dehydrogenase polypeptide is a polypeptide from the organism *Mucor circinelloides*.

159. The engineered *Y. lipolytica* strain of any one of claims 144-156, wherein the phytoene synthase/lycopene cyclase polypeptide is a polypeptide from an organism of the genus *Mucor* or *Neurospora*.

160. The engineered *Y. lipolytica* strain of claim 159, wherein the phytoene synthase/lycopene cyclase polypeptide is a polypeptide from the organism *Mucor circinelloides* or *Neurospora crassa*.

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161. The engineered *Y. lipolytica* strain of any one of claims 144-160, wherein the strain produces β-carotene.

162. The engineered *Y. lipolytica* strain of claim 161, wherein the produced β-carotene accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

163. The engineered *Y. lipolytica* strain of claim 161, wherein the produced β-carotene accumulates to levels that are greater than at least about 2.0% of the dry weight of the cells.

164. The engineered *Y. lipolytica* strain of claim 161, wherein the produced β-carotene accumulates to levels that are greater than at least about 3.0% of the dry weight of the cells.

165. The engineered *Y. lipolytica* strain of claim 161, wherein the produced β-carotene accumulates to levels that are greater than at least about 5.0% of the dry weight of the cells.

166. The engineered *Y. lipolytica* strain of claim 144, further comprising a second carotenogenic modification of increased expression or activity of a carotenoid ketolase polypeptide, and wherein the strain produces a compound selected from the group consisting of echinenone, canthaxanthin, and combinations thereof.

167. The engineered *Y. lipolytica* strain of claim 166, wherein the strain produces echinenone.

168. The engineered *Y. lipolytica* strain of claim 167, wherein the produced echinenone accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

169. The engineered *Y. lipolytica* strain of claim 167, wherein the produced echinenone accumulates to levels that are greater than at least about 3.0% of the dry weight of the cells.

170. The engineered *Y. lipolytica* strain of claim 166, wherein the strain produces canthaxanthin.

171. The engineered *Y. lipolytica* strain of claim 170, wherein the produced canthaxanthin accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

172. The engineered *Y. lipolytica* strain of claim 170, wherein the produced canthaxanthin accumulates to levels that are greater than at least about 2.5% of the dry weight of the cells.

173. The engineered *Y. lipolytica* strain of claim 170, wherein the produced canthaxanthin accumulates to levels that are greater than at least about 3.5% of the dry weight of the cells.

174. The engineered *Y. lipolytica* strain of claim 144, further comprising a second carotenogenic modification comprising increased expression or activity of a carotenoid hydroxylase polypeptide, and wherein the strain produces zeaxanthin.

175. The engineered *Y. lipolytica* strain of claim 174, wherein the produced zeaxanthin accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

176. The engineered *Y. lipolytica* strain of claim 144, further comprising:

a second carotenogenic modification comprising increased expression or activity of a carotenoid ketolase polypeptide; and

a third carotenogenic modification comprising increased expression or activity of a carotenoid hydroxylase polypeptide, and wherein the strain produces astaxanthin.

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177. The engineered *Y. lipolytica* strain of claim 176, wherein the produced astaxanthin accumulates to levels that are greater than at least about 0.1% of the dry weight of the cells.

178. The engineered *Y. lipolytica* strain of claim 176, wherein the produced astaxanthin accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

179. The engineered *Y. lipolytica* strain of any one of claims 166-176, wherein the carotenoid ketolase polypeptide is a polypeptide from an organism of a genus selected from the group consisting of *Parvularcula*, and *Aurantimonas sp. SI85-9A1*.

180. The engineered *Y. lipolytica* strain of claim 179, wherein the carotenoid ketolase polypeptide is a polypeptide from the organism *Parvularcula bermudensis*.

181. The engineered *Y. lipolytica* strain of claim 179, wherein the carotenoid ketolase polypeptide is a polypeptide from the organism *Aurantimonas sp. SI85-9A1*.

182. The engineered *Y. lipolytica* strain of any one of claims 174-175 or 179-181 wherein the carotenoid hydroxylase polypeptide is a polypeptide from an organism of a genus selected from the group consisting of *Erythrobacter, Novosphingobium, Parvularcula, Xanthobacter, Sphingopyxis, Chlamydomonas, Robiginitalea,* and *Pseudomonas*.

183. The engineered *Y. lipolytica* strain of claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Erythrobacter litoralis*.

184. The engineered *Y. lipolytica* strain of claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Novosphingobium aromaticivorans*.

185. The engineered *Y. lipolytica* strain of claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Parvularcula bermudensis*.

186. The engineered *Y. lipolytica* strain of claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Xanthobacter autotrophicus*.

187. The engineered *Y. lipolytica* strain of claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Sphingopyxis alaskensis*.

188. The engineered *Y. lipolytica* strain of a claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Chlamydomonas rheinhardtii*.

189. The engineered *Y. lipolytica* strain of a claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Erythrobacter longus*.

190. The engineered *Y. lipolytica* strain of a claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Robiginitalea biformata*.

191. The engineered *Y. lipolytica* strain of a claim 182, wherein the carotenoid hydroxylase polypeptide is a polypeptide from the organism *Pseudomonas putida*.

192. The engineered *Y. lipolytica* strain of any one of claims 144-191, wherein a carotenoid produced by the strain accumulates in lipid bodies.

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193. The engineered *Y. lipolytica* strain of claim 192, wherein the carotenoid is selected from the group consisting of: astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, and combinations thereof.

194. The engineered *Y. lipolytica* strain of claim 192, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

195. The engineered *Y. lipolytica* strain of claim 192, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

196. The engineered *Y. lipolytica* strain of claim 195, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

197. The engineered *Y. lipolytica* strain of any one of claims 192-196, wherein the carotenoid is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

198. A method of preparing a food or feed additive or a dietary supplement containing a carotenoid, the method comprising steps of:

a. cultivating the fungus of any one of claims 1-79, the strain of claims 80-86 or the engineered *Y. lipolytica* strain of claims 144-197 under conditions that allow production of the carotenoid;

b. isolating the carotenoid; and

c. combining the isolated carotenoid with one or more other food or feed additive components.

199. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one retinolic compound, and can accumulate the produced retinolic compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, which parental fungus both is not oleaginous and does not accumulate the retinolic compound to at least about 1% of its dry cell weight, the at least one modification being selected from the group consisting of retinologenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one retinolic compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one retinolic compound which the parental fungus does not produce.

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200. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one retinolic compound selected from the group consisting of retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof, and can accumulate the produced retinolic compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of retinologenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one retinolic compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one retinolic compound which the parental fungus does not naturally produce.

201. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one retinolic compound, and can accumulate the produced retinolic compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus is a member of a genus selected from the group consisting of: *Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia),* and *Yarrowia*

or is a species selected from the group consisting of:

Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), and *Yarrowia lipolytica*

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wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of retinologenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one retinolic compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one retinolic compound which the parental fungus does not naturally produce.

202. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one retinolic compound selected from the group consisting of retinol, retinal, retinoic acid, and combinations thereof, and can accumulate the produced retinolic compound to at least about 1% of its dry cell weight;

wherein the recombinant fungus is a member of a genus selected from the group consisting of:

Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia), and *Yarrowia*

or is of a species selected from the group consisting of:

Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), and *Yarrowia lipolytica*

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of retinologenic modifications, oleaginic modifications, and combinations thereof, and

wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least

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one retinolic compound to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one retinolic compound which the parental fungus does not naturally produce.

203. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a species selected from the group consisting of: *Candida utilis, Saccharomyces cerevisiae, Xanthophyllomyces dendrorhous (Phaffia rhodozyma),* and *Yarrowia lipolytica.*

204. The recombinant fungus of claim 203 wherein the recombinant fungus of the species *Candida utilis.*

205. The recombinant fungus of claim 203 wherein the recombinant fungus of the species *Saccharomyces cerevisiae.*

206. The recombinant fungus of claim 203 wherein the recombinant fungus of the species *Xanthophyllomyces dendrorhous (Phaffia rhodozyma).*

207. The recombinant fungus of claim 203 wherein the recombinant fungus of the species *Yarrowia lipolytica.*

208. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Aspergillus, Candida, Cunninghamella, Kluyveromyces, Lipomyces, Mortierella, Pichia (Hansenula), Rhodosporidium, Rhodotorula, Trichoderma,* and *Trichosporon.*

209. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a species selected from the group consisting of: *Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Cunninghamella echinulata, Cunninghamella elegans, Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Pichia pastoris, Rhodosporidium toruloides, Rhodotorula glutinis, Trichoderma reesei,* and *Trichosporon pullans.*

210. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Cercospora, Fusarium (Gibberella), Mucor, Neurospora, Penicillium, Phycomyces, Puccinia,* and *Pythium.*

211. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a species selected from the group consisting of: *Cercospora nicotianae, Fusarium fujikuroi (Gibberella zeae), Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Puccinia distincta, Pythium irregulare, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis,* and *Trichosporon cutaneum.*

212. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a member of a genus selected from the group consisting of : *Botrytis, Cryptococcus,* and *Sclerotium*

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213. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a species selected from the group consisting of: *Botrytis cinerea, Cryptococcus curvatus, Sclerotium rolfsii.*

214. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus grows as a single cell.

215. The recombinant fungus of any one of claims 199-202 wherein the recombinant fungus is a yeast.

216. The recombinant fungus of any one of claims 199-215 wherein the retinolic compound is retinol.

217. The recombinant fungus of any one of claims 199-215 wherein the retinolic compound is retinal.

218. The recombinant fungus of any one of claims 199-215 wherein the retinolic compound is retinoic acid.

219. The recombinant fungus of any one of claims 199-215 wherein the retinolic compound is retinyl palmitate.

220. The recombinant fungus of 199-219 wherein the parental fungus is oleaginous.

221. The recombinant fungus of 199-219 wherein the parental fungus is not oleaginous.

222. The recombinant fungus of any one of claims 199-221 wherein the parental fungus does not naturally produce the at least one retinolic compound.

223. The recombinant fungus of any one of claims 199-221 wherein the recombinant fungus grows as a single cell.

224. The recombinant fungus of any one of claims 199-221 wherein the recombinant fungus is a yeast.

225. The recombinant fungus of any one of claims 199-224 wherein the recombinant fungus contains at least one oleaginic modification.

226. The recombinant fungus of claim 225 wherein the at least one oleaginic modification confers oleaginy upon the fungus.

227. The fungus of claim 225 wherein the at least one oleaginic modification alters oleaginicity of the fungus.

228. The recombinant fungus of claim 225 wherein the recombinant fungus further comprises at least one retinologenic modification wherein the retinologenic modification confers to the recombinant fungus the ability to produce the at least one retinolic compound to a level at least about 1% of its dry cell weight or confers to the recombinant fungus the ability to produce at least one retinolic compound which the parental fungus does not naturally produce.

229. The recombinant fungus of any one of claims 225-228 wherein the at least one oleaginic modification increases expression or activity of at least one oleaginic polypeptide.

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230. The recombinant fungus of any one of claims 225-228 wherein the at least one oleaginic modification decreases expression or activity of at least one oleaginic polypeptide.

231. The recombinant fungus of c any one of claims 225-228 wherein the at least one oleaginic modification increases expression or activity of at least one oleaginic polypeptide and decreases expression or activity of at least one other oleaginic polypeptide.

232. The recombinant fungus of claim 229 or 230, wherein the at least one oleaginic polypeptide is selected from the group consisting of acetyl-CoA carboxylase polypeptide, pyruvate decarboxylase polypeptide, isocitrate dehydrogenase polypeptide, ATP-citrate lyase polypeptide, malic enzyme polypeptide, AMP deaminase polypeptide, malate dehydrogenase polypeptide, glucose-6 -phosphate dehydrogenase polypeptide, 6-phosphogluconate dehydrogenase polypeptide, fructose 1, 6 bisphosphatase polypeptide, NADH kinase polypeptide, transhydrogenase polypeptide, acyl-CoA:diacylglycerol acyltransferase polypeptide, phospholipid:diacylglycerol acyltransferase polypeptide, acyl-CoA:cholesterol acyltransferase polypeptide, triglyceride lipase polypeptide, acyl-coenzyme A oxidase polypeptide and combinations thereof.

233. The recombinant fungus of claim 229 or 230 wherein the least one oleaginic polypeptide is at least one polypeptide selected from the group consisting of a polypeptide in any one of Tables 1 through 6 or 31-47.

234. The recombinant fungus of any one of claims 229-231, wherein the at least one oleaginic modification comprises expression of at least one heterologous oleaginic polypeptide in the fungus.

235. The recombinant fungus of claim 234, wherein the at least one oleaginic modification comprises expression of at least one heterologous gene encoding the at least one heterologous oleaginic polypeptide.

236. The recombinant fungus of claim 234, wherein the at least one heterologous oleaginic polypeptide comprises an animal polypeptide, a mammalian polypeptide, an insect polypeptide, a plant polypeptide, a fungal polypeptide, a yeast polypeptide, an algal polypeptide, a bacterial polypeptide, a cyanobacterial polypeptide, an archaebacterial polypeptide, or a protozoal polypeptide.

237. The recombinant fungus of claim 234, wherein the at least one heterologous oleaginic polypeptide comprises at least two heterologous oleaginic polypeptides.

238. The recombinant fungus of claim 237, wherein the at least two heterologous oleaginic are from the same source organism.

239. The recombinant fungus of claim 237, wherein the at least two heterologous oleaginic polypeptides are from at least two different source organisms.

240. The recombinant fungus of any one of claims 199-239 wherein the fungus contains at least one retinologenic modification.

241. The recombinant fungus of claim 240 wherein the at least one retinologenic modification confers to the recombinant fungus the ability to produce the at least one retinolic compound to a level at least about 1% of its dry cell weight.

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242. The recombinant fungus of claim 240 wherein the at least one retinologenic modification confers to the fungus the ability to produce at least one retinolic compound which the parental fungus does not naturally produce.

243. The recombinant fungus of claim 240 wherein the recombinant fungus further comprises at least one oleaginic modification wherein the oleaginic modification alters oleaginicity of the recombinant fungus or confers to the recombinant fungus oleaginy.

244. The recombinant fungus of any one of claims 240-243, wherein the at least one retinologenic modification confers the ability to the recombinant fungus to produce the at least one retinolic compound to a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the dry cell weight of the recombinant fungus.

245. The recombinant fungus of any one of claims 240-243, wherein the at least one retinologenic modification confers the ability to the recombinant fungus to produce the at least one retinolic compound such that total retinolic compound production by the recombinant fungus occurs at a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the dry cell weight of the recombinant fungus.

246. The recombinant fungus of any one of claims 240-244, wherein the at least one retinologenic modification increases expression or activity of a retinologenic polypeptide.

247. The recombinant fungus of any one of claims 240-244, wherein the at least one retinologenic modification decreases expression or activity of a retinologenic polypeptide.

248. The recombinant fungus of any one of claims 240-244, wherein the at least one retinologenic modification increases expression or activity of at least one retinologenic polypeptide and decreases expression or activity of at least one other retinologenic polypeptide.

249. The recombinant fungus of any one of claims 246-248, wherein the at least one retinologenic modification comprises expression of at least one heterologous retinologenic polypeptide.

250. The recombinant fungus of claim 249 wherein the at least one retinologenic modification comprises expression of at least one heterologous gene encoding the at least one heterologous retinologenic polypeptide.

251. The recombinant fungus of claim 246 or 247, wherein the retinologenic polypeptide is selected from the group consisting of: retinolic compound biosynthesis polypeptides, isoprenoid biosynthesis polypeptides, carotenoid biosynthesis polypeptides, isoprenoid biosynthesis competitor polypeptides, and combinations thereof.

252. The recombinant fungus of claim 251 wherein the isoprenoid biosynthesis polypeptides are selected from the group consisting of: acetoacetyl-CoA thiolase polypeptide, HMG-CoA synthase polypeptide, HMG-CoA reductase polypeptide, mevalonate kinase polypeptide, phosphomevalonate kinase polypeptide, mevalonate pyrophosphate decarboxylase polypeptide, IPP isomerase polypeptide, FPP synthase polypeptide, and GGPP synthase polypeptide, and combinations thereof.

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253. The recombinant fungus of claim 251, wherein the carotenoid biosynthesis polypeptides are selected from the group consisting of: phytoene synthase polypeptide, phytoene dehydrogenase polypeptide, lycopene cyclase polypeptide, carotenoid ketolase polypeptide, carotenoid hydroxylase polypeptide, astaxanthin synthase polypeptide, carotenoid epsilon hydroxylase polypeptide, carotenoid glucosyltransferase polypeptide, lycopene cyclase (beta and epsilon subunits) polypeptides, and acyl CoA:diacyglycerol acyltransferase polypeptide, and combinations thereof.

254. The recombinant fungus of claim 251, wherein the isoprenoid biosynthesis competitor polypeptides are selected from the group consisting of squalene synthase polypeptide, prenyldiphosphate synthase and PHB polyprenyltransferase, and combinations thereof.

255. The recombinant fungus of claim 251, wherein the carotenogenic polypeptide is selected from the group consisting of any of the polypeptides of any one of Tables 7-25, Table 29, and Table 30, and combinations thereof.

256. The recombinant fungus of claim 251, wherein the retinolic compound biosynthesis polypeptides are selected from the group consisting of beta-carotene 15, 15'-monooxygenase polypetides, retinol dehydrogenase polypeptides, and combinations thereof.

257. The recombinant fungus of claim 256, wherein the retinolic compound biosynthesis polypeptides are selected from the group consisting of any of the polypeptides of any one of Table 67 or 68, and combinations thereof.

258. The recombinant fungus of claim 249, wherein the at least one heterologous retinologenic polypeptide comprises an animal polypeptide, a mammalian polypeptide, an insect polypeptide, a plant polypeptide, a fungal polypeptide, a yeast polypeptide, an algal polypeptide, a bacterial polypeptide, cyanobacterial polypeptide, an archaebacterial polypeptide, or a protozoal polypeptide.

259. The recombinant fungus of claim 249, wherein the at least one heterologous retinologenic polypeptide comprises at least two heterologous carotenogenic polypeptides.

260. The recombinant fungus of claim 259, wherein the at least two heterologous retinologenic polypeptides are from a single source organism.

261. The recombinant fungus of claim 259, wherein the at least two heterologous retinologenic polypeptides are from at least two different source organisms.

262. A recombinant fungus according to any one of claims 199-261 wherein the fungus accumulates the produced at least one retinolic compound to a level selected from the group consisting of: above about 1%, above about 2%, above about 3%, above about 5%, and above about 10% of the dry cell weight of the recombinant fungus.

263. A recombinant fungus according to any one of claims 199-262 characterized in that the fungus accumulates lipid in the form of cytoplasmic bodies.

264. The recombinant fungus of claim 263 wherein the at least one retinolic compound accumulates in the cytoplasmic oil bodies.

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265. A strain of *Yarrowia lipolytica* comprising one or more modifications selected from the group consisting of an oleaginic modification, a retinologenic modification, and combinations thereof, such that the strain accumulates from 1% to 15% of its dry cell weight as at least one retinolic compound.

266. The strain of claim 265 further characterized in that it accumulates from 20% to 50% of its dry cell weight as lipid.

267. The strain of claim 266, wherein the strain accumulates from 20% to 50% of its dry cell weight as lipid in the form of cytoplasmic oil bodies.

268. The strain of claim 265, wherein the strain comprises a retinologenic modification selected from the group consisting of: expression of a polypeptide selected from a group consisting of a beta-carotene 15, 15'-monooxygenase, a retinol dehydrogenase, and combinations thereof.

269. The strain of any one of claims 265-268, wherein the strain accumulates 1-15% of its dry cell weight as retinol.

270. The strain of any one of claims 265-268, wherein the strain accumulates 1-15% of its dry cell weight as retinol, retinal, retinoic acid, and combinations thereof.

271. A method of producing a retinolic compound, the method comprising steps of:

a. cultivating the fungus of any one of claims 199-264 or the strain of any one of claims 265-270 under conditions that allow production of the retinolic compound;

b. and isolating the produced retinolic compound.

272. The method of claim 271, wherein the step of cultivating comprising cultivating under conditions and for a time sufficient that the retinolic compound accumulates to a level above at least about 1% of the dry cell weight of the fungus.

273. The method of claim 271 or 272, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus accumulates lipid bodies to a level above about 20% of its dry cell weight.

274. The method of any one of claims 271-273, wherein the retinolic compound is selected from the group consisting of retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof.

275. The method of any one of claims 271-274, wherein the step of cultivating comprises growing cells under conditions of excess carbon and limiting non-carbon nutrient.

276. The method of claim 275, wherein the limiting non-carbon nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, and combinations thereof.

277. The method of claim 275 wherein the limiting non-carbon nutrient comprises nitrogen.

278. The method of claim 277 wherein the carbon:nitrogen ratio is within the range selected from the group consisting of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 6-:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, and 10:1.

279. The method of claim 277 wherein the carbon:nitrogen ratio is less than about 10:1.

280. The method of any one of claims 271-279, wherein the step of cultivating comprises growing under conditions of controlled dissolved oxygen concentration.

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281. The method of any one of claims 271-280, wherein the step of cultivating comprises growing under conditions between a pH of 7.0 and 8.0.

282. The method of claim 281, wherein the step of cultivating comprises increasing the pH during the course of cultivation.

283. The method of 281 or 282, wherein the pH is increased at a rate of about 0.021 pH units/hour.

284. The method of 281 or 282, wherein the pH is increased at a rate of about 0.042 pH units/hour.

285. The method of any one of claims 281-284, wherein production of the retinolic compound is increased relative to retinolic compound production that would be observed if the fungus were grown under at a pH below 7.0 or above 8.0.

286. The method of any one of claims 281-284, wherein the produced retinolic compound is hydroxylated, and wherein the retinolic compound is hydoxylated to a greater extent than would be observed if the fungus were grown under at a pH below 7.0 or above 8.0.

287. The method of claim 271, wherein the step of cultivating comprises modulating feed rate to maintain a specific level of dissolved oxygen.

288. The method of claim 271, wherein the step of cultivating comprises a first phase of growing under conditions of excess carbon and limiting oxygen, followed by a second phase of growing under conditions of excess oxygen and limiting carbon.

289. The method of claim 271, wherein the step of isolating comprises homogenizing cells and subjecting them to extraction.

290. The method of claim 289, wherein the step of isolating comprises extracting with a solvent selected from the group consisting of acetone, supercritical fluids, propane, xenon, ethane, propylene, methane, ethylene, ethanol, carbon dioxide, chloroform, ethanol, ethyl acetate, heptane, hexane, isopropanol, methanol, methylene chloride, octane, tetrahydrofuran (THF), cyclohexane, isobutyl acetate, methyl ketone, ethyl ketone, toluene, cyclohexanone, benzene, propylene glycol, vegetable oils, and combinations thereof.

291. The method of claim 289, wherein the step of isolating comprises extracting with a supercritical fluid.

292. The method of claim 291, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

293. The method of claim 292, wherein the supercritical fluid comprises carbon dioxide.

294. The method of claim 289, wherein the step of isolating comprises extracting with propylene glycol.

295. The method of any one of claims 271-294, wherein the produced retinolic compound is retinol.

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296. The method of any one of claims 271-294, wherein the produced retinolic compound is retinyl palmitate.

297. The method of claim 289, wherein the step of isolating comprises extracting with vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

298. The method of claim 289, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

299. The method of claim 289, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

300. The method of claim 299, wherein the step of isolating comprises extracting with a combination of an alcohol and hexane.

301. The method of claim 299, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

302. The method of claim 300 or 301, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

303. The method of claim 289, wherein the step of isolating comprises disrupting the cells by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the cells to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

304. The method of claim 303, wherein the step of isolating comprises disrupting the cells by mechanical disruption.

305. The method of claim 304, wherein mechanical disruption is achieved by subjecting the cells to a bead mill/mashing at high pressure.

306. The method of claim 305, wherein wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

307. The method of claim 289, wherein the retinolic compound in the cell accumulates in lipid bodies.

308. The method of claim 307, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

309. The method of claim 307, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

310. The method of claim 309, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

311. The method of claim 271, wherein the step of isolating comprises fractionating the cultivation medium to obtain at least one carotenoid-enriched fraction.

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312. The method of claim 271, wherein: the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the carotenoid in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

313. The method of claim 271, wherein the retinolic compound is selected from the group consisting of retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof.

314. The method of claim 271, wherein the retinolic compound comprises retinol.

315. The method of claim 271, wherein the step of isolating comprises concentrating the retinolic compound.

316. The method of claim 315, wherein the step of isolating comprises concentrating the retinolic compound until it is at least about 5-fold more concentrated.

317. The method of any one of claims 271-316, further comprising a step of chemically modifying the retinolic compound.

318. The method of claim 317, wherein the step of chemically modifying comprises esterifying or de-esterifying the retinolic compound.

319. The method of any one of claims 271-316, further comprising a step of combining the retinolic compound with one or more other agents in a composition.

320. The method of claim 319, wherein the step of combining comprises combining the retinolic compound with one or more other agents selected from the group consisting of binders, fillers, and combinations thereof.

321. The method of claim 319, wherein the step of combining comprises combining the retinolic compound with one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

322. An engineered *Y. lipolytica* strain that produces a retinolic compound, the strain containing one or more retinologenic modifications selected from the group consisting of:

a. increased expression or activity of a beta-carotene 15, 15'-monooxygenase polypeptide;
b. increased expression or activity of a retinol dehydrogenase polypeptide;
c. and combinations thereof.

323. The engineered Y. lipolytica strain of claim 322, wherein the produced retinolic compound accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

324. The engineered Y. lipolytica strain of claim 322, wherein the produced retinolic compound accumulates to levels that are greater than at least about 2.0% of the dry weight of the cells.

325. The engineered Y. lipolytica strain of claim 322, wherein the produced retinolic compound accumulates to levels that are greater than at least about 3.0% of the dry weight of the cells.

326. The engineered Y. lipolytica strain of claim 322, wherein the produced retinolic compound accumulates to levels that are greater than at least about 5.0% of the dry weight of the cells.

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327. The engineered *Y. lipolytica* strain of any one of claims 322-326, wherein the retinolic compound produced by the strain accumulates in lipid bodies.

328. The engineered *Y. lipolytica* strain of claim 327, wherein the retinolic compound is selected from the group consisting of: retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof.

329. The engineered *Y. lipolytica* strain of claim 327, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

330. The engineered *Y. lipolytica* strain of claim 327, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

331. The engineered *Y. lipolytica* strain of claim 330, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

332. The engineered *Y. lipolytica* strain of any one of claims 322-331, wherein the retinolic compound is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

333. A method of preparing a food or feed additive or a dietary supplement containing a retinolic compound, the method comprising steps of:

a. cultivating the fungus of any one of claims 199-264, the strain of claims 265-270 or the engineered Y. lipolytica strain of claims 322-332 under conditions that allow production of the retinolic compound;

b. isolating the retinolic compound; and

c. combining the isolated retinolic compound with one or more other food or feed additive components.

334. An engineered *Y. lipolytica* strain containing a truncated HMG CoA reductase polypeptide.

335. The engineered *Y. lipolytica* strain of claim 334, wherein the HMG CoA reductase polypeptide is a *Yarrowia* polypeptide.

336. The engineered *Y. lipolytica* strain of claim 334 or 335, wherein the HMG CoA reductase polypeptide is a *Yarrowia lipolytica* polypeptide.

337. The engineered *Y. lipolytica* strain of any one of claims 334-336, further comprising a second HMG CoA reductase polypeptide from a second organism.

338. An engineered *Y. lipolytica* strain having increased expression or activity of a GGPP synthase gene.

339. The engineered *Y. lipolytica* strain of claim 338, wherein the GGPP synthase polypeptide is a *Yarrowia* polypeptide.

340. The engineered *Y. lipolytica* strain of claim 338 or 339, wherein the GGPP synthase polypeptide is a *Yarrowia lipolytica* polypeptide.

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341. The engineered *Y. lipolytica* strain of any one of claims 338-340, further comprising a second GGPP synthase polypeptide from a second organism.

342. An engineered *Y. lipolytica* strain having decreased expression or activity of a squalene synthase polypeptide.

343. The engineered *Y. lipolytica* strain of claim 342, wherein the squalene synthase polypeptide is an endogenous squalene synthase polypeptide.

344. The engineered *Y. lipolytica* strain of claim 342 or 343, wherein the squalene synthase polypeptide is a polypeptide from an organism selected from the group consisting of: *Neurospora crassa, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), Aspergillus niger, Saccharomyces cerevisiae, Mucor circinelloides, Rhotorula glutinis, Candida utilis, Mortierella alpina*, and *Yarrowia lipolytica*.

345. The engineered *Y. lipolytica* strain of any one of claims 342-344, further comprising a truncated HMG CoA reductase polypeptide selected from the group consisting of: a *Yarrowia* HMG CoA reductase polypeptide and a *Yarrowia lipolytica* HMG CoA reductase polypeptide;

and optionally comprising a second HMG CoA reductase polypeptide from a second organism.

346. An engineered *Y. lipolytica* strain containing a heterologous phytoene dehydrogenase (carB) polypeptide and a heterologous phytoene synthase/lycopene cyclase (carRP) polypeptide.

347. The engineered *Y. lipolytica strain* of any one of claims 334-344, further containing:

a heterologous phytoene dehydrogenase (carB) polypeptide; and

a heterologous phytoene synthase/lycopene cyclase (carRP) polypeptide,

wherein the strain produces β -carotene.

348. The engineered *Y. lipolytica* strain of claim 347, wherein the phytoene dehydrogenase polypeptide is a polypeptide from an organism of the genus *Mucor*.

349. The engineered *Y. lipolytica* strain of claim 347, wherein the phytoene dehydrogenase polypeptide is a polypeptide from the organism *Mucor circinelloides*.

350. The engineered *Y. lipolytica* strain of claim 347, further comprising a second phytoene dehydrogenase polypeptide from a second organism.

351. The engineered *Y. lipolytica* strain of claim 347, wherein the phytoene synthase/lycopene cyclase polypeptide is a polypeptide from an organism of the genus *Mucor*.

352. The engineered *Y. lipolytica* strain of claim 347, wherein the phytoene synthase/lycopene cyclase polypeptide is a polypeptide from the organism *Mucor circinelloides*.

353. The engineered *Y. lipolytica* strain of any one of claims 347-352, further comprising a second phytoene synthase/lycopene cyclase polypeptide from a second organism.

354. The engineered *Y. lipolytica* strain of claim 347, wherein the produced β-carotene accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

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355. The engineered *Y. lipolytica* strain of claim 347, wherein the produced β-carotene accumulates to levels that are greater than at least about 2.0% of the dry weight of the cells.

356. The engineered *Y. lipolytica* strain of claim 347, wherein the produced β-carotene accumulates to levels that are greater than at least about 3.0% of the dry weight of the cells.

357. The engineered *Y. lipolytica* strain of claim 347, wherein the produced β-carotene accumulates to levels that are greater than at least about 5.0% of the dry weight of the cells.

358. The engineered *Y. lipolytica* strain of any one of claims 347-357, wherein the produced β-carotene accumulates in lipid bodies.

359. The engineered *Y. lipolytica* strain of claim 358, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

360. The engineered *Y. lipolytica* strain of claim 358, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

361. The engineered *Y. lipolytica* strain of claim 360, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

362. The engineered *Y. lipolytica* strain of any one of claims 354-360, wherein the β-carotene is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

363. The engineered *Y. lipolytica* strain of claim 347, further comprising a heterologous carotenoid ketolase polypeptide, such that the strain produces echinenone.

364. The engineered *Y. lipolytica* strain of claim 363, wherein the produced echinenone accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

365. The engineered *Y. lipolytica* strain of claim 363, wherein the produced echinenone accumulates to levels that are greater than at least about 3.0% of the dry weight of the cells.

366. The engineered *Y. lipolytica* strain of any one of claims 363-365, wherein the produced echinenone accumulates in lipid bodies.

367. The engineered *Y. lipolytica* strain of claim 366, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

368. The engineered *Y. lipolytica* strain of claim 366, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

369. The engineered *Y. lipolytica* strain of claim 368, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

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370. The engineered *Y. lipolytica* strain of any one of claims 363-369, wherein the echinenone is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

371. The engineered *Y. lipolytica* strain of claim 347, further comprising a heterologous carotenoid ketolase polypeptide, such that the strain produces canthaxanthin.

372. The engineered *Y. lipolytica* strain of claim 371, wherein the produced canthaxanthin accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

373. The engineered *Y. lipolytica* strain of claim 371, wherein the produced canthaxanthin accumulates to levels that are greater than at least about 2.5% of the dry weight of the cells.

374. The engineered *Y. lipolytica* strain of claim 371, wherein the produced canthaxanthin accumulates to levels that are greater than at least about 3.5% of the dry weight of the cells.

375. The engineered *Y. lipolytica* strain of any one of claims 371-374, wherein the produced canthaxanthin accumulates in lipid bodies.

376. The engineered *Y. lipolytica* strain of claim 374, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

377. The engineered *Y. lipolytica* strain of claim 374, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

378. The engineered *Y. lipolytica* strain of claim 377, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

379. The engineered *Y. lipolytica* strain of any one of claims 371-378, wherein the canthaxanthin is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

380. The engineered *Y. lipolytica* strain of claim 363 or 371, further comprising a heterologous carotenoid hydroxylase polypeptide, such that the strain produces astaxanthin.

381. The engineered *Y. lipolytica* strain of claim 380, wherein the produced astaxanthin accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

382. The engineered *Y. lipolytica* strain of any one of claims 380-381, wherein the produced astaxanthin accumulates in lipid bodies.

383. The engineered *Y. lipolytica* strain of claim 382, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

384. The engineered *Y. lipolytica* strain of claim 382, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

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385. The engineered *Y. lipolytica* strain of claim 384, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

386. The engineered *Y. lipolytica* strain of any one of claims 380-385, wherein the astaxanthin is characterized by a characterized by negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

387. The engineered *Y. lipolytica* strain of claim 347, further comprising a heterologous carotenoid hydroxylase polypeptide, such that the strain produces zeaxanthin.

388. The engineered *Y. lipolytica* strain of claim 387, wherein the produced zeaxanthin accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

389. The engineered *Y. lipolytica* strain of any one of claims 387-388, wherein the produced zeaxanthin accumulates in lipid bodies.

390. The engineered *Y. lipolytica* strain of claim 389, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

391. The engineered *Y. lipolytica* strain of claim 389, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

392. The engineered *Y. lipolytica* strain of claim 391, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

393. The engineered *Y. lipolytica* strain of any one of claims 387-392, wherein the zeaxanthin is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

394. A composition comprising:
lipid bodies;
at least one carotenoid compound; and
intact fungal cells.

395. A composition comprising:
lipid bodies;
at least one retinolic compound; and
intact fungal cells.

396. The composition of claim 394 or 395, wherein not more than 5%, 4%, 3%, 2%, or 1% of the composition is intact fungal cells.

397. The composition of claim 394 or 395, wherein not more than about 5%, 4%, 3%, 2%, or 1% of the composition is water soluble cell components.

398. The composition of claim 394, wherein the carotenoid comprises at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or higher of the composition.

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399. The composition of claim 395, wherein the retinolic compound comprises at least about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or higher of the composition.

400. The composition of claim 394 or 395, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof

401. The composition of claim 394 or 395 wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

402. The composition of claim 401 wherein the fatty acids are selected from the group consisting of . C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

403. The composition of any one of claims 394, 396-398, or 400-402 wherein the carotenoid is selected from the group consisting of: antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

404. The composition of any one of claims 394, 396-398, or 400-402 wherein the carotenoid is selected from the group consisting of: astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, and combinations thereof.

405. The composition of claim 404, wherein the carotenoid is β-carotene.

406. The composition of claim 404, wherein the carotenoid is selected from the group consisting of canthaxanthin, echinenone, and combinations thereof.

407. The composition of claim 404, wherein the carotenoid is zeaxanthin or lutein.

408. The composition of claim 404, wherein the carotenoid is astaxanthin.

409. The composition of any one of claims 395-397 or 399-402 wherein the retinolic compound is selected from the group consisting of: retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof.

410. The composition of 409, wherein the retinolic compound is retinol.

411. The composition of 409, wherein the retinolic compound is retinal.

412. The composition of 409, wherein the retinolic compound is retinoic acid.

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413. The composition of any one of claims 394-412, wherein the fungal cell is selected from the group consisting of: *Yarrowia, Sacchaomyces, Phaffi, Candida,* and combinations thereof.

414. The composition of claim 413, wherein the fungal cell is *Yarrowia lipolytica.*

415. The composition of claim 413, wherein the fungal cell is *Saccharomyces cerevisiae.*

416. The composition of claim 413, wherein the fungal cell is *Phaffia rhodozyma.*

417. The composition of claim 413, wherein the fungal cell is *Candida utilis.*

418. A composition comprising:

an oil suspension comprising:

lipid bodies;

at least one carotenoid compound;

intact fungal cells; and

a binder or filler.

419. The composition of any one of claims 394, 396-398, 400-408, or 413-418 wherein the at least one carotenoid compound is characterized by a characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

420. A composition comprising:

an oil suspension comprising:

lipid bodies;

at least one carotenoid compound;

intact fungal cells; and

one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

421. The composition of any one of claims 418-420, wherein the composition is dried.

422. The composition of claim 422, formulated as a feedstuff.

423. A composition comprising:

an oil suspension comprising:

lipid bodies;

at least one retinolic compound;

intact fungal cells; and

a binder or filler.

424. The composition of any one of claims 395-397, 399-402, or 409-417 wherein the at least one retinolic compound is characterized by a characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

425. A composition comprising:

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an oil suspension comprising:

lipid bodies;

at least one retinolic compound;

intact fungal cells; and

one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

426. The composition of any one of claims 423-425, wherein the composition is dried.

427. The composition of claim 426, formulated as a feedstuff.

428. The composition of any one of claims 394-427 wherein the fungal cells are selected from group chosen from *Y. lipolytica*, *C. utilis*, and *S. cerevisiae*.

429. An isolated carotenoid composition, prepared by a method comprising steps of:

a. cultivating the fungus of any one of claims 1-79, the strain of any one of claims 80-86 or or the engineered *Y. lipolytica* strain of claims 144-197 under conditions that allow production of a carotenoid; and

b. isolating the produced carotenoid.

430. The composition of claim 429, wherein the fungus is selected from a genus of the group consisting of: *Yarrowia*, *Saccharomyces*, *Phaffia*, and *Candida*.

431. The composition of claim 430, wherein the fungus is *Yarrowia lipolytica*.

432. The composition of claim 430, wherein the fungus is *Saccharomyces cerevisiae*.

433. The composition of claim 430, wherein the fungus is *Phaffia rhodozyma*.

434. The composition of claim 430, wherein the fungus is *Candida utilis*.

435. The composition of claim 429, wherein the step of cultivating comprising cultivating under conditions and for a time sufficient that the carotenoid accumulates to a level above at least about 1% of the dry cell weight of the fungus.

436. The composition of any one of claims 429-435, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus accumulates lipid bodies to a level above about 20% of its dry cell weight.

437. The composition of any one of claims 429-436, wherein the carotenoid is selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide

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acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

438. The composition of any one of claims 429-437, wherein the step of cultivating comprises growing cells under conditions of excess carbon and limiting non-carbon nutrient.

439. The composition of claim 438, wherein the limiting non-carbon nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, and combinations thereof.

440. The composition of claim 438 wherein the limiting non-carbon nutrient comprises nitrogen.

441. The composition of claim 440 wherein the carbon:nitrogen ratio is within the range selected from the group consisting of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 6-:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, and 10:1.

442. The composition of claim 440 wherein the carbon:nitrogen ratio is less than about 10:1.

443. The composition of any one of claims 429-442, wherein the step of cultivating comprises growing under conditions of controlled dissolved oxygen concentration.

444. The composition of claim 443, wherein the step of cultivating comprises modulating feed rate to maintain a specific level of dissolved oxygen.

445. The composition of claim 429, wherein the step of cultivating comprises a first phase of growing under conditions of excess carbon and limiting oxygen, followed by a second phase of growing under conditions of excess oxygen and limiting carbon.

446. The composition of claim 429, wherein the step of isolating comprises homogenizing cells and subjecting them to extraction.

447. The composition of claim 446, wherein the step of isolating comprises extracting with a supercritical fluid.

448. The composition of claim 447, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

449. The composition of claim 448, wherein the supercritical fluid comprises carbon dioxide.

450. The composition of claim 446, wherein the step of isolating comprises extracting with propylene glycol.

451. The composition of claim 429-450, wherein the produced carotenoid is a xanthophyll.

452. The composition of claim 451, wherein the xanthophyll comprises canthaxanthin, echinenone, or both.

453. The composition of claim 446, wherein the step of isolating comprises extracting with vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

454. The composition of claim 446, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

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455. The composition of claim 446, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

456. The composition of claim 455, wherein the step of isolating comprises extracting with a combination of an alcohol and hexane.

457. The composition of claim 455, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

458. The composition of claim 456 or 457, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

459. The composition of claim 446, wherein the step of isolating comprises disrupting the fungus by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the host cell to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

460. The composition of claim 459, wherein the step of isolating comprises disrupting the fungus by mechanical disruption.

461. The composition of claim 460, wherein mechanical disruption is achieved by subjecting the fungus to a bead mill/mashing at high pressure.

462. The composition of claim 461, wherein wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

463. The composition of any one of claims 429-462, wherein the carotenoid accumulates in a lipid body.

464. The composition of claim 463, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

465. The composition of claim 463, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

466. The composition of claim 465, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

467. The composition of claim 429, wherein the step of isolating comprises substantially separating the fungus from the cultivation medium to obtain at least one carotenoid-enriched fraction.

468. The composition of claim 429, wherein: the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the carotenoid in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

469. The composition of claim 429, wherein the carotenoid is selected from the group consisting of astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin and combinations thereof.

470. The composition of claim 469, wherein the carotenoid comprises β-carotene.

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471. The composition of claim 469, wherein the carotenoid is selected from the group consisting of canthaxanthin, echinenone, β-cryptoxanthin, and combinations thereof..

472. The composition of claim 469, wherein the carotenoid comprises zeaxanthin or lutein.

473. The composition of claim 469, wherein the carotenoid comprises astaxanthin.

474. The composition of claim 429, wherein the step of isolating comprises concentrating the carotenoid.

475. The composition of claim 474, wherein the step of isolating comprises concentrating the carotenoid until it is at least about 5-fold more concentrated.

476. The composition of claim 429 or any one of claims 474-475, further comprising a step of chemically modifying the carotenoid.

477. The composition of claim 476, wherein the step of chemically modifying comprises esterifying or de-esterifying the carotenoid.

478. The composition of claim 429 or any one of claims 474-475, further comprising a step of combining the carotenoid with one or more other agents in a composition.

479. The composition of claim 478, wherein the step of combining comprises combing the carotenoid with one or more other agents selected from the group consisting of binders, fillers, and combinations thereof.

480. The composition of claim 478, wherein the step of combining comprises combining the carotenoid with one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

481. The composition of any one of claims 429-480, further comprising one or more binders or fillers.

482. The composition of any one of claims 429-480, further comprising one or more chelating agents, pigments, salts, surfactants , moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, etc., and combinations thereof.

483. The composition of any one of claims 429-482 wherein the composition is formulated as a feedstuff.

484. An isolated retinolic compound composition, prepared by a method comprising steps of:

a. cultivating the fungus of any one of claims 221-264,the strain of any one of claims 265-270, or the engineered Y. lipolytica strain of claims 322-332 under conditions that allow production of a retinolic compound; and

b. isolating the produced retinolic compound.

485. The composition of claim 484, wherein the fungus is selected from a genus of the group consisting of: *Yarrowia*, *Saccharomyces*, *Phaffia*, and *Candida*.

486. The composition of claim 485, wherein the fungus is *Yarrowia lipolytica*.

487. The composition of claim 485, wherein the fungus is *Saccharomyces cerevisiae*.

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488. The composition of claim 485, wherein the fungus is *Phaffia rhodozyma*.

489. The composition of claim 485, wherein the fungus is *Candida utilis*.

490. The composition of claim 484, wherein the step of cultivating comprising cultivating under conditions and for a time sufficient that the retinolic compound accumulates to a level above at least about 1% of the dry cell weight of the fungus.

491. The composition of any one of claims 484-490, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus accumulates lipid bodies to a level above about 20% of its dry cell weight.

492. The composition of any one of claims 484-491, wherein the retinolic compound is selected from the group consisting of retinol, retinal, retinoic acid, and combinations thereof.

493. The composition of any one of claims 484-492, wherein the step of cultivating comprises growing cells under conditions of excess carbon and limiting non-carbon nutrient.

494. The composition of claim 493, wherein the limiting non-carbon nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, and combinations thereof.

495. The composition of claim 493 wherein the limiting non-carbon nutrient comprises nitrogen.

496. The composition of claim 493 wherein the carbon:nitrogen ratio is within the range selected from the group consisting of about 200:1, 150:1, 125:1, 100:1, 95:1, 90:1, 85:1, 80:1, 75:1, 70:1, 65:1, 6-:1, 55:1, 50:1, 45:1, 40:1, 35:1, 30:1, 25:1, 20:1, 15:1, and 10:1.

497. The composition of claim 493 wherein the carbon:nitrogen ratio is less than about 10:1.

498. The composition of claims 484-497, wherein the step of cultivating comprises growing under conditions of controlled dissolved oxygen concentration.

499. The composition of claim 498, wherein the step of cultivating comprises modulating feed rate to maintain a specific level of dissolved oxygen.

500. The composition of claim 484, wherein the step of cultivating comprises a first phase of growing under conditions of excess carbon and limiting oxygen, followed by a second phase of growing under conditions of excess oxygen and limiting carbon.

501. The composition of claim 484, wherein the step of isolating comprises homogenizing cells and subjecting them extraction.

502. The composition of claim 501, wherein the step of isolating comprises extracting with a supercritical fluid.

503. The composition of claim 502, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

504. The composition of claim 503, wherein the supercritical fluid comprises carbon dioxide.

505. The composition of claim 501, wherein the step of isolating comprises extracting with propylene glycol.

506. The composition of claim 505, wherein the produced carotenoid is a xanthophyll.

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507. The composition of claim 506, wherein the xanthophyll comprises canthaxanthin, echinenone, or both.

508. The composition of claim 501, wherein the step of isolating comprises extracting with vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

509. The composition of claim 501, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

510. The composition of claim 501, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

511. The composition of claim 510, wherein the step of isolating comprises extracting with a combination of an alcohol and hexane.

512. The composition of claim 510, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

513. The composition of claim 510, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

514. The composition of claim 501, wherein the step of isolating comprises disrupting the fungus by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the host cell to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

515. The composition of claim 514, wherein the step of isolating comprises disrupting the fungus by mechanical disruption.

516. The composition of claim 515, wherein mechanical disruption is achieved by subjecting the fungusl to a bead mill/mashing at high pressure.

517. The composition of claim 516, wherein wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

518. The composition of claim 501, wherein the retinolic compound accumulates in a lipid body.

519. The composition of claim 518, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

520. The composition of claim 518, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

521. The composition of claim 518, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

522. The composition of claim 484, wherein the step of isolating comprises substantially separating the fungus from the cultivation medium to obtain at least one retinolic compound-enriched fraction.

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523. The composition of claim 484, wherein: the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the retinolic compound in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

524. The composition of claim 484, wherein the retinolic compound comprises retinol.

525. The composition of claim 484, wherein the step of isolating comprises concentrating the retinolic compound.

526. The composition of claim 525, wherein the step of isolating comprises concentrating the retinolic compound until it is at least about 5-fold more concentrated.

527. The composition of claim 484 or any one of claims 525-526, further comprises a step of chemically modifying the retinolic compound.

528. The composition of claim 527, wherein the step of chemically modifying comprises esterifying or de-esterifying the retinolic compound.

529. The composition of claim 484 or any one of claims 525-526, further comprising a step of combining the retinolic compound with one or more other agents in a composition.

530. The composition of claim 529, wherein the step of combining comprises combing the retinolic compound with one or more other agents selected from the group consisting of binders, fillers, and combinations thereof.

531. The composition of claim 529, wherein the step of combining comprises combining the retinolic compound with one or more other agents selected from the group consisting of chelating agents, pigments, salts, surfactants, moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, and combinations thereof.

532. The composition of any one of claims 484-531, further comprising one or more binders or fillers.

533. The composition of any one of claims 484-531, further comprising one or more chelating agents, pigments, salts, surfactants , moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, etc., and combinations thereof.

534. The composition of any one of claims 484-533 wherein the composition is formulated as a feedstuff.

535. A feedstuff comprising:

a carotenoid in lipid bodies;

wherein the carotenoid is selected from the group consisting of astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin and combinations thereof.

536. The feedstuff of claim 535, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

537. The feedstuff of claim 535, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

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538. The feedstuff of claim 537, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

539. The feedstuff of any one of claims 535-538, wherein the carotenoid is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

540. A feedstuff comprising:

a retinolic compound in lipid bodies;

wherein the retinolic compound is selected from the group consisting of retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof.

541. The feedstuff of claim 540, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

542. The feedstuff of claim 540, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

543. The feedstuff of claim 542, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

544. The feedstuff of any one of claims 540-543, wherein the reinolic compound is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

545. A carotenoid composition comprising:

a *Y. lipolytica* cell containing at least 1% carotenoids by weight.

546. A carotenoid composition comprising:

Y lipolytica lipid bodies; and

at least one carotenoid compound,

where the at least one carotenoid compound is present at a level that is at least 1% by weight of the lipid bodies.

547. The carotenoid composition of either claim 545 or claim 546, comprising a carotenoid compound selected from the group consisting of: antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

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548. The carotenoid composition of either claim 545 or claim 546, comprising a carotenoid compound selected from the group consisting of: astaxanthin, β-carotene, canthaxanthin, zeaxanthin, lutein, lycopene, echinenone, β-cryptoxanthin, and combinations thereof.

549. The carotenoid composition of claim 548 wherein the carotenoid is β-carotene.

550. The carotenoid composition of claim 548, wherein the carotenoid is selected from the group consisting of canthaxanthin, echinenone, β-cryptoxanthin and combinations thereof.

551. The carotenoid composition of claim 548, wherein the carotenoid is zeaxanthin or lutein.

552. The carotenoid composition of claim 548, wherein the carotenoid is astaxanthin.

553. The carotenoid composition of any one of claims 545-552, further comprising one or more binders or fillers.

554. The carotenoid composition of any one of claims 545-552, further comprising one or more chelating agents, pigments, salts, surfactants , moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, etc., and combinations thereof.

555. The carotenoid composition of any one of claims 545-554, wherein the composition is formulated as a feedstuff.

556. A retinolic compound composition comprising:

a *Y. lipolytica* cell containing at least 1% carotenoids by weight.

557. A retinolic compound composition comprising:

Y lipolytica lipid bodies; and

at least one retinolic compound,

where the at least one retinolic compound is present at a level that is at least 1% by weight of the lipid bodies.

558. The retinolic compound composition of either claim 556 or claim 557, comprising a retinolic compound selected from the group consisting of: retinol, retinal, retinoic acid, retinyl palmitate, and combinations thereof.

559. The retinolic compound composition of any one of claims 556-558, further comprising one or more binders or fillers.

560. The retinolic compound composition of any one of claims 556-558, further comprising one or more chelating agents, pigments, salts, surfactants , moisturizers, viscosity modifiers, thickeners, emollients, fragrances, preservatives, etc., and combinations thereof.

561. The retinolic compound composition of any one of claims 556-560, wherein the composition is formulated as a feedstuff.

562. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one small molecule lipophilic agent selected from the group consisting of retinolic compounds, carotenoids, ubiquinone,

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vitamin K, vitamin E, squalene, lanosterol, zymosterol, ergosterol, 7-dehydrocholesterol (provitamin D3), and combinations thereof and can accumulate the produced small molecule lipophilic agent to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of retinologenic modifications, carotenogenic modifications, oleaginic modifications, and combinations thereof, and wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one small molecule lipophilic agent to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one small molecule lipophilic agent which the parental fungus does not naturally produce.

563. A recombinant fungus characterized by:

a. the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight; and

b. the recombinant fungus produces at least one small molecule lipophilic agent characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%, and combinations thereof and can accumulate the produced small molecule lipophilic agent to at least about 1% of its dry cell weight; wherein the recombinant fungus comprises at least one modification as compared with a parental fungus, the at least one modification being selected from the group consisting of retinologenic modifications, carotenogenic modifications, oleaginic modifications, and combinations thereof, and wherein the at least one modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one small molecule lipophilic agent to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one small molecule lipophilic agent which the parental fungus does not naturally produce.

564. A genetically modified *Y. lipolytica* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of acetyl-CoA thiolase, increased activity or expression of HMG-CoA synthase, increased activity or expression of HMG-CoA reductase, increased activity or expression of mevalonate kinase, increased activity or expression of phosphomevalonate kinase, increased activity or expression of mevalonate PP decarboxylase, decreased activity or expression of acetyl-CoA carboxylase, increased activity or expression of IPP isomerase, increased activity or expression of GPP synthase, increased activity or expression of FPP synthase, increased activity or expression of squalene synthase, decreased activity or expression of squalene synthase, increased activity or expression of GGPP synthase, decreased activity or expression of GGPP synthase, increased activity or expression of glucose-6 –phosphate

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dehydrogenase, increased activity or expression of 6-phosphogluconate dehydrogenase, increased activity or expression of fructose 1, 6 bisphosphatase, increased activity or expression of NADH kinase, increased activity or expression of transhydrogenase, and combinations thereof.

565. The genetically modified *Y. lipolytica* of claim 564, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

566. The genetically modified *Y. lipolytica* of claim 565, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

567. The genetically modified *Y. lipolytica* of claim 565, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

568. A genetically modified *Candida utilis* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of acetyl-CoA thiolase, increased activity or expression of HMG-CoA synthase, increased activity or expression of HMG-CoA reductase, increased activity or expression of mevalonate kinase, increased activity or expression of phosphomevalonate kinase, increased activity or expression of mevalonate PP decarboxylase, decreased activity or expression of acetyl-CoA carboxylase, increased activity or expression of IPP isomerase, increased activity or expression of GPP synthase, increased activity or expression of FPP synthase, increased activity or expression of squalene synthase, decreased activity or expression of squalene synthase, increased activity or expression of GGPP synthase, decreased activity or expression of GGPP synthase, increased activity or expression of glucose-6 –phosphate dehydrogenase, increased activity or expression of 6-phosphogluconate dehydrogenase, increased activity or expression of fructose 1, 6 bisphosphatase, increased activity or expression of NADH kinase, increased activity or expression of transhydrogenase, and combinations thereof.

569. The genetically modified *Candida utilis* of claim 568, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

570. The genetically modified *Candida utilis* of claim 569, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

571. The genetically modified *Candida utilis* of claim 569, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

572. A genetically modified *Saccharomyces cerevisiae* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of acetyl-CoA thiolase, increased activity or expression of HMG-CoA synthase, increased activity or expression of HMG-CoA reductase, increased activity or expression of mevalonate kinase, increased activity or expression of phosphomevalonate kinase, increased activity or expression of

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mevalonate PP decarboxylase, decreased activity or expression of acetyl-CoA carboxylase, increased activity or expression of IPP isomerase, increased activity or expression of GPP synthase, increased activity or expression of FPP synthase, increased activity or expression of squalene synthase, decreased activity or expression of squalene synthase, increased activity or expression of GGPP synthase, decreased activity or expression of GGPP synthase, increased activity or expression of glucose-6 –phosphate dehydrogenase, increased activity or expression of 6-phosphogluconate dehydrogenase, increased activity or expression of fructose 1, 6 bisphosphatase, increased activity or expression of NADH kinase, increased activity or expression of transhydrogenase, and combinations thereof.

573. The genetically modified *Saccharomyces cerevisiae* of claim 572, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

574. The genetically modified *Saccharomyces cerevisiae* of claim 573, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

575. The genetically modified *Saccharomyces cerevisiae* of claim 573, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

576. A genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of acetyl-CoA thiolase, increased activity or expression of HMG-CoA synthase, increased activity or expression of HMG-CoA reductase, increased activity or expression of mevalonate kinase, increased activity or expression of phosphomevalonate kinase, increased activity or expression of mevalonate PP decarboxylase, decreased activity or expression of acetyl-CoA carboxylase, increased activity or expression of IPP isomerase, increased activity or expression of GPP synthase, increased activity or expression of FPP synthase, increased activity or expression of squalene synthase, decreased activity or expression of squalene synthase, increased activity or expression of GGPP synthase, decreased activity or expression of GGPP synthase, increased activity or expression of glucose-6 –phosphate dehydrogenase, increased activity or expression of 6-phosphogluconate dehydrogenase, increased activity or expression of fructose 1, 6 bisphosphatase, increased activity or expression of NADH kinase, increased activity or expression of transhydrogenase, and combinations thereof.

577. The genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of claim 576, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

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578. The genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of claim 577, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

579. The genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of claim 577, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

580. A method comprising steps of:

a. cultivating a host cell selected form the group consisting of: the recombinant fungus of any one of claims 1-79, the engineered *Y. lipolytica* strain of any one of claims 334-393 or claims 144-197, the strain of *Y. lipolytica* of any one of claims 80-86, the recombinant fungus of claim 562 or claim 563, the genetically modified *Y. lipolytica* of any one of claims 564-567, the genetically modified *Candida utilis* of any one of claims 568-571, the genetically modified *Saccharomyces cerevisiae* of any one of claims 572-575, and the genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of any one of claims 576-579, under conditions that allow production of the carotenoid;

b. and isolating the produced carotenoid.

581. The method of claim 580 wherein the produced carotenoid is b-carotene

582. The method of claim 580 wherein the produced carotenoid it astaxanthin.

583. The method of claim 580 wherein the step of isolating comprises extracting with an organic or a non-organic solvent.

584. The method of claim 580 wherein the step of isolating comprises extracting with a solvent selected from the group consisting of acetone, supercritical fluids, propane, xenon, ethane, propylene, methane, ethylene, ethanol, carbon dioxide, chloroform, ethanol, ethyl acetate, heptane, hexane, isopropanol, methanol, methylene chloride, octane, tetrahydrofuran (THF), cyclohexane, isobutyl acetate, methyl ketone, ethyl ketone, toluene, cyclohexanone, benzene, propylene glycol, vegetable oils, and combinations thereof.

585. The method of claim 584, wherein the step of isolating comprises extracting with a supercritical fluid.

586. The method of claim 585, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

587. The method of claim 586, wherein the supercritical fluid comprises carbon dioxide.

588. The method of claim 584, wherein the step of isolating comprises extracting with propylene glycol.

589. The method of any one of claims 580-588, wherein the produced carotenoid is a xanthophyll.

590. The method of claim 589, wherein the xanthophyll comprises canthaxanthin, echinenone, or both.

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591. The method of claim 584, wherein the step of isolating comprises extracting with vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

592. The method of claim 584, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

593. The method of claim 584, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

594. The method of claim 593, wherein the step of isolating comprises extracting with a combination of an alcohol and hexane.

595. The method of claim 593, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

596. The method of claim 594 or 595, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

597. The method of claim 580, wherein the step of isolating comprises disrupting the host cell by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the host cell to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

598. The method of claim 597, wherein the step of isolating comprises disrupting the host cell by mechanical disruption.

599. The method of claim 598, wherein mechanical disruption is achieved by subjecting the host cell to a bead mill/mashing at high pressure.

600. The method of claim 599, wherein wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

601. The method of claim 580 wherein the step of cultivating comprises growing under conditions of limiting nutrient, where the limiting nutrient is selected from the group consisting of carbon, nitrogen, phosphate, magnesium, or combinations thereof.

602. The method of claim 601 wherein the limiting nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, or combinations thereof, and carbon is in excess.

603. The method of claim 601 wherein the limiting nutrient is carbon.

604. The method of claim 601 wherein the limiting nutrient is phosphate and phosphate addition is controlled so that production of canthazanthin as compared with echinenone is altered.

605. The method of any one of claims 580-604 wherein the step of cultivating comprises growing under conditions where at least one environmental parameter is controlled for at least a portion of the cultivating.

606. The method of claim 605 wherein the controlled environmental parameter is selected from the group consisting of amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, and combinations thereof.

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607. The method of any one of claims 580-606 wherein at least one environmental parameter is not controlled during at least a portion of the cultivating.

608. The method of claim 607 wherein the controlled environmental parameter is selected from the group consisting of amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, and combinations thereof.

609. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at about 20-40 degrees.

610. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at about 20-30 degrees.

611. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating at about 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30 °C or above.

612. The method of claim any one of claims 580-608wherein the step of cultivating comprises cultivating within a pH range of about pH 4-7.5.,

613. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 4-6.5.

614. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 3.5-7.

615. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 3.5-4

616. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH, 4-4.5.

617. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 4.5-5.

618. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 5-5.5.

619. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 5.5-6.

620. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 6-6.5.

621. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating within a pH range of about pH 6.5-7.

622. The method of claim any one of claims 580-608 wherein the step of cultivating comprises cultivating at a pH of about pH 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5 or above.

623. The method of any one of claims 580-622 wherein temperature is varied during the culture period.

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624. The method of any one of claims 580-622 wherein pH is varied during the culture period.

625. The method of claim 623 or claim 624 wherein the variation is gradual.

626. The method of claim 623 or claim 624 wherein the variation is stepwise.

627. The method of claim 623 or claim 624 wherein the variation is sometimes gradual and sometimes stepwise.

628. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 5-30%.

629. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 5-20%

630. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 10-25%.

631. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 10-30%.

632. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 15-25%

633. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 15-30%.

634. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration of about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, or more.

635. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at an oxygen concentration above about 20%.

636. The method of any one of claims 580-608 wherein the step of cultivating comprises cultivating at about pH 5.5 and at a temperature between about 28-30 °C.

637. The method of claim 636 wherein the step of cultivating comprises cultivating at an oxygen concentration above about 20%.

638. The method of any one of claims 580-637 wherein the step of isolating comprises crystallizing the carotenoid.

639. The method of claim 638 wherein the step of isolating comprises collecting crystals.

640. The method of claim 639 wherein the step of collecting comprises filtering or centrifuging or both.

641. The method of any one of claims 580-640 further comprising formulating the isolated carotenoid.

642. The method of claim 641 wherein the step of formulating comprises preparing as a cold-water dispersible powder.

643. The method of claim 641 wherein the step of formulating comprises preparing as a suspension of crystals in oil.

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644. The method of claim 643 wherein the oil is vegetable oil.

645. The method of claim 643 or 644 wherein the step of formulating comprises preparing as a 5%-30% w/w suspension of crystals in oil.

646. The method of claim 643 or 644 wherein the step of formulating comprises preparing as a 1%-30% w/w suspension of crystals in oil.

647. The method of claim 643 or 644 wherein the step of formulating comprises preparing as a 10%-30% w/w suspension of crystals in oil.

648. A genetically modified *Y. lipolytica* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of beta-carotene 15, 15'-monooxygenase, increased expression or activity of retinol dehydrogenase, and combinations thereof.

649. The genetically modified *Y. lipolytica* of claim 648, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

650. The genetically modified *Y. lipolytica* of claim 649, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

651. The genetically modified *Y. lipolytica* of claim 649, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

652. A genetically modified *Candida utilis* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of beta-carotene 15, 15'-monooxygenase, increased expression or activity of retinol dehydrogenase,, and combinations thereof.

653. The genetically modified *Candida utilis* of claim 652, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

654. The genetically modified *Candida utilis* of claim 653, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

655. The genetically modified *Candida utilis* of claim 653, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

656. A genetically modified *Saccharomyces cerevisiae* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of beta-carotene 15, 15'-monooxygenase, increased expression or activity of retinol dehydrogenase, and combinations thereof.

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657. The genetically modified *Saccharomyces cerevisiae* of claim 656, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

658. The genetically modified *Saccharomyces cerevisiae* of claim 657, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

659. The genetically modified Saccharomyces cerevisiae of claim Q657, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

660. A genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* comprising an altered activity or expression of one or more enzymes when compared to an unmodified strain, wherein the altered activity or expression of one or more enzymes is selected from the group consisting of: increased activity or expression of beta-carotene 15, 15'-monooxygenase, increased expression or activity of retinol dehydrogenase, and combinations thereof.

661. The genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of claim 660, wherein the altered activity or expression of one or more enzymes is caused by an overexpression of one or more endogenous genes.

662. The genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of claim 661, wherein the overexpression of one or more endogenous genes is caused by altered regulation of an endogenous gene, increased copy number of an endogenous gene, or both.

663. The genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of claim 661, wherein the overexpression of one or more endogenous genes is caused by expression of a heterologous gene.

664. A method comprising steps of:

a. cultivating a host cell selected form the group consisting of: the recombinant fungus of any one of claims 199-264, the engineered *Y. lipolytica* strain of any one of claims 322-332, the strain of Y. lipolytica of any one of claims 265-270, the recombinant fungus of claim 562 or claim 563, the genetically modified *Y. lipolytica* of any one of claims 648-651, the genetically modified *Candida utilis* of any one of claims 652-655, the genetically modified *Saccharomyces cerevisiae* of any one of claim 656-659, and the genetically modified *Xanthophyllomyces dendrorhous (Phaffia rhodozyma)* of any one of claim 660-663, under conditions that allow production of the retinolic compound;

b. and isolating the produced retinolic compound.

665. The method of claim 664 wherein the produced retinolic compound is retinol.

666. The method of claim 664 wherein the produced retinolic compound it retinal

667. The method of claim 664 wherein the produced retinolic compound it retinoic acid.

668. The method of claim 664 wherein the step of isolating comprises extracting with an organic or a non-organic solvent.

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669. The method of claim 664 wherein the step of isolating comprises extracting with a solvent selected from the group consisting of acetone, supercritical fluids, propane, xenon, ethane, propylene, methane, ethylene, ethanol, carbon dioxide, chloroform, ethanol, ethyl acetate, heptane, hexane, isopropanol, methanol, methylene chloride, octane, tetrahydrofuran (THF), cyclohexane, isobutyl acetate, methyl ketone, ethyl ketone, toluene, cyclohexanone, benzene, propylene glycol, vegetable oils, and combinations thereof.

670. The method of claim 669, wherein the step of isolating comprises extracting with a supercritical fluid.

671. The method of claim 670, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

672. The method of claim 671, wherein the supercritical fluid comprises carbon dioxide.

673. The method of claim 669, wherein the step of isolating comprises extracting with propylene glycol.

674. The method of claim 673, wherein the produced retinolic compound is a retinol.

675. The method of claim 669, wherein the step of isolating comprises extracting with vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

676. The method of claim 669, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

677. The method of claim 669, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

678. The method of claim 677, wherein the step of isolating comprises extracting with a combination of alcohol and hexane.

679. The method of claim 677, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

680. The method of claim 678 or 679, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

681. The method of claim 664, wherein the step of isolating comprises disrupting the host cell by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the host cell to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

682. The method of claim 681, wherein the step of isolating comprises disrupting the host cell by mechanical disruption.

683. The method of claim 682, wherein mechanical disruption is achieved by subjecting the host cell to a bead mill/mashing at high pressure.

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684. The method of claim 683, wherein wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

685. The method of claim 664 wherein the step of cultivating comprises growing under conditions of limiting nutrient, where the limiting nutrient is selected from the group consisting of carbon, nitrogen, phosphate, magnesium, or combinations thereof.

686. The method of claim 685 wherein the limiting nutrient is selected from the group consisting of nitrogen, phosphate, magnesium, or combinations thereof, and carbon is in excess.

687. The method of claim 685 wherein the limiting nutrient is carbon.

688. The method of any one of claims 664-687 wherein the step of cultivating comprises growing under conditions where at least one environmental parameter is controlled for at least a portion of the cultivating.

689. The method of claim 688 wherein the controlled environmental parameter is selected from the group consisting of amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, and combinations thereof.

690. The method of any one of claims 664-689 wherein at least one environmental parameter is not controlled during at least a portion of the cultivating.

691. The method of claim 690 wherein the controlled environmental parameter is selected from the group consisting of amount of a particular nutrient, pH, temperature, pressure, oxygen concentration, timing of feeds, content of feeds, and combinations thereof.

692. The method of claim any one of claims 664-691 wherein the step of cultivating comprises cultivating at about 20-40 degrees.

693. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at about 20-30 degrees.

694. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at about 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30 °C or above.

695. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 4-7.5.,

696. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 4-6.5.

697. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 3.5-7.

698. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 3.5-4

699. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH, 4-4.5.

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700. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 4.5-5.

701. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 5-5.5.

702. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 5.5-6.

703. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 6-6.5.

704. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating within a pH range of about pH 6.5-7.

705. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at a pH of about pH 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5 or above.

706. The method of any one of claims 664-705 wherein temperature is varied during the culture period.

707. The method of any one of claims 664-705 wherein pH is varied during the culture period.

708. The method of claim 706 or claim 707 wherein the variation is gradual.

709. The method of claim 706 or claim 707 wherein the variation is stepwise.

710. The method of claim 706 or claim 707 wherein the variation is sometimes gradual and sometimes stepwise.

711. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 5-30%.

712. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 5-20%

713. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 10-25%.

714. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 10-30%.

715. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 15-25%

716. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration within the rage of about 15-30%.

717. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration of about 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, or more.

718. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at an oxygen concentration above about 20%.

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719. The method of any one of claims 664-691 wherein the step of cultivating comprises cultivating at about pH 5.5 and at a temperature between about 28-30 °C.

720. The method of claim 719 wherein the step of cultivating comprises cultivating at an oxygen concentration above about 20%.

721. The method of any one of claims 664-720 wherein the step of isolating comprises crystallizing the retinolic compound.

722. The method of claim 721 wherein the step of isolating comprises collecting crystals.

723. The method of claim 722 wherein the step of collecting comprises filtering or centrifuging or both.

724. The method of any one of claims 664-723 further comprising formulating the isolated retinolic compound.

725. The method of claim 724 wherein the step of formulating comprises preparing as a cold-water dispersible powder.

726. The method of claim 724 wherein the step of formulating comprises preparing as a suspension of crystals in oil.

727. The method of claim 726 wherein the oil is vegetable oil.

728. The method of claim 726 or 727 wherein the step of formulating comprises preparing as a 5%-30% w/w suspension of crystals in oil.

729. The method of claim 726 or 727 wherein the step of formulating comprises preparing as a 1%-30% w/w suspension of crystals in oil.

730. The method of claim 726 or 727 wherein the step of formulating comprises preparing as a 10%-30% w/w suspension of crystals in oil.

731. A recombinant fungus wherein the fungus produces at least one carotenoid, and can accumulate the produced carotenoid to at least about 1% of its dry cell weight;

wherein the recombinant fungus comprises at least a first modification as compared with a parental fungus, wherein the mutation comprises a mutation in one or more genes that encode proteins comprising a SAGA complex.

732. The recombinant fungus of claim 731, wherein the recombinant fungus is oleaginous in that it can accumulate lipid to at least about 20% of its dry cell weight.

733. The recombinant fungus of claim 731 or 732, wherein the parental fungus both is not oleaginous and does not accumulate the carotenoid to at least about 1% of its dry cell weight;

and wherein the recombinant fungus comprises at least a second modification as compared with a parental fungus, the second modification selected from the group consisting of: carotenogenic modifications, oleaginic modifications, and combinations thereof;

wherein the second modification alters oleaginicity of the recombinant fungus, confers to the recombinant fungus oleaginy, confers to the recombinant fungus the ability to produce the at least one

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carotenoid to a level at least about 1% of its dry cell weight, or confers to the recombinant fungus the ability to produce at least one carotenoid which the parental fungus does not produce.

734. The recombinant fungus of claim 731-733, wherein the at least one carotenoid is selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

735. The recombinant fungus of claim 731-734, wherein the at least one carotenoid comprises β-carotene.

736. The recombinant fungus of any one of claims 731-735, wherein the recombinant fungus is a member of a genus selected from the group consisting of:

Aspergillus, Blakeslea, Botrytis, Candida, Cercospora, Cryptococcus, Cunninghamella, Fusarium (Gibberella), Kluyveromyces, Lipomyces, Mortierella, Mucor, Neurospora, Penicillium, Phycomyces, Pichia (Hansenula), Puccinia, Pythium, Rhodosporidium, Rhodotorula, Saccharomyces, Sclerotium, Trichoderma, Trichosporon, Xanthophyllomyces (Phaffia), and *Yarrowia;*

or is a species selected from the group consisting of:

Aspergillus terreus, Aspergillus nidulans, Aspergillus niger, Blakeslea trispora, Botrytis cinerea, Candida japonica, Candida pulcherrima, Candida revkaufi, Candida tropicalis, Candida utilis, Cercospora nicotianae, Cryptococcus curvatus, Cunninghamella echinulata, Cunninghamella elegans, Fusarium fujikuroi (Gibberella zeae), Kluyveromyces lactis, Lipomyces starkeyi, Lipomyces lipoferus, Mortierella alpina, Mortierella ramanniana, Mortierella isabellina, Mortierella vinacea, Mucor circinelloides, Neurospora crassa, Phycomyces blakesleanus, Pichia pastoris, Puccinia distincta, Pythium irregulare, Rhodosporidium toruloides, Rhodotorula glutinis, Rhodotorula graminis, Rhodotorula mucilaginosa, Rhodotorula pinicola, Rhodotorula gracilis, Saccharomyces cerevisiae, Sclerotium rolfsii, Trichoderma reesei, Trichosporon cutaneum, Trichosporon pullans, Xanthophyllomyces dendrorhous (Phaffia rhodozyma), and *Yarrowia lipolytica.*

737. The recombinant fungus of any one of claims 731-736 wherein the recombinant fungus is a species selected from the group consisting of: *Candida utilis, Saccharomyces cerevisiae, Xanthophyllomyces dendrorhous (Phaffia rhodozyma),* and *Yarrowia lipolytica.*

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738. The recombinant fungus of any one of claims 731-737, wherein the first modification comprises a mutation in a gene selected from the group consisting of: *spt-3, spt-7, spt-8, spt-20, ada-2, ada-3, gcn-5, ada-1, spt-15*, and combinations thereof.

739. The recombinant fungus of claim 738, wherein the first modification comprises a mutation in the *spt-8* gene.

740. The recombinant fungus of claim 739, wherein the first modification reduces *spt-8* expression, *spt-8* activity, or both.

741. The recombinant fungus of any one of claims 732-740, wherein the first modification confers the ability to the recombinant fungus to produce the at least one carotenoid to a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the dry cell weight of th fractionating the cultivation medium e recombinant fungus.

742. The recombinant fungus of any one of claims 732-741, wherein the first modification confers the ability to the recombinant fungus to produce the at least one carotenoid such that total carotenoid production by the recombinant fungus occurs at a level selected from the group consisting of at least about 2%, at least about 3%, at least about 5%, and at least about 10% of the dry cell weight of the recombinant fungus.

743. A strain of *Yarrowia lipolytica* comprising a mutation in one or more genes that encode proteins comprising a SAGA complex

744. The strain of claim 743, wherein the mutation comprises a mutation in a gene selected from the group consisting of: *spt-3, spt-7, spt-8, spt-20, ada-2, ada-3, gcn-5, ada-1, spt-15*, and combinations thereof.

745. The strain of claim 744, wherein the first modification comprises a mutation in the *spt-8* gene.

746. The strain of claim 745, wherein the first modification reduces *spt-8* expression, *spt-8* activity, or both.

747. The strain of any one of claims 743-746, wherein the strain accumulates from 1% to 15% of its dry cell weight as at least one carotenoid.

748. The strain of claim 747, wherein the carotenoid is selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

749. The strain of claim 748, wherein the carotenoid comprises β-carotene.

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750. A method of producing a carotenoid, the method comprising steps of:

a. cultivating the fungus of any one of claims 731-742 or the strain of claims 743-749 under conditions that allow production of the carotenoid;

b. and isolating the produced carotenoid.

751. The method of claim 750, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the carotenoid accumulates to a level above at least about 1% of the dry cell weight of the fungus or strain.

752. The method of claim 750 or 751, wherein the step of cultivating comprises cultivating under conditions and for a time sufficient that the fungus or strain accumulates lipid bodies to a level above about 20% of its dry cell weight.

753. The method of any one of claims claim 750-752, wherein the carotenoid is selected from the group consisting of antheraxanthin, adonirubin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, α-carotene, β,ψ-carotene, δ-carotene, ε-carotene, echinenone, 3-hydroxyechinenone, 3'-hydroxyechinenone, γ-carotene, ψ-carotene, 4-keto- γ-carotene, ζ-carotene, α-cryptoxanthin, deoxyflexixanthin, diatoxanthin, 7,8-didehydroastaxanthin, didehydrolycopene, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene, lactucaxanthin, lutein, lycopene, myxobactone, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, phytofluene, rhodopin, rhodopin glucoside, 4-keto-rubixanthin, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, torulene, 4-keto-torulene, 3-hydroxy-4-keto-torulene, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, a C30 carotenoid, and combinations thereof.

754. The method of claim 753, wherein the carotenoid comprises β-carotene.

755. The method any one of claims claim 750-754, wherein the step of isolating comprises homogenizing the fungus or strain and subjecting it to extraction.

756. The method of claim 755, wherein the step of isolating comprises extracting with a solvent selected from the group consisting of acetone, supercritical fluids, propane, xenon, ethane, propylene, methane, ethylene, ethanol, carbon dioxide, chloroform, ethanol, ethyl acetate, heptane, hexane, isopropanol, methanol, methylene chloride, octane, tetrahydrofuran (THF), cyclohexane, isobutyl acetate, methyl ketone, ethyl ketone, toluene, cyclohexanone, benzene, propylene glycol, vegetable oils, and combinations thereof.

757. The method of claim 756, wherein the step of isolating comprises extracting with a supercritical fluid.

758. The method of claim 757, wherein the supercritical fluid comprises a fluid selected from the group consisting of: carbon dioxide, propane, xenon, ethane, propylene, methane, ethylene, ethanol, and combinations thereof.

759. The method of claim 758, wherein the supercritical fluid comprises carbon dioxide.

760. The method of claim 756, wherein the step of isolating comprises extracting with propylene glycol.

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761. The method of claim 760, wherein the produced carotenoid is a xanthophyll.

762. The method of claim 761, wherein the xanthophyll comprises canthaxanthin, echinenone, or both.

763. The method of claim 756, wherein the step of isolating comprises extracting with vegetable oils selected from the group consisting of soybean oil, rapeseed oil, corn oil, cottonseed oil, canola oil, and combinations thereof.

764. The method of claim 756, wherein the step of isolating comprises extracting with a combination of hexane and ethyl acetate.

765. The method of claim 756, wherein the step of isolating comprises extracting with a combination of a polar and non-polar solvent.

766. The method of claim 765, wherein the step of isolating comprises extracting with a combination of an alcohol and hexane.

767. The method of claim 765, wherein the step of isolating comprises extracting with a combination of an alcohol and ethyl acetate.

768. The method of claim 766 or 767, wherein the alcohol is selected from the group consisting of: ethanol, isopropanol, methanol, and combinations thereof.

769. The method of claim 750, wherein the step of isolating comprises disrupting the cells by a process selected from the group consisting of: mechanical disruption, enzymatic disruption, chemical disruption, subjecting the cells to a reducting agent, high pressure homogenization/shearing, changing pH, and combinations thereof.

770. The method of claim 769, wherein the step of isolating comprises disrupting the cells by mechanical disruption.

771. The method of claim 770, wherein mechanical disruption is achieved by subjecting the cells to a bead mill/mashing at high pressure.

772. The method of claim 771, wherein wherein extraction takes place at 25K, 10K-30K, 15K-25K, or 20-25K pound-force per square inch (psi).

773. The method of any one of claims 750-772, wherein the carotenoid in the cell accumulates in a lipid body.

774. The method of claim 773, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

775. The method of claim 773, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

776. The method of claim 775, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

777. The method of claim any one of claims 750-776, wherein the step of isolating comprises fractionating the cultivation medium to obtain at least one carotenoid-enriched fraction.

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778. The method of claim any one of claims 750-776, wherein: the step of cultivating comprises cultivating the fungus under conditions that allow accumulation of the carotenoid in cytoplasmic oil bodies; and the step of isolating comprises isolating oil derived from the cytoplasmic oil bodies.

779. An engineered *Y. lipolytica* strain that produces lutein, the strain containing one or more carotenogenic modifications selected from the group consisting of:

a. increased expression or activity of a GGPP synthase polypeptide;

b. increased expression or activity of an HMG CoA reductase polypeptide;

c. decreased expression or activity of a squalene synthase polypeptide;

d. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide;

e. increased expression or activity of a phytoene dehydrogenase polypeptide;

f. increased expression or activity of an lycopene epsilon cyclase polypeptide;

g. increased expression or activity of an carotene epsilon hydroxylase polypeptide;

h. increased expression or activity of a carotenoid hydroxylase polypeptide; and combinations thereof.

780. An engineered *Y. lipolytica* strain that produces lutein, the strain containing one or more carotenogenic modifications selected from the group consisting of:

a. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide;

b. increased expression or activity of a phytoene dehydrogenase polypeptide;

c. increased expression or activity of an lycopene epsilon cyclase polypeptide;

d. increased expression or activity of an carotene epsilon hydroxylase polypeptide;

e. increased expression or activity of a carotenoid hydroxylase polypeptide; and combinations thereof.

781. An engineered *Y. lipolytica* strain that produces lutein, the strain containing the carotenogenic modifications:

a. increased expression or activity of a phytoene synthase/lycopene cyclase polypeptide;

b. increased expression or activity of a phytoene dehydrogenase polypeptide;

c. increased expression or activity of an lycopene epsilon cyclase polypeptide;

d. increased expression or activity of an carotene epsilon hydroxylase polypeptide;

e. increased expression or activity of a carotenoid hydroxylase polypeptide; and combinations thereof.

782. The engineered *Y. lipolytica* strain of claim 780 or 781, further comprising one or more carotenogenic modifications selected from the group consisting of:

a. increased expression or activity of a GGPP synthase polypeptide;

b. increased expression or activity of an HMG CoA reductase polypeptide;

c. decreased expression or activity of a squalene synthase polypeptide; and combinations thereof.

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783. The engineered *Y. lipolytica* strain of any one of claims 779-782, wherein the produced lutein accumulates to levels that are greater than at least about 1.0% of the dry weight of the cells.

784. The engineered *Y. lipolytica* strain of any one of claims 779-782, wherein the produced lutein accumulates to levels that are greater than at least about 2.0% of the dry weight of the cells.

785. The engineered *Y. lipolytica* strain of any one of claims 779-782, wherein the produced lutein accumulates to levels that are greater than at least about 3.0% of the dry weight of the cells.

786. The engineered *Y. lipolytica* strain of any one of claims 779-782, wherein the produced lutein accumulates to levels that are greater than at least about 5.0% of the dry weight of the cells.

787. The engineered *Y. lipolytica* strain of any one of claims 779-786, wherein lutein produced by the strain accumulates in lipid bodies.

788. The engineered *Y. lipolytica* strain of claim 797, wherein the lipid bodies are characterized by major components selected from the group consisting of triacylglycerols, ergosteryl esters, other steryl esters, free ergosterol, phospholipids, and combinations thereof.

789. The engineered *Y. lipolytica* strain of claim 787, wherein the lipid bodies comprise fatty acids, which fatty acids are selected from the group consisting of C16 and C18 fatty acids, and combinations thereof.

790. The engineered *Y. lipolytica* strain of claim 789, wherein the fatty acids are selected from the group consisting of C16:0, C16:1, C18:0, C18:1, C18:2 and combinations thereof.

791. The engineered *Y. lipolytica* strain of any one of claims 779-790, wherein the lutein is characterized by a negligible solubility in water and solubility in oil within the range of about <0.001% - 0.2%; 0.004%-0.15%; 0.005-0.1%; or 0.005-0.5%.

792. The engineered *Y. lipolytica* strain of any one of claims 779-791, wherein the GGPP synthase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

793. The engineered *Y. lipolytica* strain of any one of claims 779-792, wherein the truncated HMG CoA reductase polypeptide is a polypeptide from the species *Yarrowia lipolytica*.

794. The engineered *Y. lipolytica* strain of any one of claims 779-793, wherein the phytoene dehydrogenase polypeptide is a polypeptide from an organism of the genus *Mucor*.

795. The engineered *Y. lipolytica* strain of any one of claims 779-793, wherein the phytoene dehydrogenase polypeptide is a polypeptide from the species *Mucor circinelloides*.

796. The engineered *Y. lipolytica* strain of any one of claims 779-795, wherein the phytoene synthase/lycopene cyclase polypeptide is a polypeptide from an organism of the genus *Mucor* or *Neurospora*.

797. The engineered *Y. lipolytica* strain of any one of claims 779-795, wherein the phytoene synthase/lycopene cyclase polypeptide is a polypeptide from the organism *Mucor circinelloides* or *Neurospora crassa*.

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798. The engineered *Y. lipolytica* strain of any one of claims 779-797, wherein the lycopene epsilon cyclase polypeptide is a polypeptide from the species *Ostreococcus lucimarinus*.

799. The engineered *Y. lipolytica* strain of any one of claims 779-799, wherein the carotene epsilon hydroxylase polypeptide is a polypeptide from the species *Ostreococcus tauri*.

800. The engineered *Y. lipolytica* strain of any one of claims 779-799, wherein the carotenoid hydroxylase polypeptide is a polypeptide from an organism of a genus selected from the group consisting of *Erythrobacter, Novosphingobium, Parvularcula, Xanthobacter, Sphingopyxis, Chlamydomonas, Robiginitalea,* and *Pseudomonas*.

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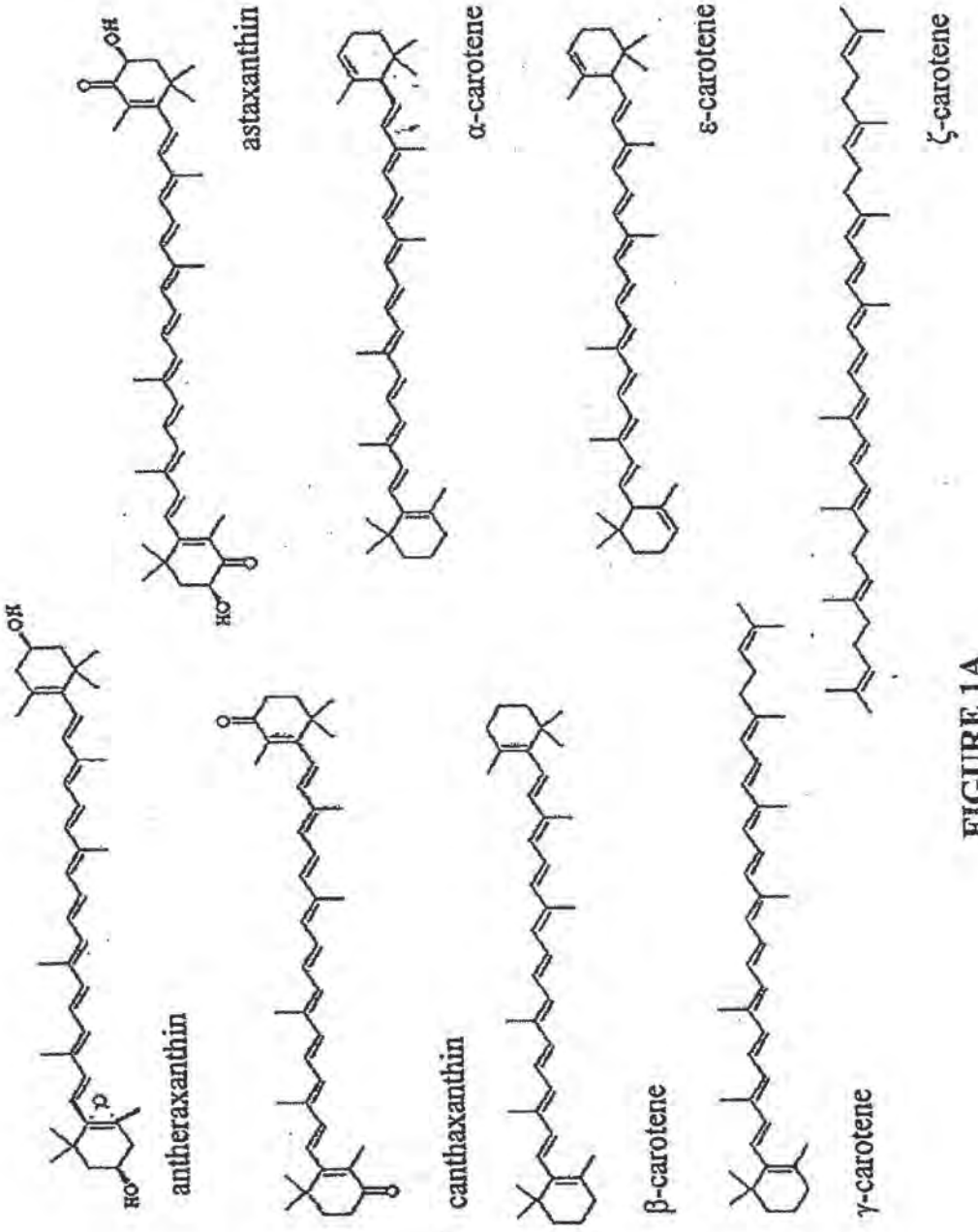


FIGURE 1A

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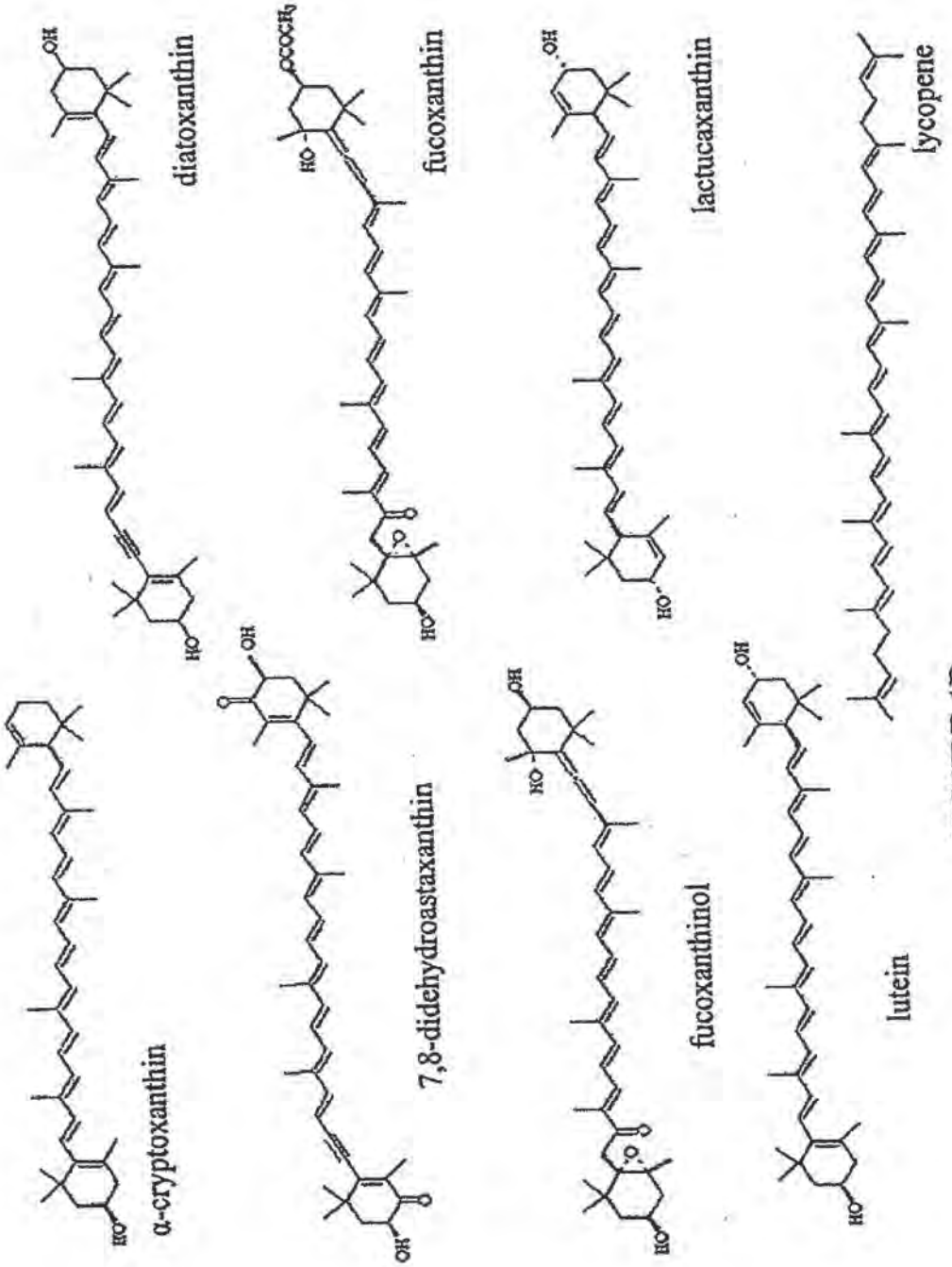


FIGURE 1B

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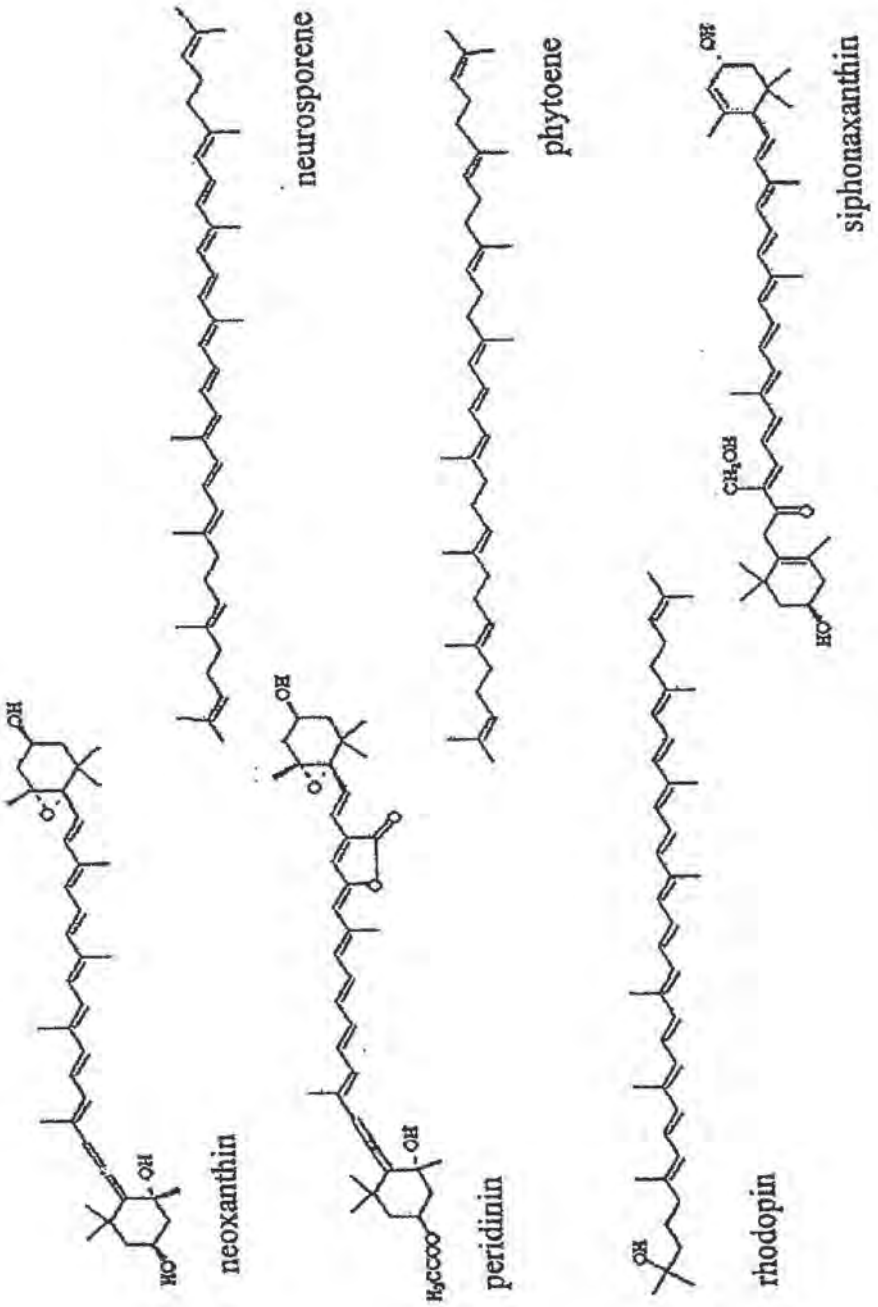


FIGURE 1C

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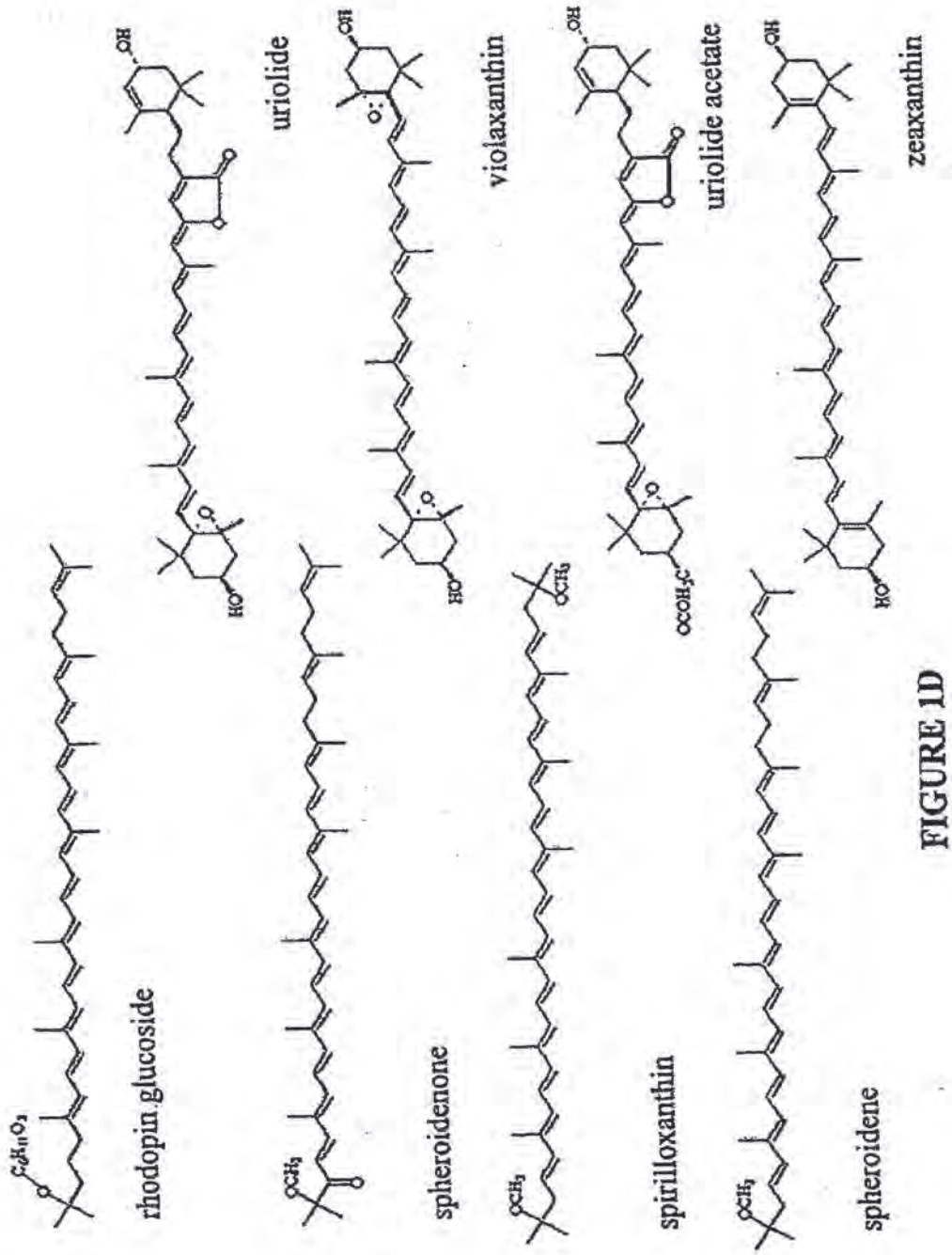


FIGURE 1D

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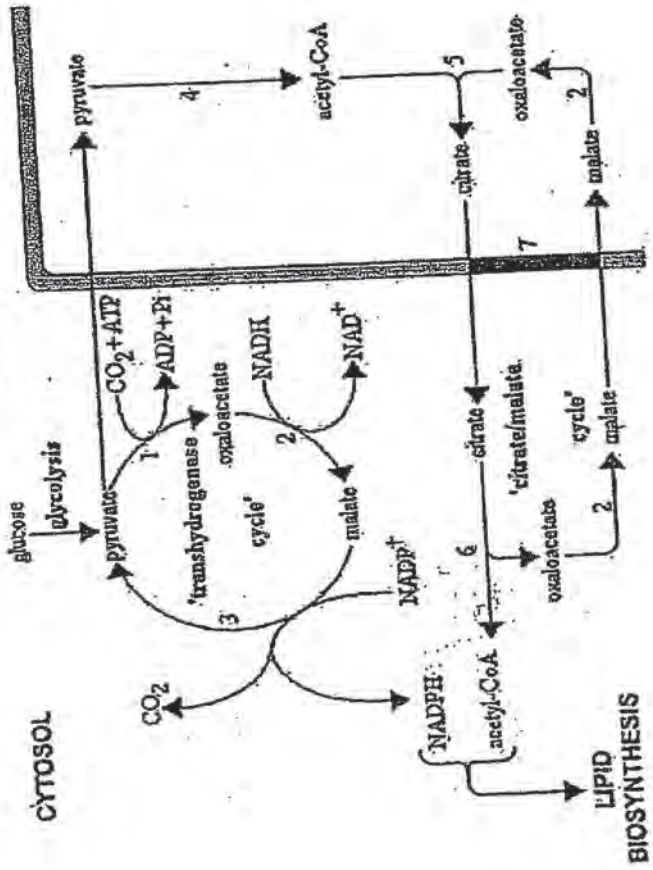
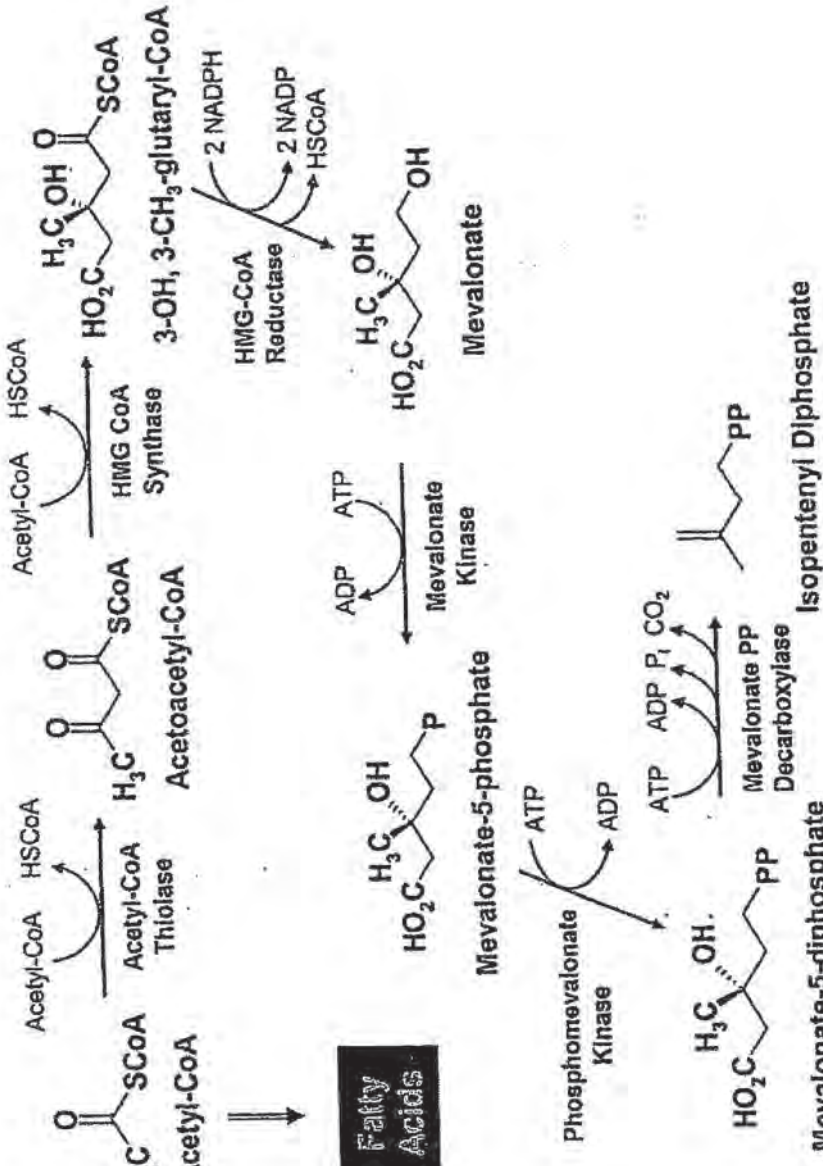


FIGURE 2

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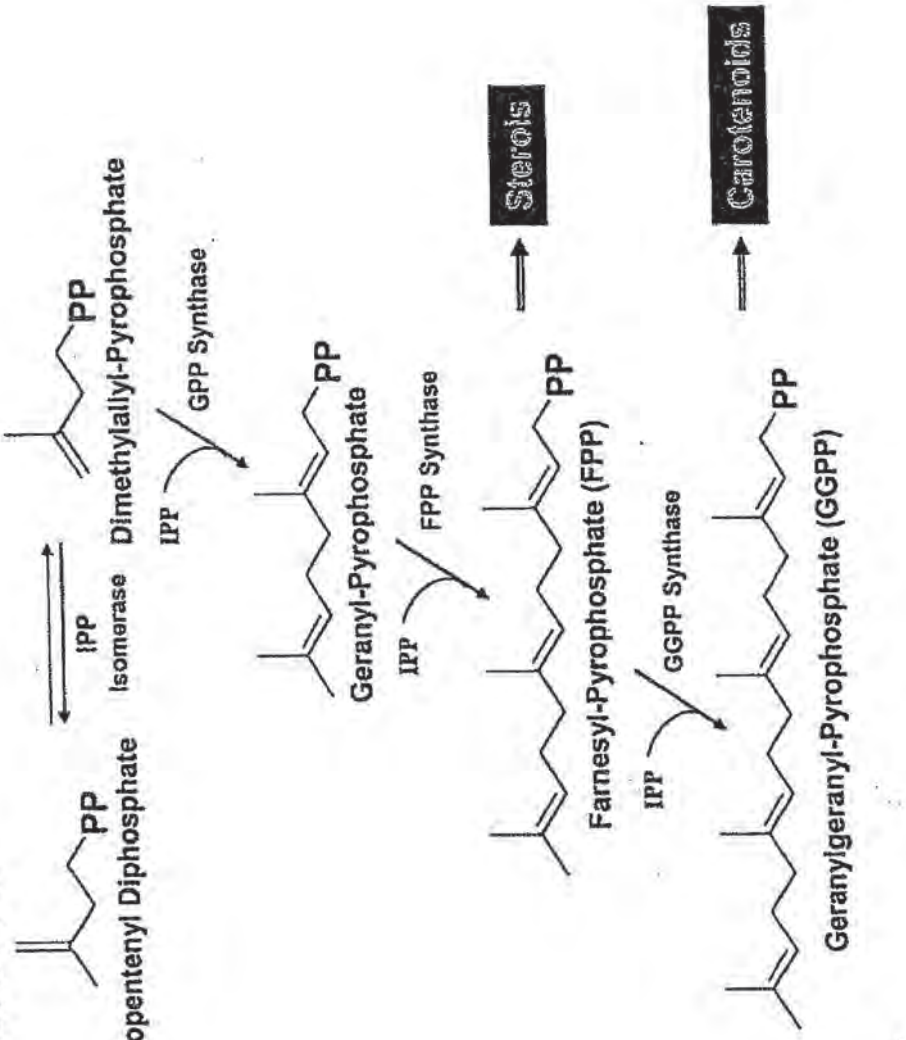
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Fig 3A. Mevalonate Pathway to Isoprenoids



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Fig 3B. Mevalonate Pathway to Isoprenoids



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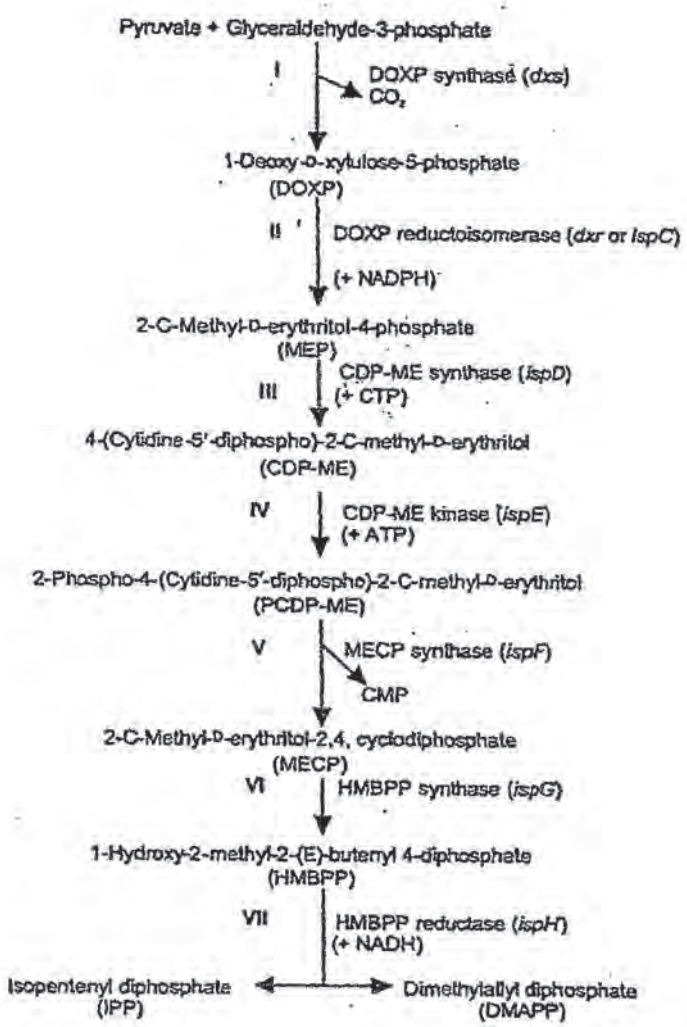


FIGURE 4

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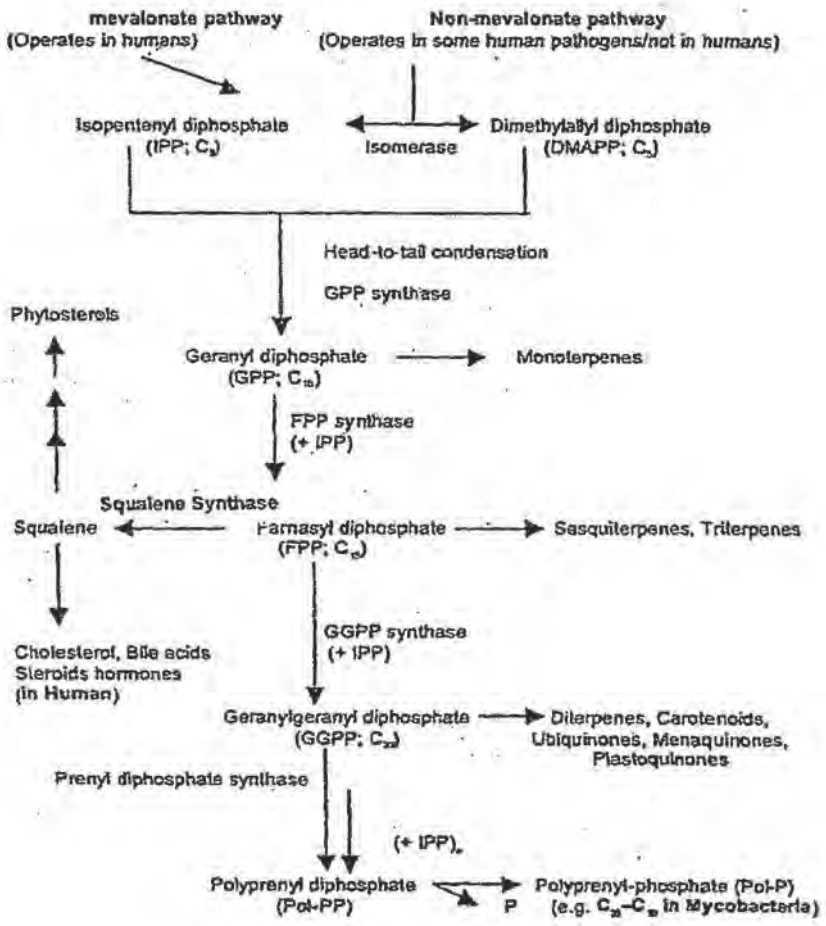


FIGURE 5

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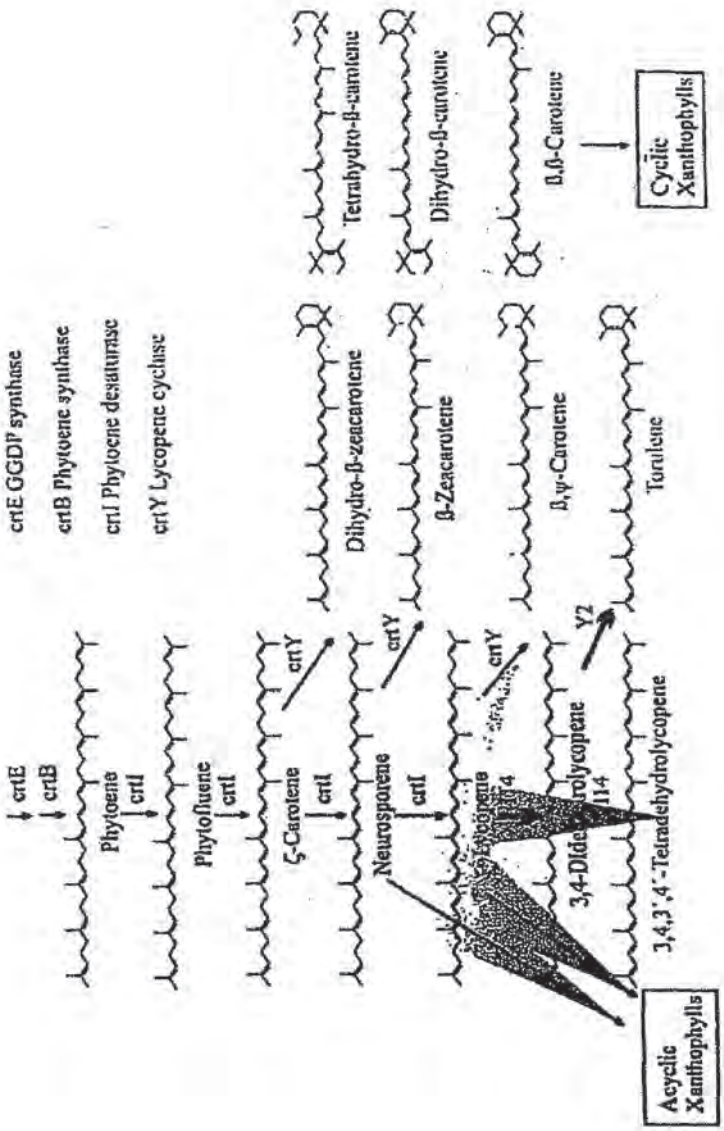


FIGURE 6A

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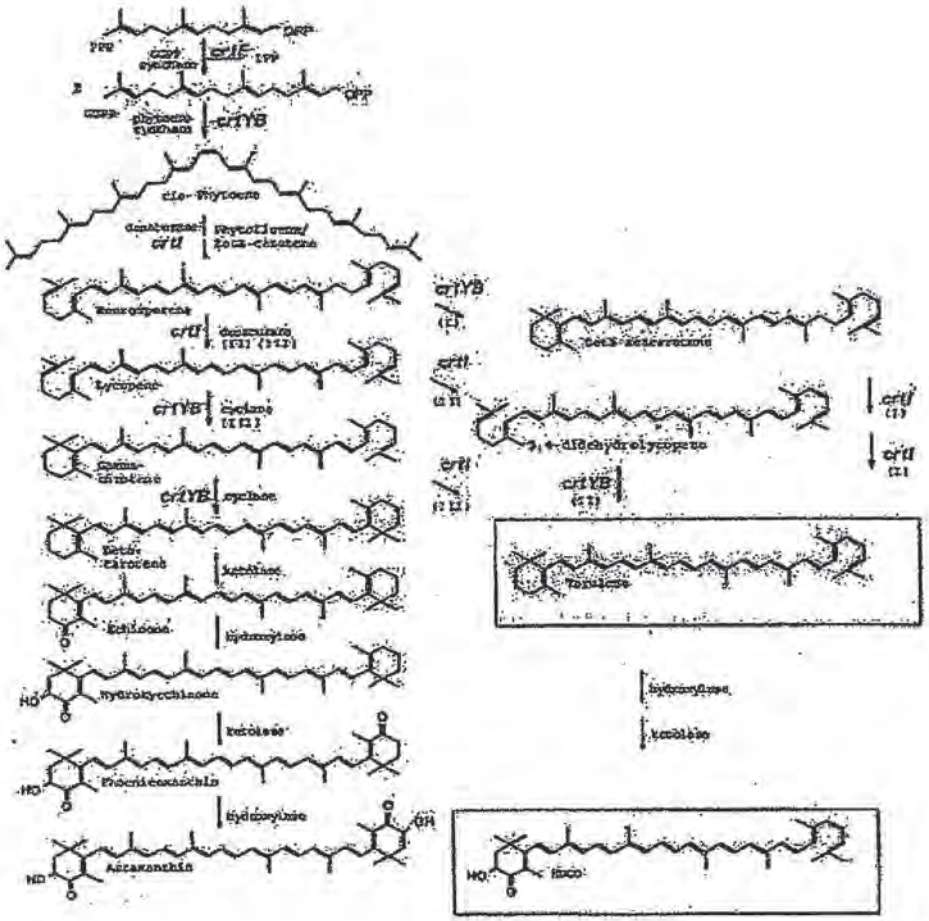


FIGURE 6B

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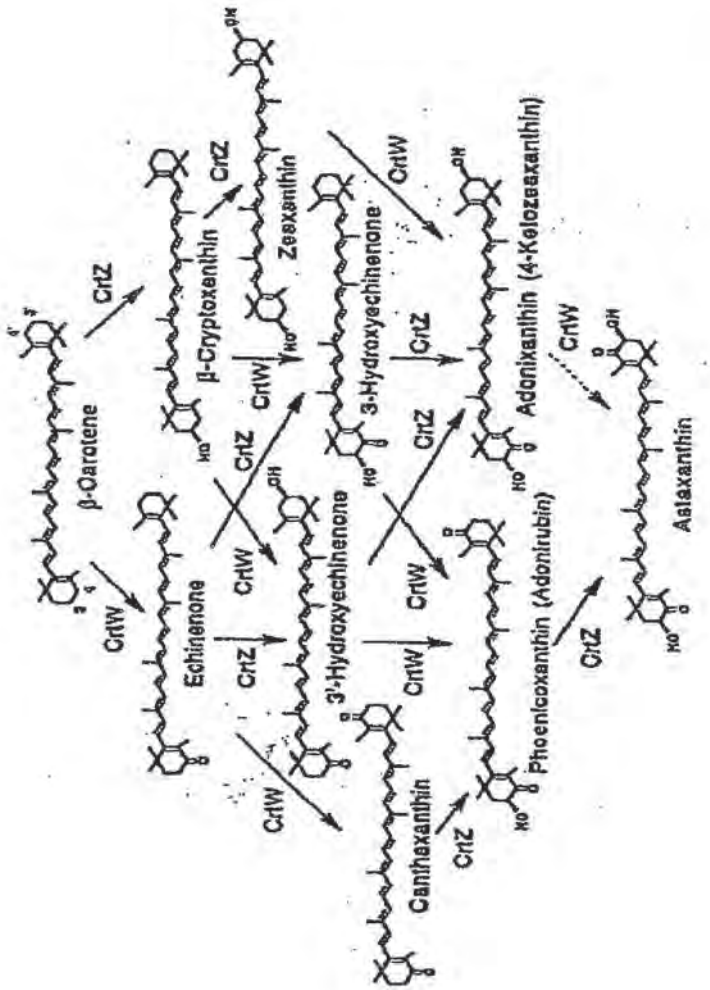


FIGURE 6C

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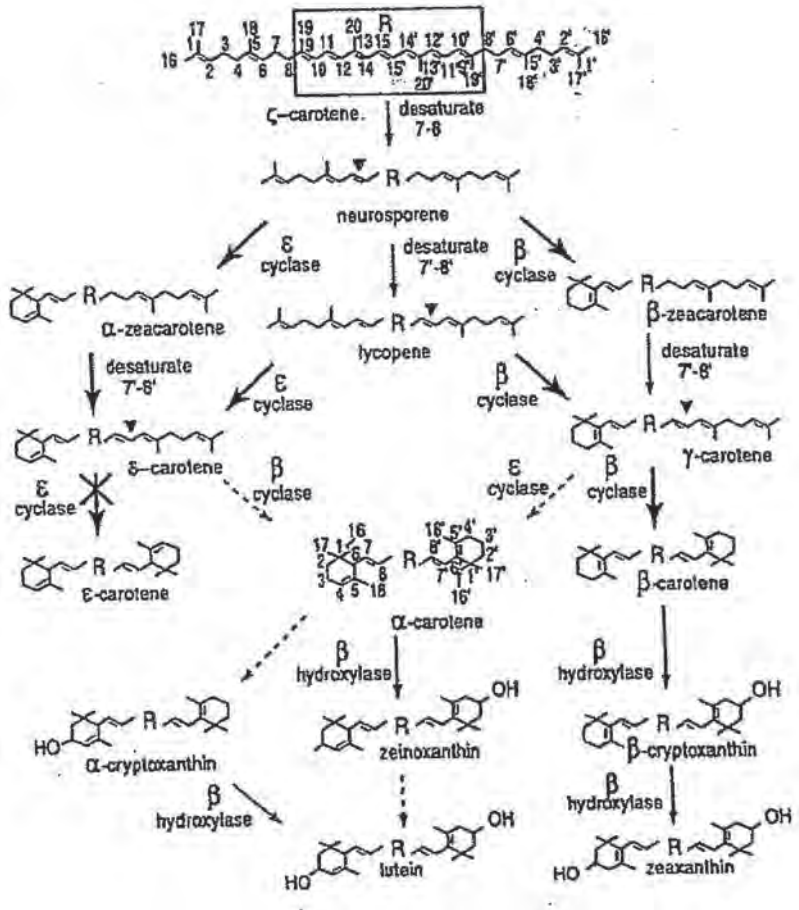


FIGURE 6D

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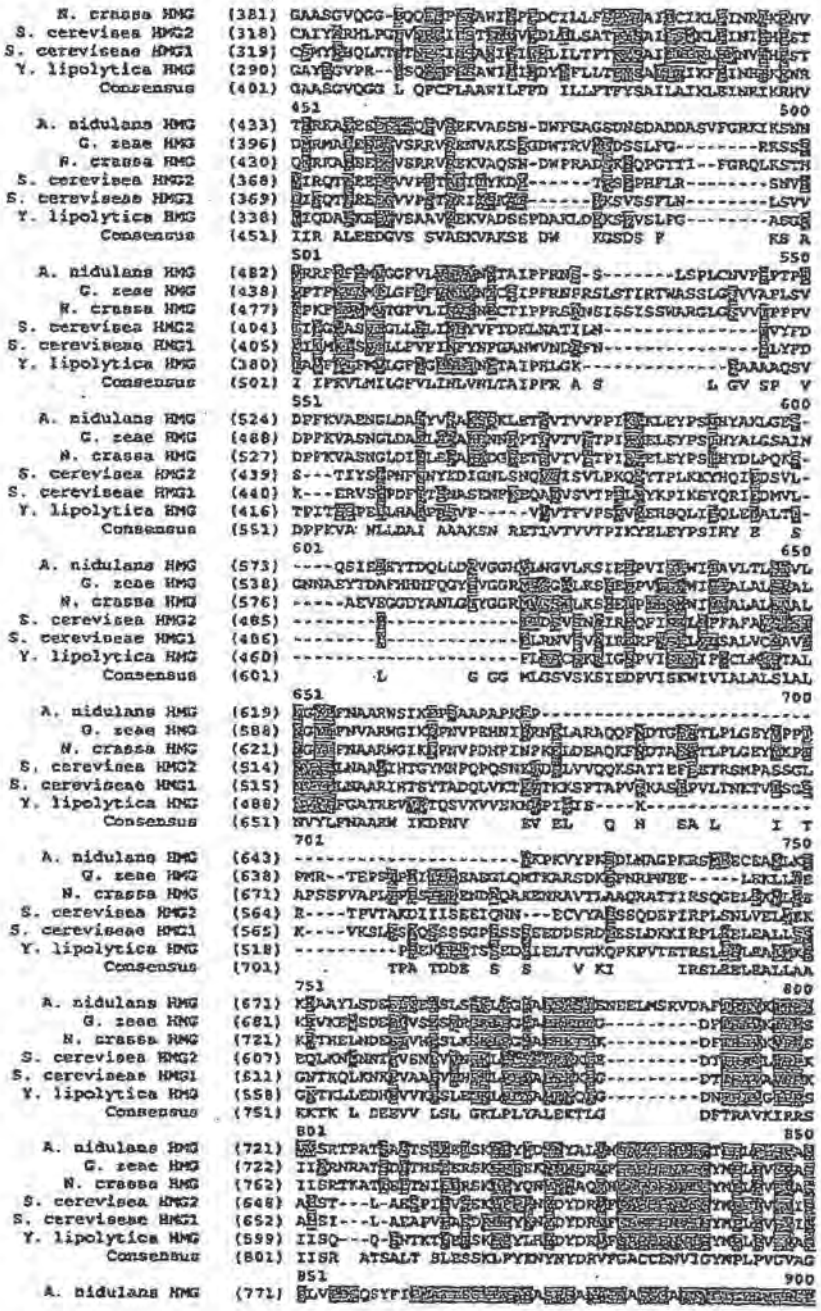
FIGURE 7A

Alignment of representative fungal HMG-CoA reductase polypetides.



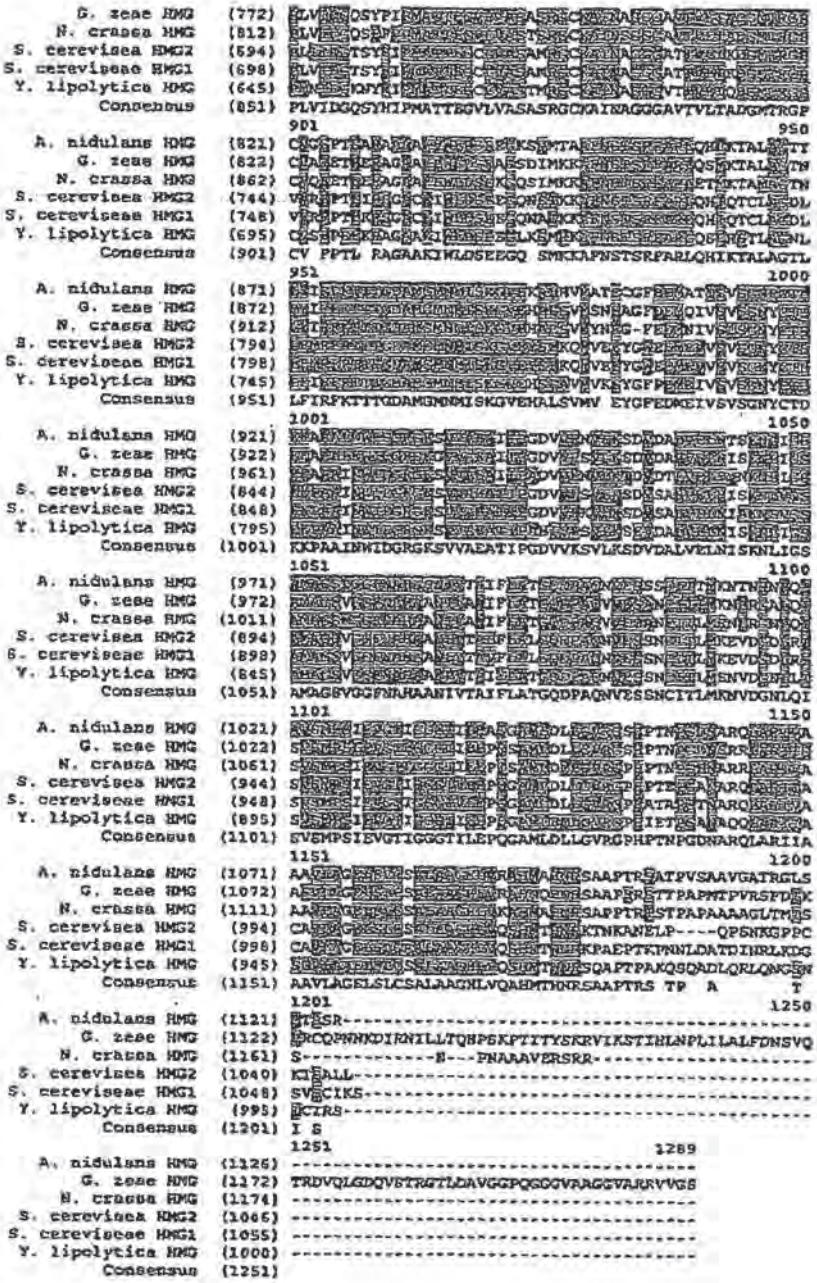
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FIGURE 7B



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FIGURE 7C



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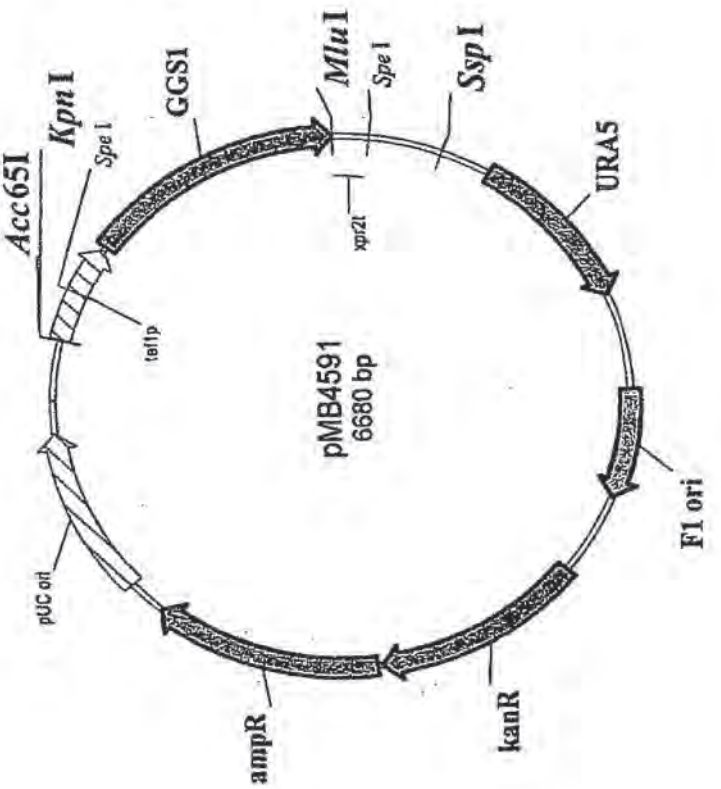


Figure 8A

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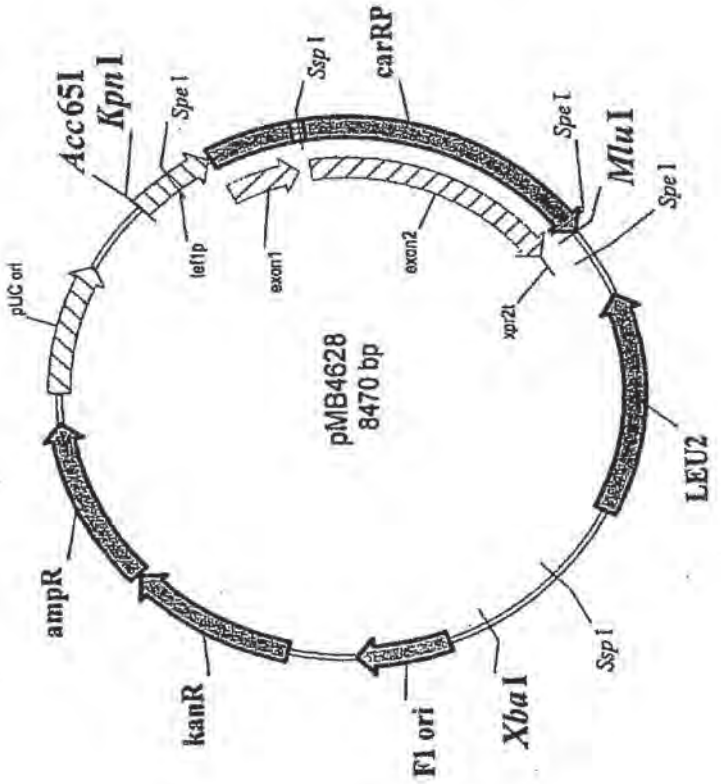


Figure 8B

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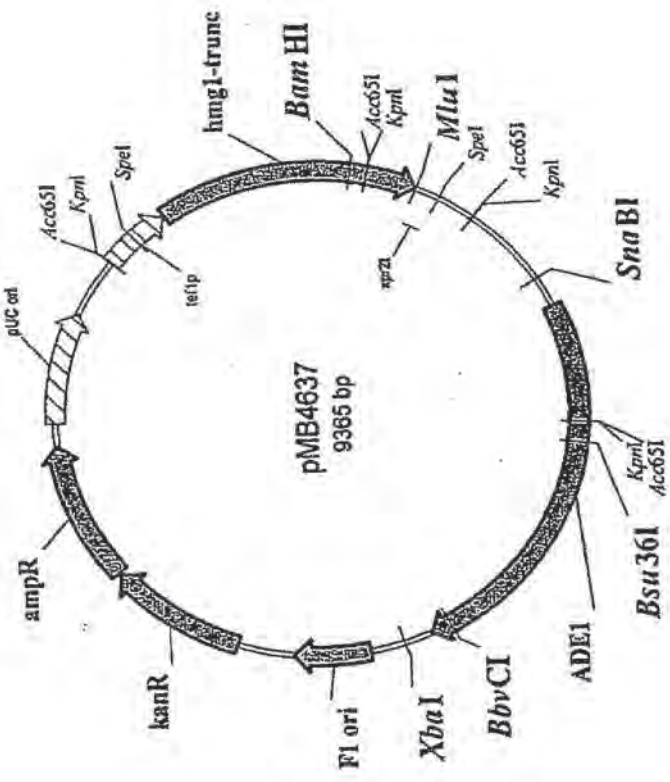


Figure 8C

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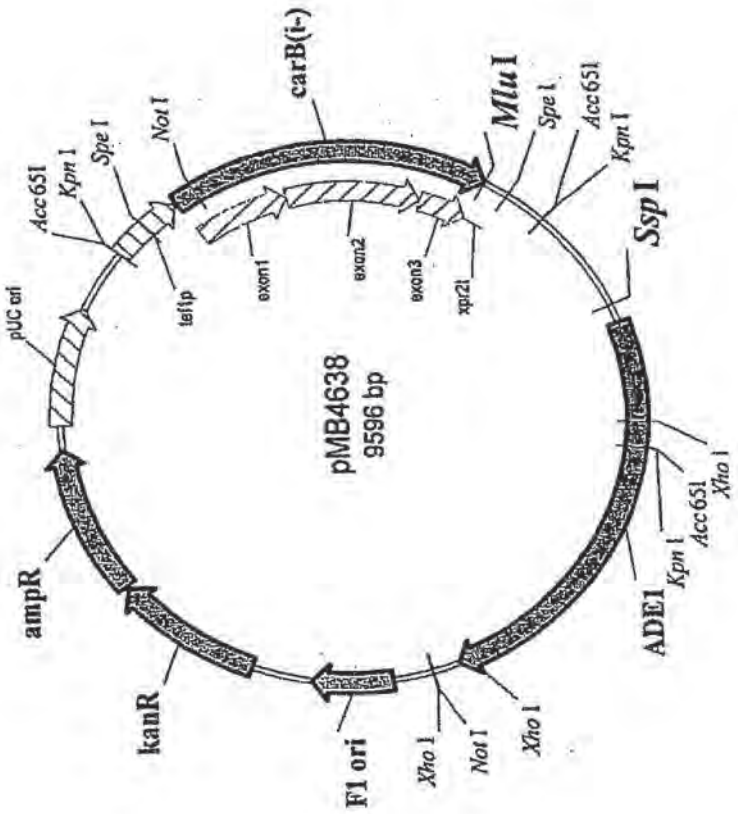


Figure 8D

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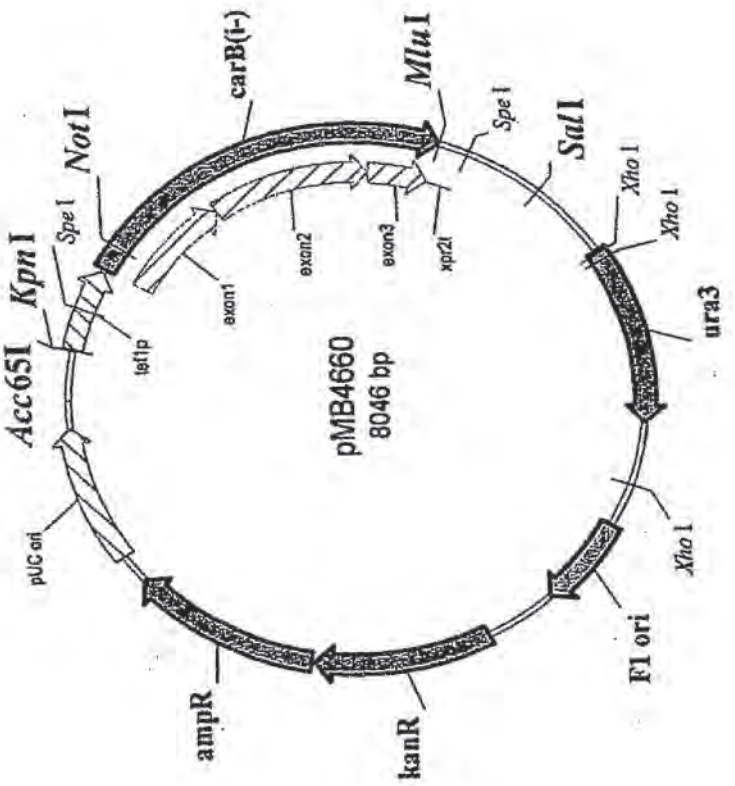


Figure 8E

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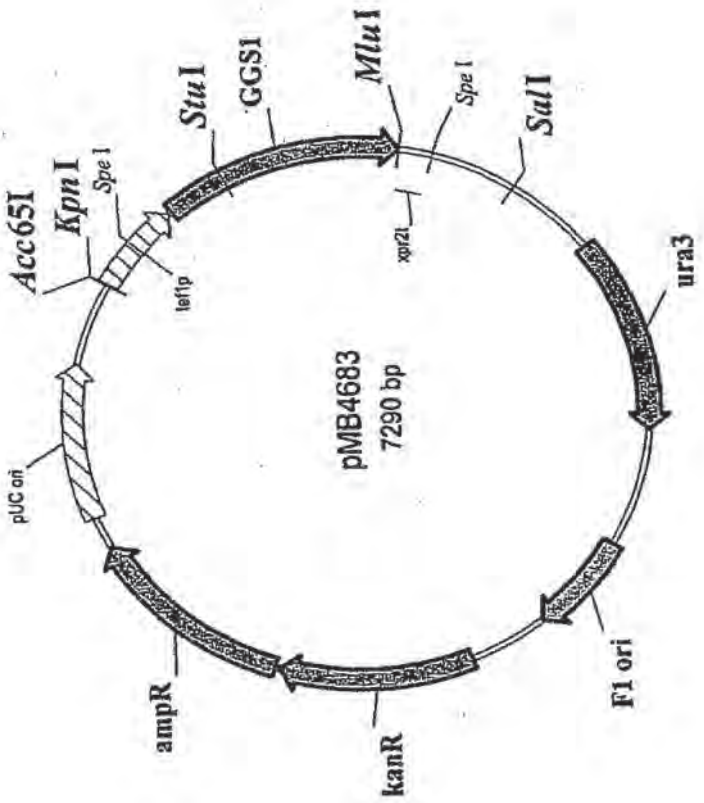


Figure 8F

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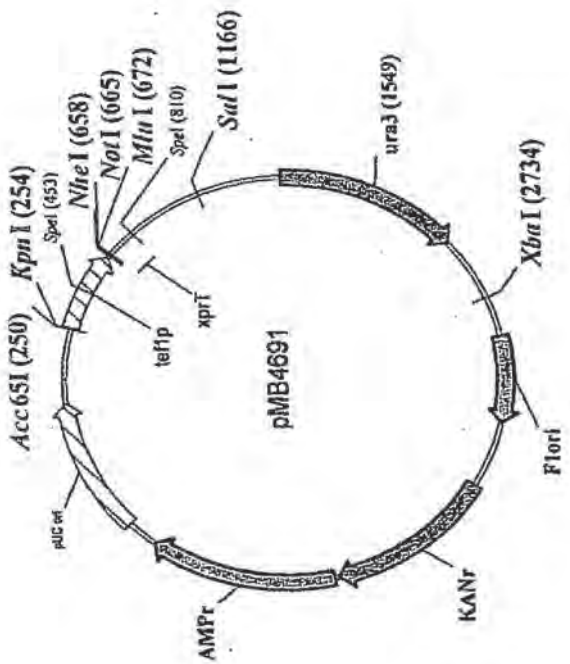


Figure 8G

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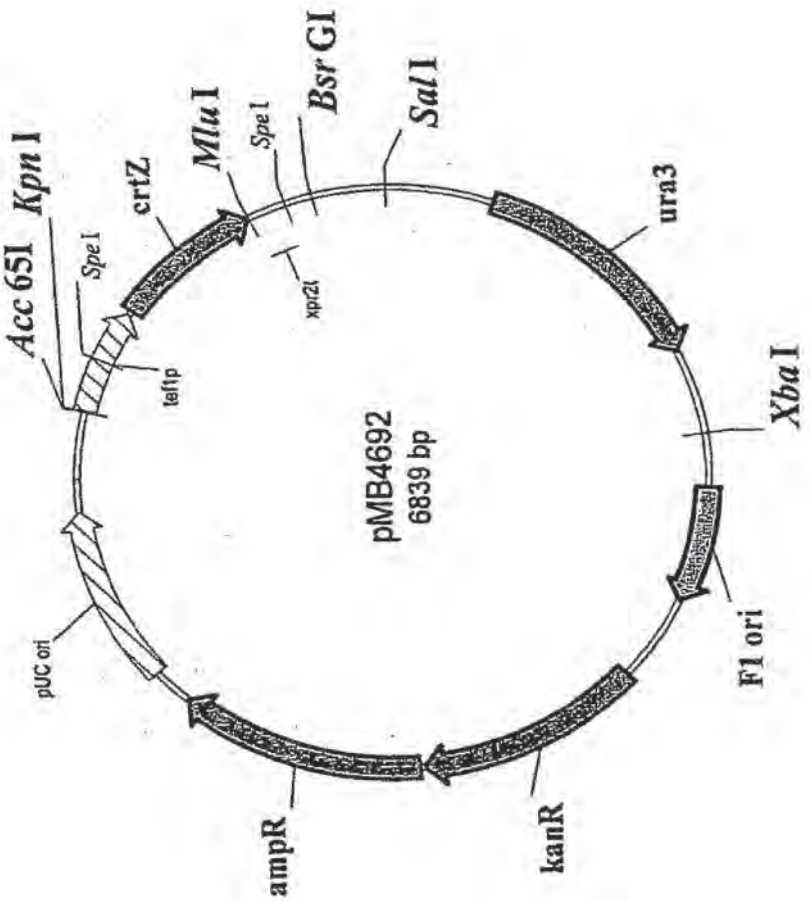


Figure 8H

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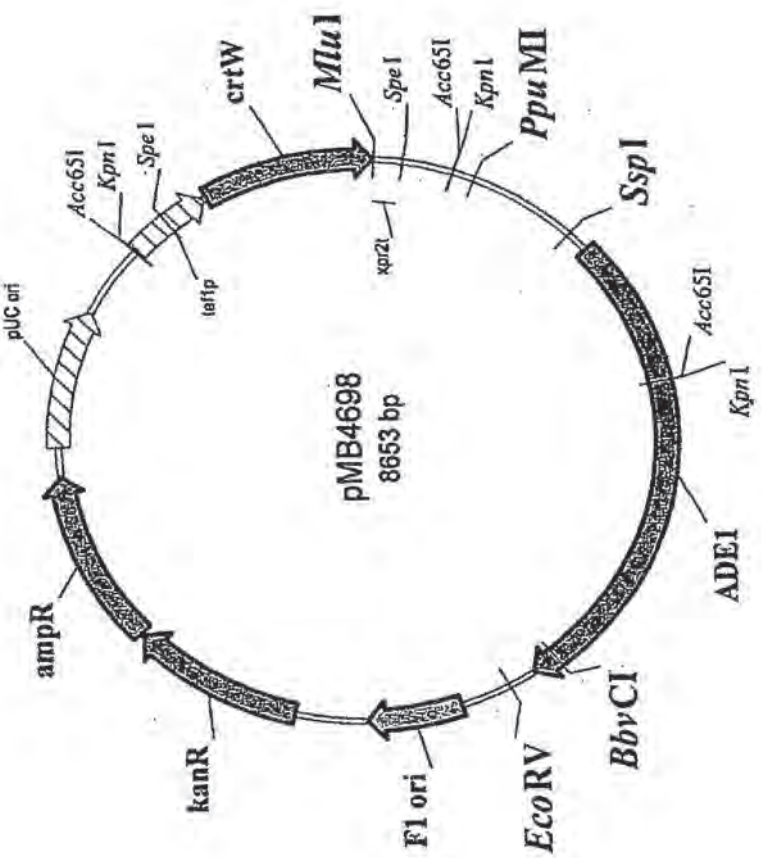


Figure 8I

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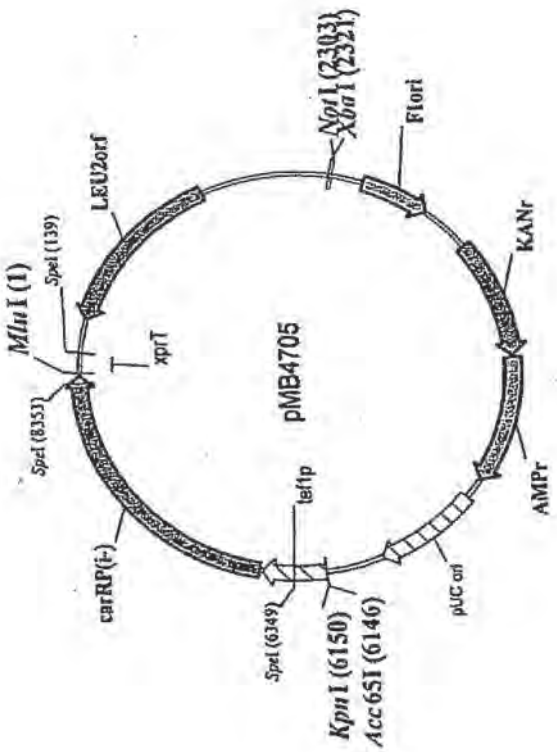


Figure 8J

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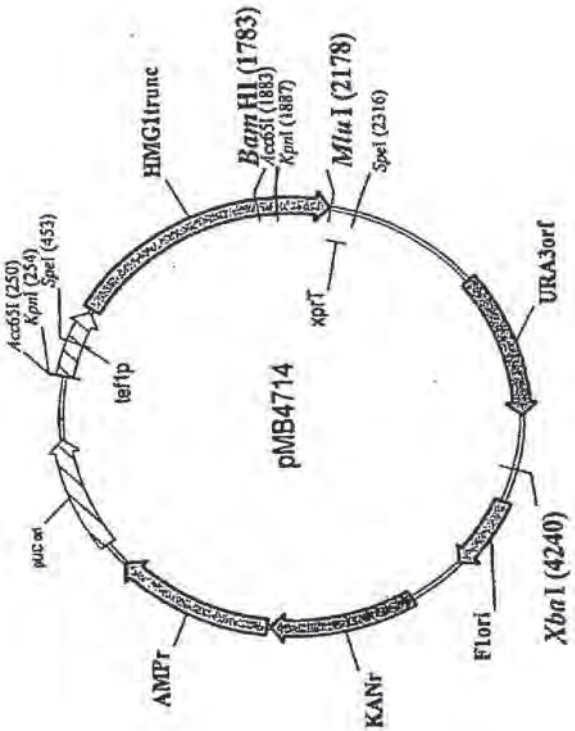


Figure 8K

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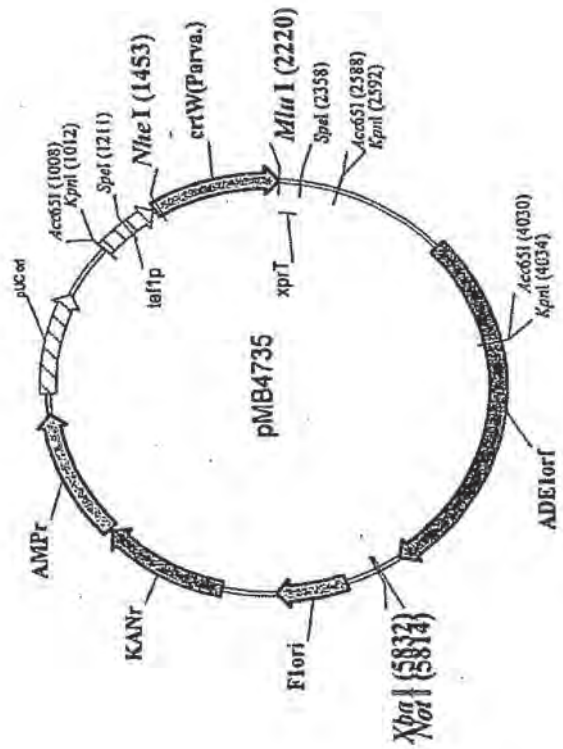


Figure 8L

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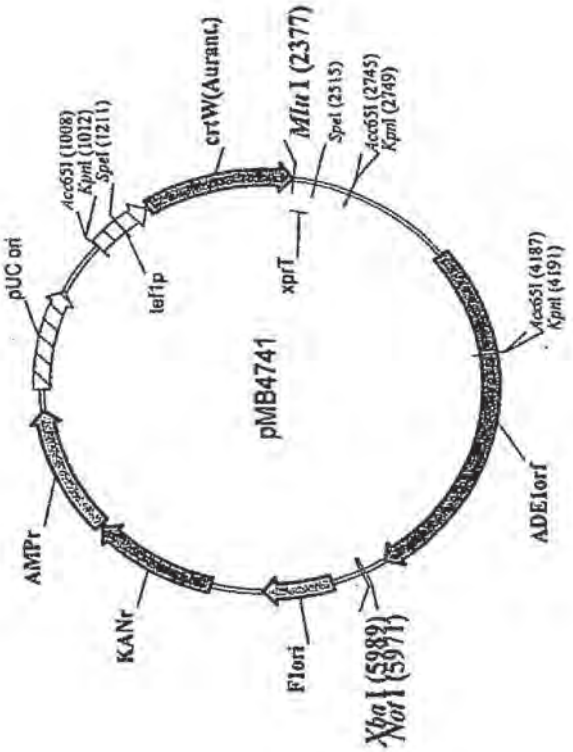


Figure 8M

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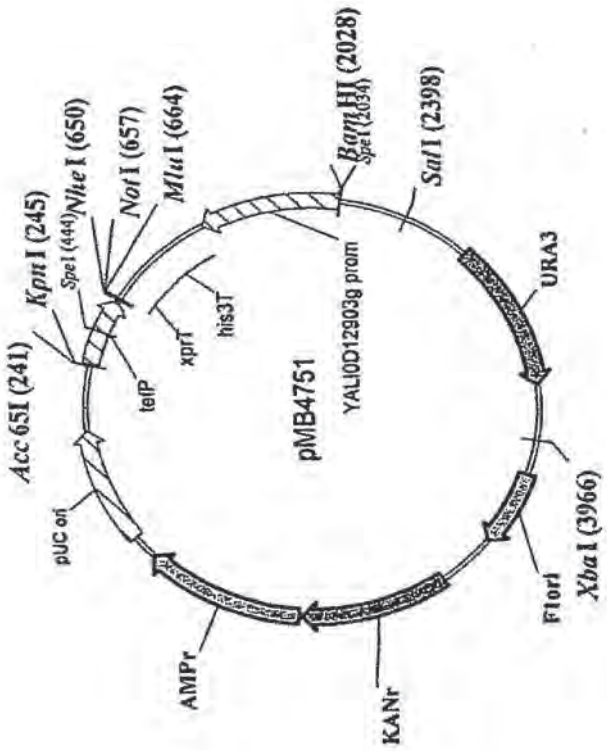


Figure 8N

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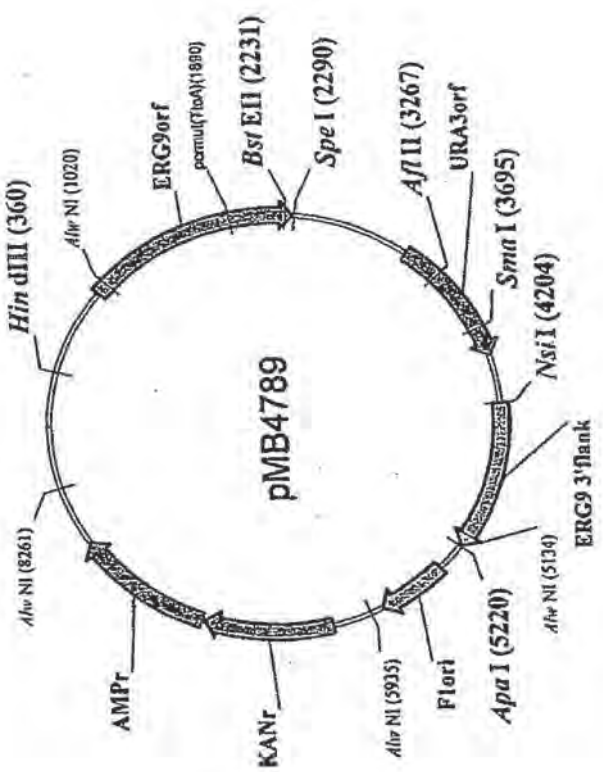


Figure 8O

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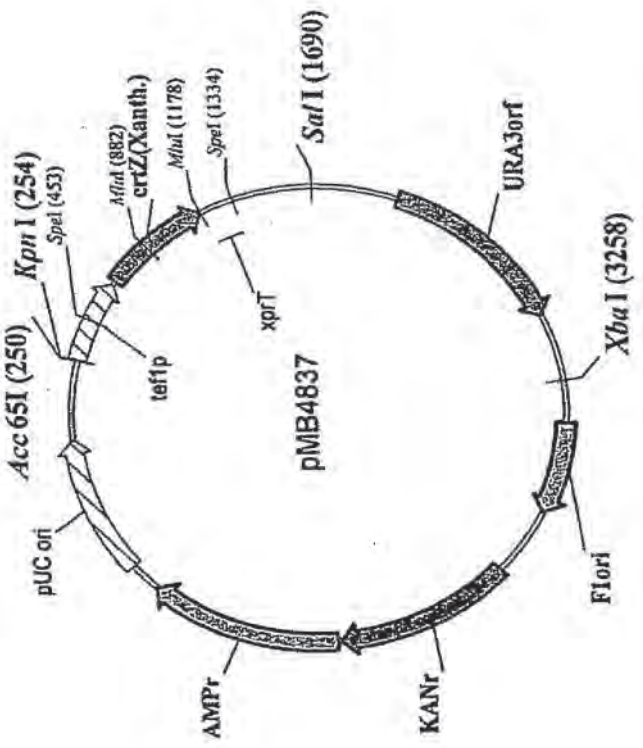
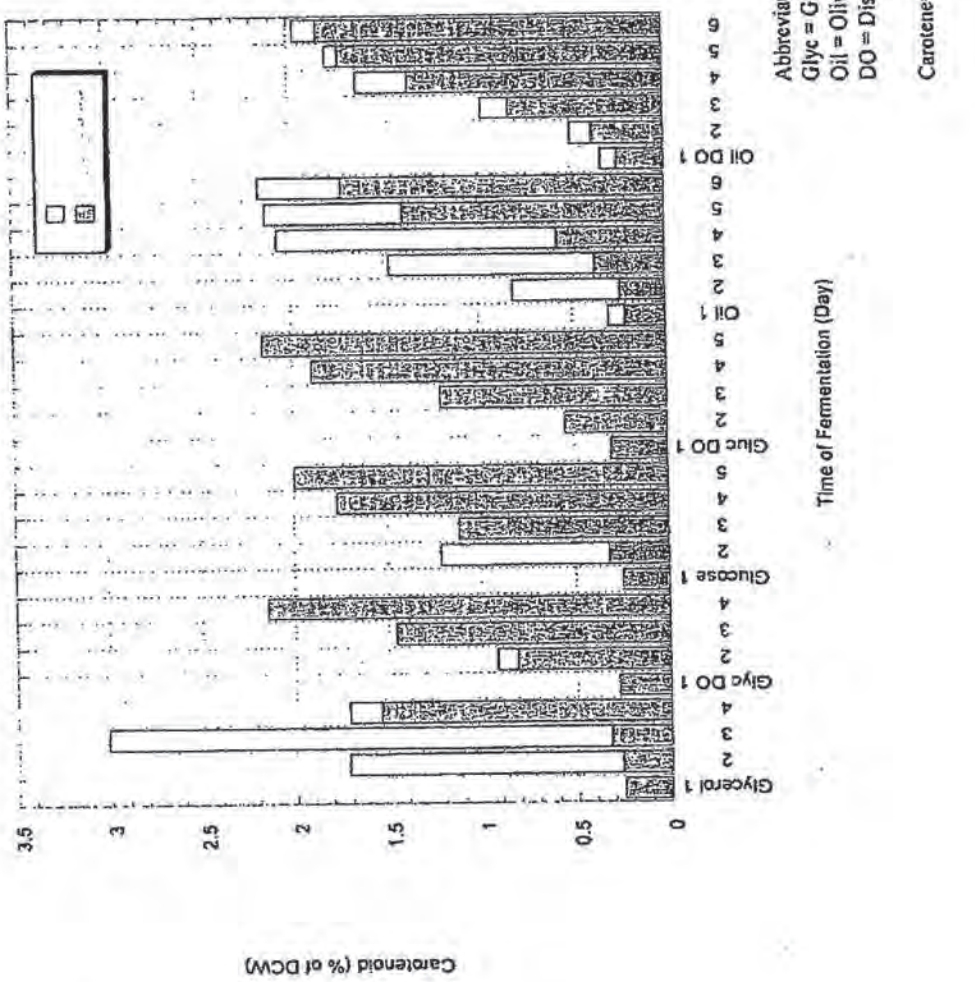


Figure 8P

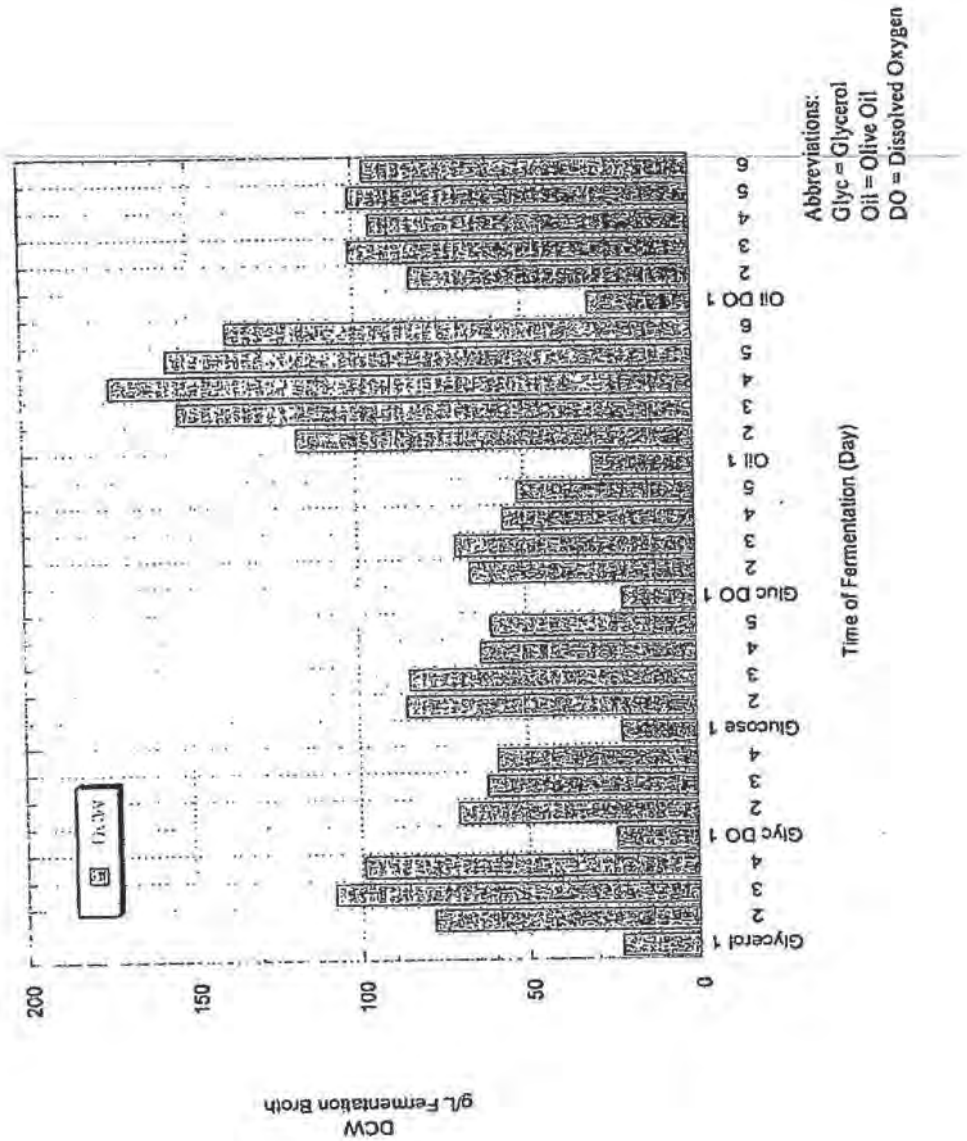
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Figure 9a. β-Carotene and phytoene production of Strain MF760 when grown in glycerol, glucose or olive oil



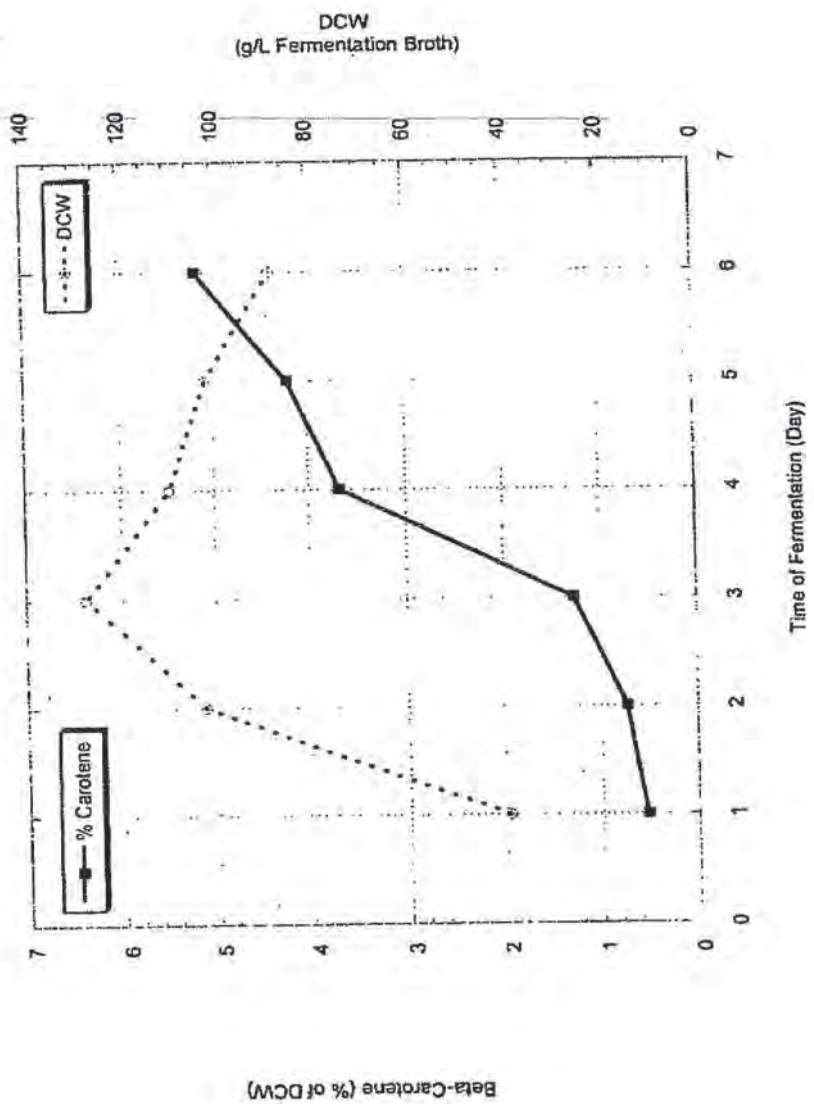
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Figure 9b. Dry cell weight accumulation of strain MF760 when grown in glycerol, glucose or olive oil



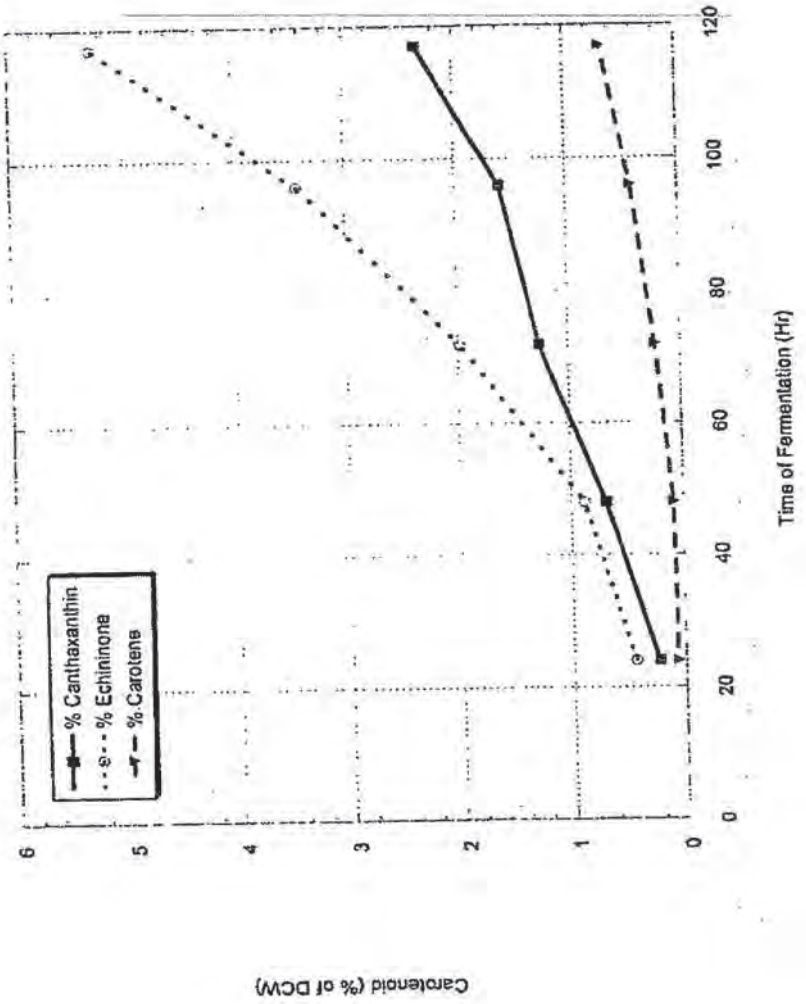
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Figure 9c. β-Carotene and dry cell weight analysis of strain MF760 when grown in the presence of a combination of olive oil and glucose



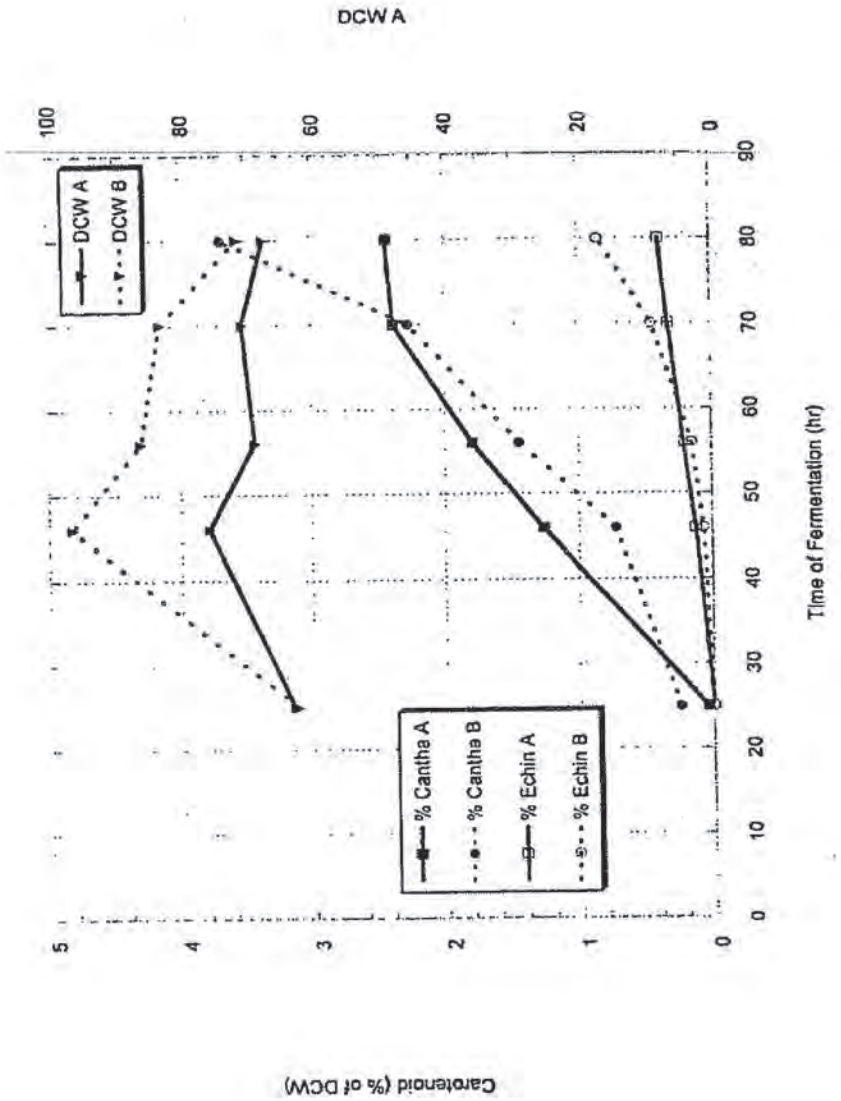
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Figure 9d. Canthaxanthin, echinenone and β-carotene production of strain MF840



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Figure 9e. Canthaxanthin and echinenone production of strain MF838 in a 2 phase feeding protocol



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Figure 10A Y. *Lipolytica* Genes (1 of 3)

Genbank protein GI number	Genbank protein Accession Number	polypeptide	Y. lipolytica gene	Oligo 1	Oligo 2
50557288	XP_506052	HMG-CoA synthase	YALI0F30481g	MO4890-5'ctctagacacaaaaatgtcgcaaccccagaacgt	MO4891-5'cacgcgtctactgcttgatctcgtact
50546973	XP_500956	Mevalonate Kinase	YALI0B16038g	MO4982-5'cgctagcccacaaaaatggactacatcatttcggcgc	MO4983-5'cacgcgtctaatgggtccagggaccga
50552418	XP_503619	Phosphomevalonate kinase	YALI0E06193g	MO4984-5'ctctagacacaaaaatgaccacctattcggctccg	MO4985-5'cggcgcgccctactgaacccttctcga
50555265	XP_505041	Mevalonate Pyrophosphate Decarboxylase	YALI0F05632g	MO4986-5'ctctagacacaaaaatgatcccaccaggccctccacca	MO4987-5'cacgcgtctactgctgttcttcagag
50555131	XP_504974	IPP Isomerase	YALI0F04015g	MO4988-5'ctctagacacaaaaatgacgacgtcttacagcga	MO4989-5'cacgcgtctacttgatccacccgccgaa
50552378	XP_503599	FPP synthase	YALI0E05753	MO4990-5'ctctagacacaaaaatgtccaaggcgaaattcgaa	MO4991-5'cacgcgtctacttctgtcgcttgtaaa
50553402	XP_504112	Malic Enzyme	YALI0E18634g	MO4992-5'ctctagacacaaaaatgttacgactacgaaccat	MO4993-5'cacgcgtctagtcgtaatcccgcacat

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Figure 10B Y. Lipolytica Genes (2 of 3)

50552824	XP_503822	AMP Deaminase	YALI0E11495g	MO4996- 5'cgctagccacaaaaatgccgcagcaagcaatgga	MO4997- 5'cacgcgttaaccatgcagccgctcaa
50550873	XP_502909	Malate Dehydrogenase Homolog	YALI0D16753g	MO5000- 5'ctctagacacaaaaatgttccgaacccgagttac	MO5001- 5'cacgcgttaagggttcgctgctgacaa
50550839	XP_502892	Isocitrate Dehydrogenase	YALI0D16247g	MO5004- 5'ctctagacacaaaaatgacacaaacgcacaatct	MO5005- 5'cacgcgttacatcttgtacgcagggt
50545147	XP_500111	Fructose 1,6 bisphosphatase	YALI0A15972g	MO5008- 5'ctctagacacaaaaatgaagccaaccccgaagt	MO5009- 5'cacgcgttcatttcagaaggtacttct
50552796	XP_503808	Acetoacetyl CoA thiolase	YALI0E11099g	MO4852- 5'ctctagacacaaaaatgcgactcactctgccc	MO4853- 5'cacgcgtctactcgacagaagagaccttc
50554757	XP_504787	ATP citrate lyase subunit 1	YALI0E34793g	MO4741- 5'ttctagacccaaaaatgtctgccaacgagaacatct c	MO4743- 5'aacgcgtctatgatcgagtcttggccttg
50551515	XP_503231	ATP citrate lyase subunit 2	YALI0D24431g	MO4760- 5'ttctagacacaaaaatgtcagcgaaatccattcacg a	MO4861- 5'cacgcgttaaactccgagaggagtgg
50553046	XP_503933	Malate Dehydrogenase	YALI0E14190g	MO4994- 5'ctctagacacaaaagtggttaagctgtcgttgc	MO4995- 5'cacgcgtttactttggcaggaggaggt

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Figure 10. *Y. Lipolytica* Genes (3 of 3)

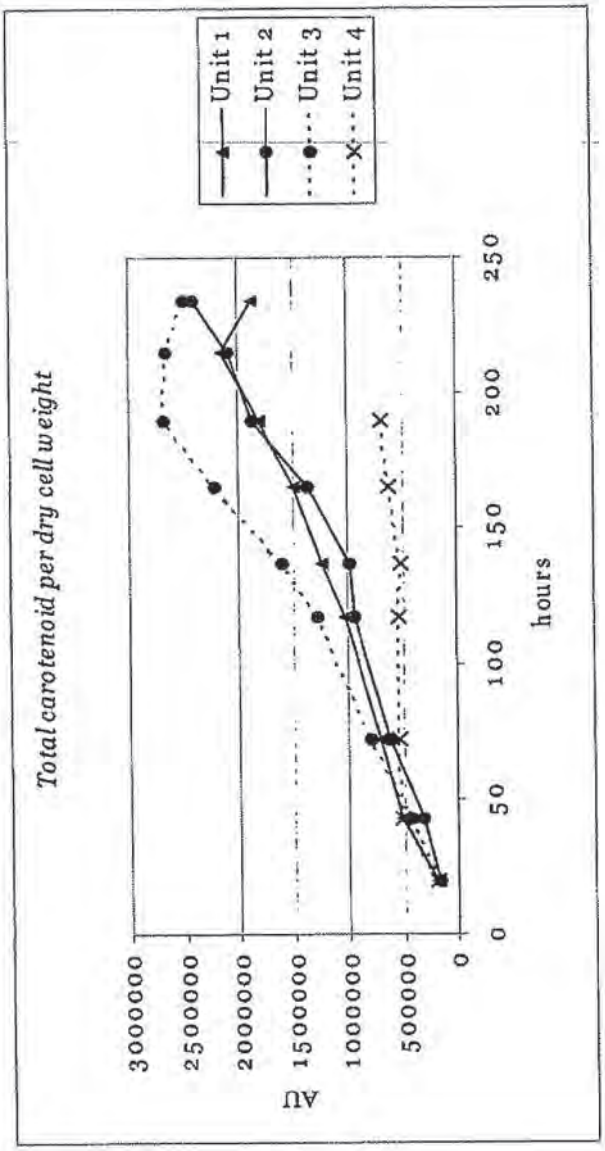
50553728	XP_504275	Glucose 6 Phosphate Dehydrogenase	YALI0E22649g	MO4998- 5'ctctagacacaaaaatgactggcaccttaccaa	MO4999- 5'cacgcgttcacgaggagccccttggtga
50546937	XP_500938	6-phosphogluconate dehydrogenase	YALI0B15598g	MO5002- 5'ctctagacacaaaaatgactgacacttcaaacat	MO5003- 5'cacgcgttaagcatcgtaagtggaag
50550013	XP_502479	Isocitrate dehydrogenase	YALI0D06303g	MO5006- 5'ctctagacacaaaaatgctcaaccttagaaccgc	MO5007- 5'cacgcgtctacttgagtcgcttgataa

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Figure 11

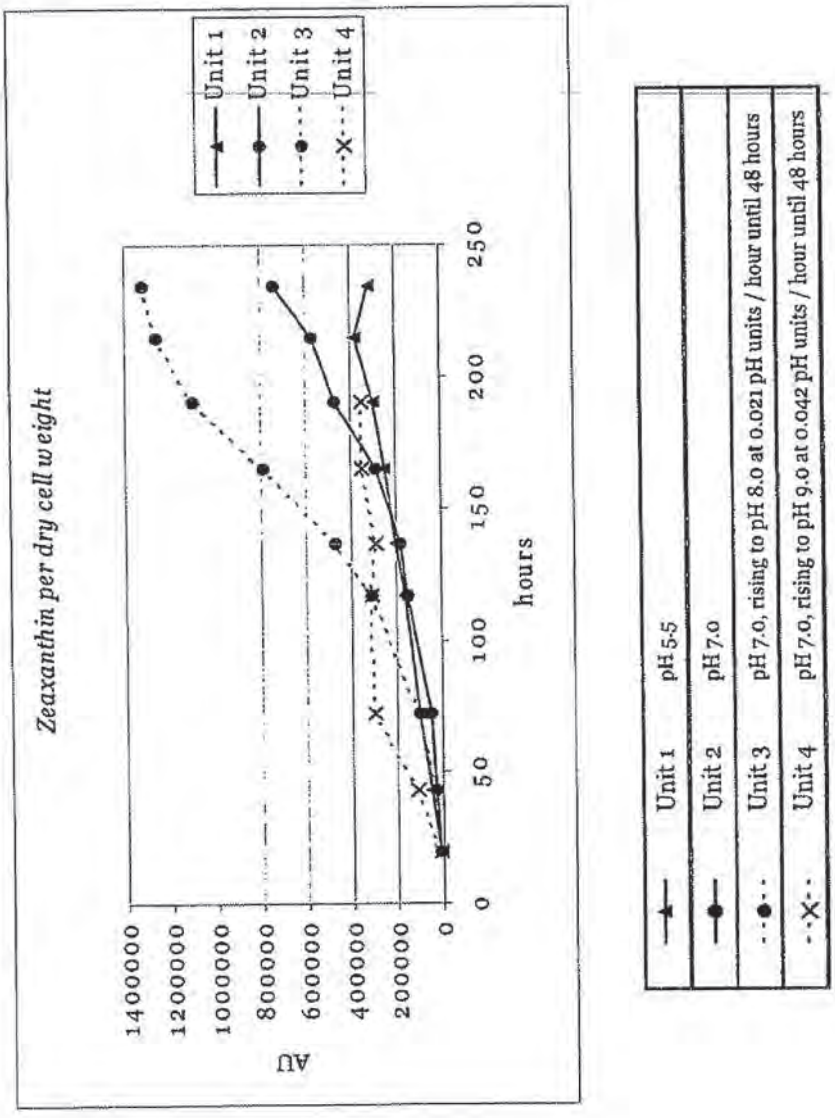
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Figure 12a. Total carotenoid accumulation in ML1011 grown under varying pH conditions



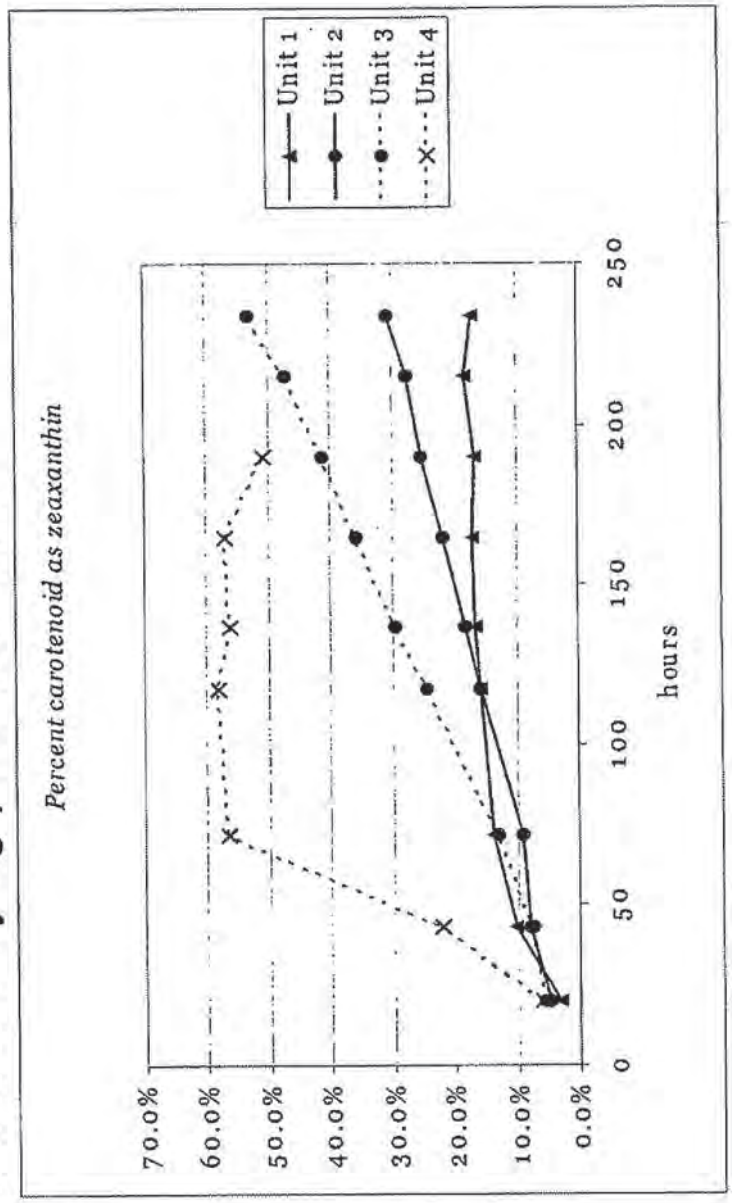
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Figure 12b. Zeaxanthin accumulation in ML1011 grown under varying pH conditions



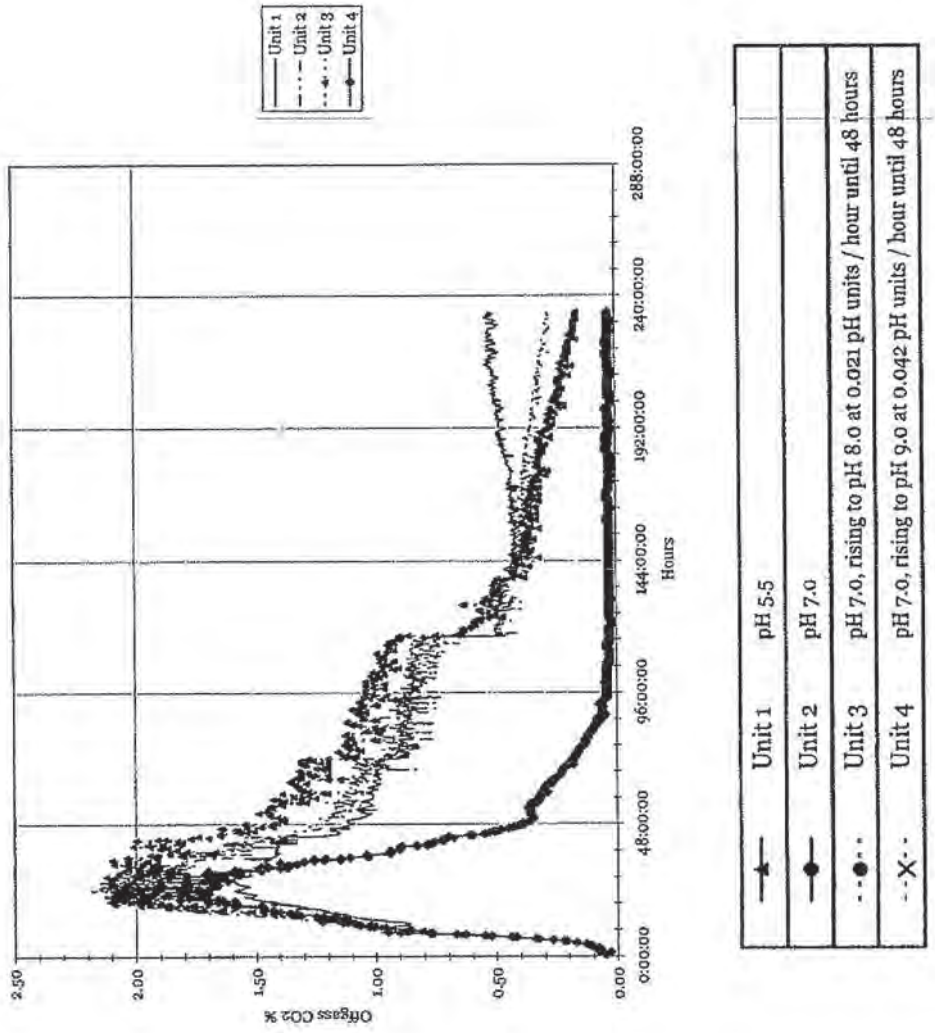
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Figure 12c. Fraction of carotenoid as zeaxanthin in ML1011 grown under varying pH conditions



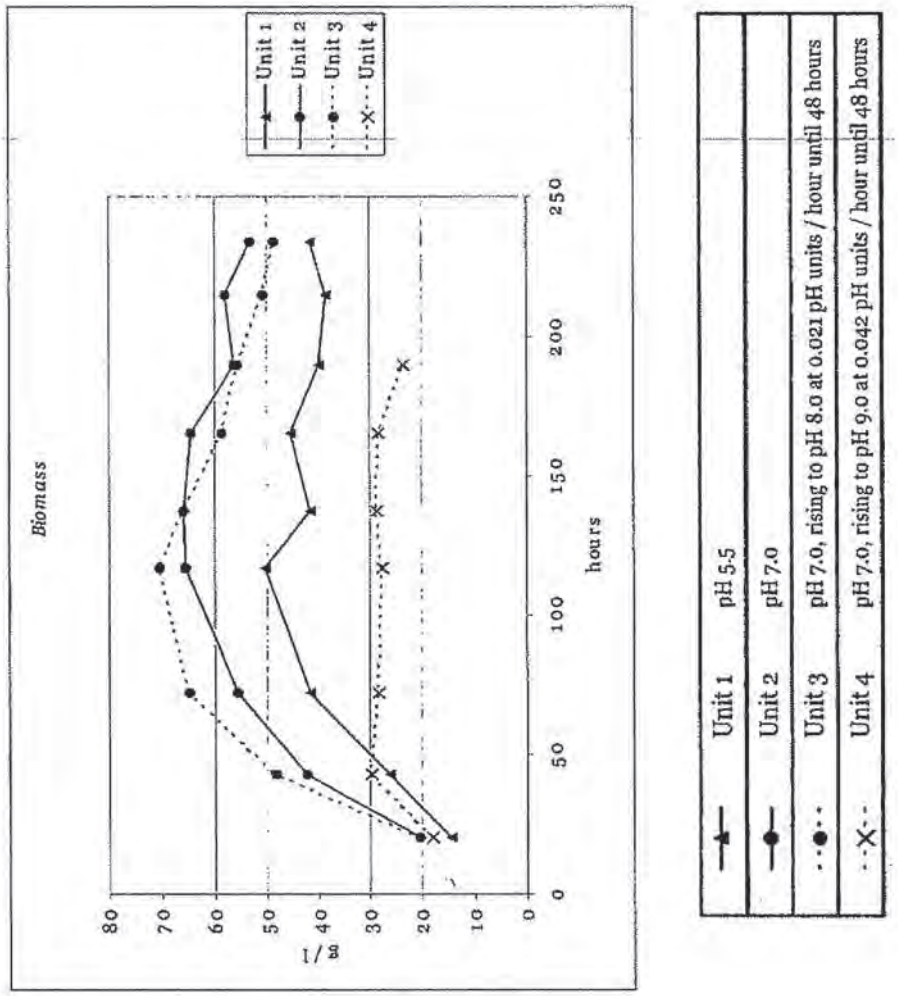
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Figure 12d. Carbon dioxide evolution of ML1011 grown under varying pH conditions



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Figure 12e. Biomass accumulation in ML1011 grown under varying pH conditions



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