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BLAST[®] >> **Global Alignment** >> results for RID-THTJHT47114

Job Title	DiNunno_Eprotein...
RID	THTJHT47114 Search expires on 12-15 03:53 am
Program	Needleman-Wunsch alignment of two sequences
Query ID	lcl Query_33461 (amino acid)
Query Descr	DiNunno_Eprotein...
Query Length	500

Subject ID

lcl|Query_33463 (amino acid)

Subject Descr

[SEQ_ID_NO73...](#)

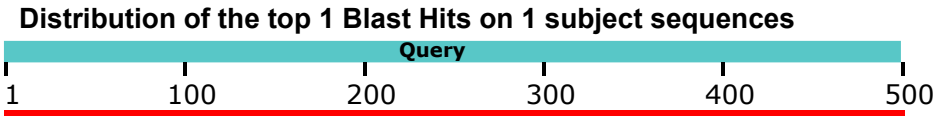
Subject Length

3423

Descriptions

Description	Score	Percent Ident	Accession
SEQ_ID_NO73	-3284.0	14.00%	Query_33463

Graphic Summary



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SEQ_ID_NO73

Sequence ID: Query_33463 Length: 3423 Number of Matches: 1

Range 1: 1 to 3423

NW Score	Identities	Positives	Gaps	Frame
-3284	486/3423(14%)	494/3423(14%)	4/3423(0%)	
Sbjct 1	MKNPKKKSGGFRIVNMLKRGVARVSPFGGLKRLPAGLLLGHGPIRMVLAILAFLRFTAIK			60
Sbjct 61	PSLGLINRWGSVGKKEAMEIICKFKKDLAAMLRIINARKEKKRRGADTSVGIVGLLLTTA			120
Sbjct 121	MAAEVTRRGSAYMYLDRNDAGEAISFP TTLGMNKC YIQIMDLGHMCDATMSYEC PMLDE			180
Sbjct 181	GVEPDDVDCWNTTSTWVVYGTCHHKKGAEARRSRAVTLPSHSTRKLQTRSQTWLESREY			240
Query 1			IRCIGVSNRD IRCIGVSNRD	10
Sbjct 241	TKHLIRVENWIFRNPGFALAAAAIAWLLGSSTSQKVIYLVMIILLIAPAYSIRCIGVSNRD			300
Query 11	FVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMAS			70
Sbjct 301	FVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMAS			360
Query 71	DSRCPTQGEAYLDKQSDTQYVCKRTLVDRGWGNCGLFGKGS LVTCAKFTCSKKMTGKSI			130
Sbjct 361	DSRCPTQGEAYLDKQSDTQYVCKRTLVDRGWGNCGLFGKGS LVTCAK FCSKKMTGKSI			420
Query 131	QPENLEYRIMLSVHGSQHSGMI - - - -GYETDEDRAKVEVTPNSPRAEATLGGFGSLGLDC			186
Sbjct 421	QPENLEYRIMLSVHGSQHSGMI G+ETDE+RAKVE+TPNSPRAEATLGGFGSLGLDC			480
Query 187	EPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHA			246
Sbjct 481	EPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNKEALVEFKDAHA			540
Query 247	KRQTVVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCR LKMDKLR LKGVSYSLCTA			306
Sbjct 541	KRQTVVVLGSQEGAVHTALAGALEAEMDGAKGRL SGHLKCR LKMDKLR LKGVSYSLCTA			600
Query 307	AFTFTKVPAETLHGTVTVEVQYAGTDGPCKIPVQMAVDMQTLTPVGR LITANPVITESTE			366
Sbjct 601	AFTFTKIPAE TLHGTVTVEVQYAGTDGPCKVPAQMAVDMQTLTPVGR LITANPVITESTE			660
Query 367	NSKMMLELDPFGDSYIVIGVGDKKITHHWHRS GSTIGKA FEATVRGAKRMAVLGDTAWD			426
Sbjct 661	NSKMMLELDPFGDSYIVIGVG+KKITHHWHRS GSTIGKA FEATVRGAKRMAVLGDTAWD			720
Query 427	FGSVGGVFNSLKGKIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISL TCLA			486
Sbjct 721	FGSVGG NSLKGKIHQIFGA AFKSLFGGMSWFSQILIGTLL+WLGLNTKNGSISL CLA			780
Query 487	LGGVMIFLSTAVSA LGGV+IFLSTAVSA			500

Sbjct	781	LGGVLI ^{FL} LSTAVSADVGCSVDFSKKETRCGTGVFVYNDVEAWRDYKYHPDSPRRLAAAV	840
Sbjct	841	KQAWEDGICGISSVSRMENIMWRSVEGELNAILEENGVLQTVVVGSVKNPMWRGPQRLPV	900
Sbjct	901	PVNELPHGWKAWGKSYFVRAAKTNNSFVVDGDTLKECPLKHRAWNSFLVEDHGFVGFHTS	960
Sbjct	961	VWLKVREDYSLECDPAVIGTAVKGKEAVHSDLGWIESEKNDTWRLKRAHLIEMKTCEWP	1020
Sbjct	1021	KSHTLWTDGIEESDLIIPKSLAGPLSHHNTREGYRTQMKGPWHSEEELEIRFECPGKTVH	1080
Sbjct	1081	VEETCGTRGPSLRSTTASGRVIEEWCCRECTMPPLSFRAKDGCWYGMEIRPRKEPESNLV	1140
Sbjct	1141	RSMVTAGSTDHMDHFSLGVLVILLMVQEGKKRMTTKIIISTMAVLVAMILGGFSMSDL	1200
Sbjct	1201	AKLAILMGATFAEMNTGGDVAHLALIAAFKVRPALLVSFIFRANWTPRESMLLALASCLL	1260
Sbjct	1261	QTAISALEGLDMVLINGFALAWLAIRAMVVPRTDNITLAILAALTPLARGTLLVAWRAGL	1320
Sbjct	1321	ATCGGFMLLSLKKGKSVKKNLPFVMALGLTAVRLVDPINVVGLLLLTRSGKRSWPPSEVL	1380
Sbjct	1381	TAVGLICALAGGFAKADIEMAGPMAAVGLLIVSYVVGSKSVDMYIERAGDITWEKDAEVT	1440
Sbjct	1441	GNSPRLDVALDESGDFSLVEDDGPPMREIILKVVLMTICGMNPIAIPFAAGAWYVYVKTG	1500
Sbjct	1501	KRSGALWDVPAPKEVKKGETTDGVYRVMTRRLLGSTQVGVGMQEGVFHTMWHVTKGSAL	1560
Sbjct	1561	RSGEGRLDOPYWGDVQDLVSYCGPWKLDAAWDGHSEVQLLAVPPGERARNIQTLPGIFKT	1620
Sbjct	1621	KDGDIGAVALDYPAGTSGSPILDKCGRVIGLYGNGVVIKNGSYVSAITQGRREEETPVEC	1680
Sbjct	1681	FEPSMLKKKQLTVLDLHPGAGKTRRVLPFIVREAIKTRLRTVILAPTRVAAEMEEALRG	1740
Sbjct	1741	LPVRYMTTAVNVTHSGTEIVDLMCHATFTSRLQLPIRVPNYLYIMDEAHFTDPSSIAAR	1800
Sbjct	1801	GYISTRVEMGEAAAIFMTATPPGTRDAFPDSNSPIMDTEVEVPERAWSSGFDWTDHSGK	1860
Sbjct	1861	TVWFVPSVRNGNEIAACLTAKGKRVIQLSRKTFETEFQKTKHQEWDFVVTDDISEMGANF	1920
Sbjct	1921	KADRVIDSRRCLKPVILDGERVILAGPMPVTHASAAQRRGRIGRNPNKPGDEYLYGGGCA	1980
Sbjct	1981	ETDEDAHMLEARMLLDNIYLQDGLIASLYRPEADKVAIEGEFKLRTEQRKTFVELMKR	2040
Sbjct	2041	GDLPVWLAYQVASAGITYTDRRWCFDGTNTNTIMEDSVPAEVWTRHGEKRVLPKPRWMDAR	2100
Sbjct	2101	VCSHAAALKSFKEFAAGKRGAAFGVMEALGTLPGHMTERFQEAIDNLAVLMRAETGSRPY	2160
Sbjct	2161	KAAAAQLPETLETIMLLGLLGTVSLGIFVLMRNKGIGKMGFGMVTLGASAWLMWLSEIE	2220
Sbjct	2221	PARIACVLIVVFLLLVVLIPPEKQRSPODNQMAIIMVAVGLLGLITANELGWLERTKS	2280
Sbjct	2281	DLSHLMGRREEGATIGFSMDIDLRPASAWAIYAALTTFITPAVQHAVTTSYNNYSLMAMA	2340
Sbjct	2341	TQAGVLFGMGKMPFYAWDFGVPLLMIGCYSQLTPLTLIVAIILLVAHYMYLIPGLQAAA	2400
Sbjct	2401	ARAAQKRTAAGIMKNPVVDGIVVTDIDTMTIDPQVEKKMGQVLLIAVAVSSAILSRTAWG	2460
Sbjct	2461	WGEAGALITAATSTLWEGSPNKYWNSSSTATSLCNIFRGSYLAGASLIYVTRNAGLVKRR	2520
Sbjct	2521	GGGTGETLGEKWKARLNQMSALEFYSYKKSIGITEVCREEARRALKDGVATGGHAVSRGSA	2580
Sbjct	2581	KLRWLVERGYLQPYGKVIDLGCGRGGWSYYAATIRKVQEVKGYTKGGPGHEPMLVQSYG	2640
Sbjct	2641	WNIVRLKSGVDVFHMAAEPCDTLLCDIGESSSSPEVEEARTLRVLSMVGDWLEKRPGAF	2700
Sbjct	2701	IKVLCPYTSTMMETLERLQRRYGGGLVRVPLSRNSTHEMYWVSGAKSNTIKSVSTTSQLL	2760
Sbjct	2761	LGRMDGPRRPVKYEEEDVNLGSGTRAVVSCAEAPNMKIIGNRIERIRSEHAETWFFDENHP	2820
Sbjct	2821	YRTWAYHGSYEAPTQGSASSLINGVVRLLSKPVDVVTGVTGIAMTDTTPYGQQRVFKEKV	2880
Sbjct	2881	DTRVPDPQEGTRQVMSMVSSWLWELGKHKRPRVCTKEEFINKVRSNAALGAIFEEKEW	2940
Sbjct	2941	KTAVEAVNDPRFWALVDKEREHLRGECQSCVYNNMGKREKKQGEFGKAKGSRAIWMWL	3000
Sbjct	3001	GARFLEFEALGLFNEDHWMGRENSGGGVEGLGLQRLGYVLEEMSRIPEGGRMYADDTAGWD	3060
Sbjct	3061	TRISRFDLNEALITNQMEKGHRALALAIKYTYQNKVVKVLRPAEKGTVMIDIISRDQ	3120
Sbjct	3121	RGSQGVVTYALNTFTNLVVQLIRNMEAEEVLEMQDLWLLRRSEKVTNWLQSNQWDRKRM	3180
Sbjct	3181	AVSGDDCVVKPIDDRFAHALRFLNDMGKVRKDTQEWKPGSTGWDNWEVFPFCSHHFNKLHL	3240
Sbjct	3241	KDGRSIVVPCRHQDELIGRARVSPGAGWSIRETACLAKSYAQMWQLLYFHRRDLRLMANA	3300
Sbjct	3301	ICSSVPVDWVPTGRTTWSIHGKGEWMTTEDMLVVWNRVWIEENDHMEKTPVTKWDIPY	3360
Sbjct	3361	LGKREDLWCGSLIGHRPRTTWAENIKNTVMVRRRIIGDEEKYMDYLSTQVRYLGEEGSTP	3420
Sbjct	3421	GVL 3423	

Taxonomy

Reports

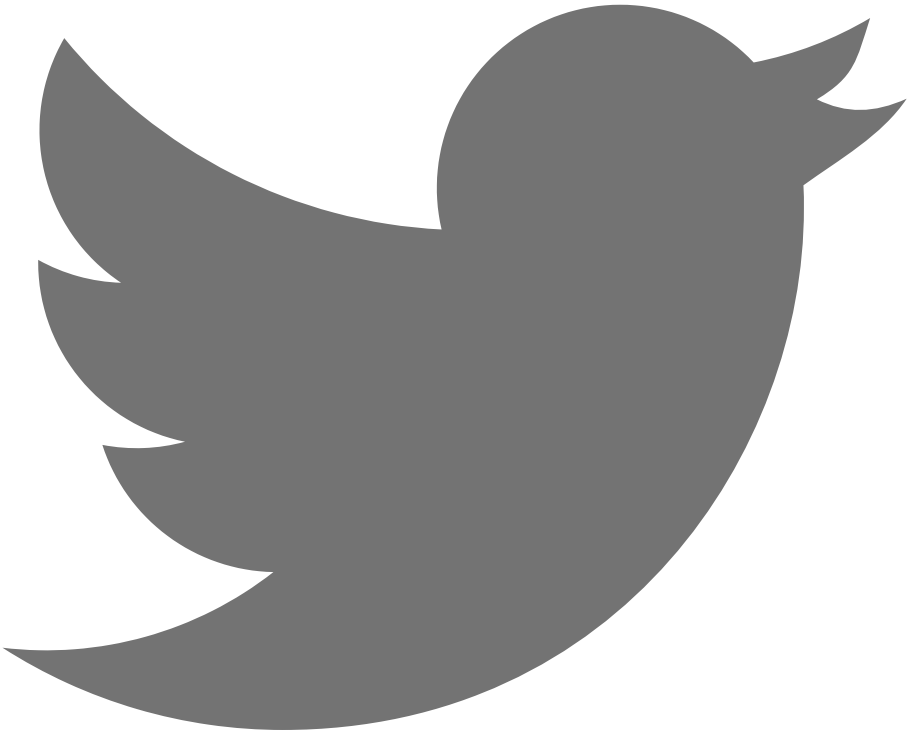
- Lineage
- Organism
- Taxonomy

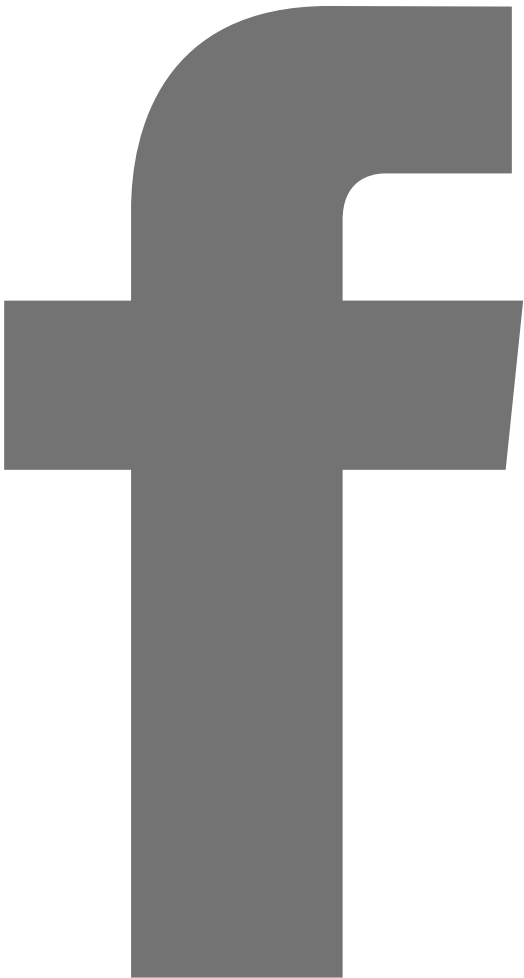
Dot Plot

Plot of lcl|Query_33461 vs lcl|Query_33463

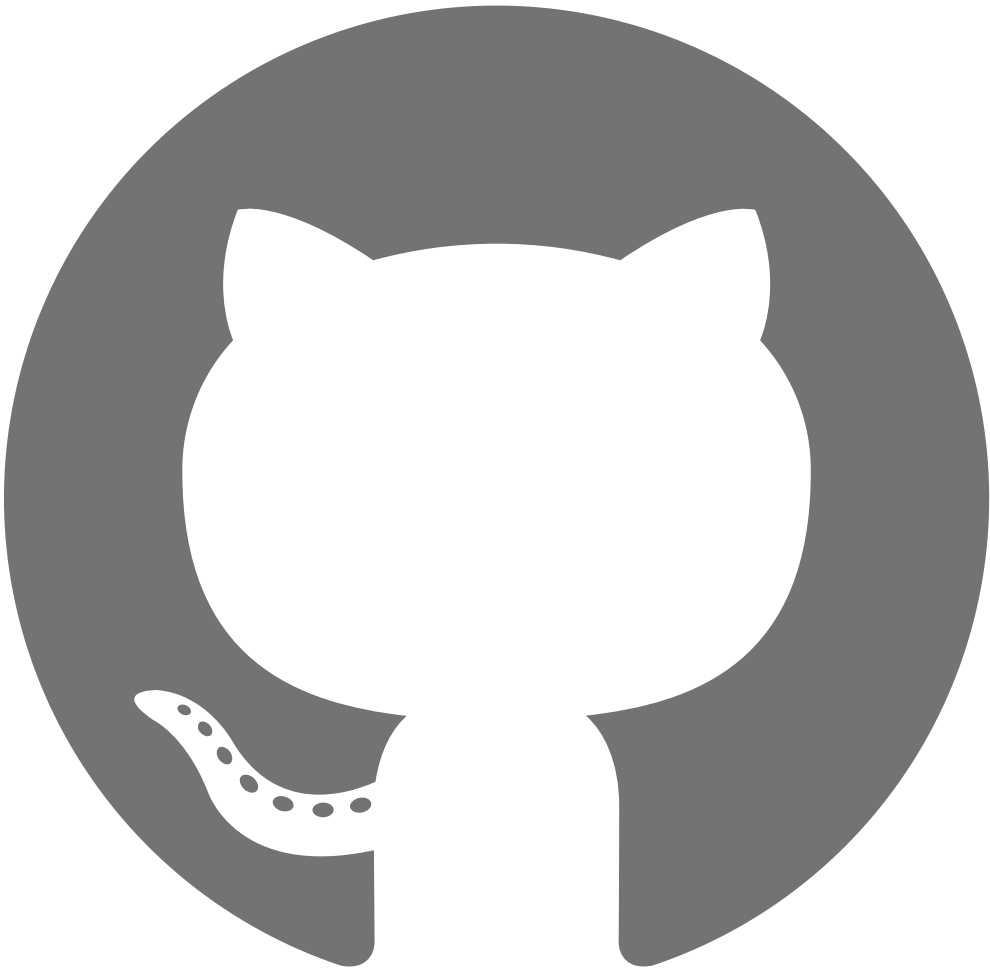
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