

Protein

COVID-19 is an emerging, rapidly evolving situation.

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GenPept

RecName: Full=(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; Short=RdpA;
AltName: Full=(R)-dichlorprop/(R)-mecoprop dioxygenase; AltName: Full=Alpha-
ketoglutarate-dependent dioxygenase; AltName: Full=Dichlorprop/alpha-ketoglutarate-
dioxygenase; AltName...

UniProtKB/Swiss-Prot: Q8KSC8.2

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LOCUS RDP_A_SPHHM 295 aa linear BCT 11-DEC-2019

DEFINITION RecName:
 Full=(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase;
 Short=RdpA; AltName: Full=(R)-dichlorprop/(R)-mecoprop dioxygenase;
 AltName: Full=Alpha-ketoglutarate-dependent dioxygenase; AltName:
 Full=Dichlorprop/alpha-ketoglutarate-dioxygenase; AltName:
 Full=Mecoprop/alpha-ketoglutarate-dioxygenase.

ACCESSION Q8KSC8

VERSION Q8KSC8.2

DBSOURCE UniProtKB: locus RDP_A_SPHHM, accession [Q8KSC8](#);
 class: standard.
 created: Oct 29, 2014.
 sequence updated: Mar 1, 2004.
 annotation updated: Dec 11, 2019.
 xrefs: AF516752.2, AAM90965.2, AJ628859.1, CAF32811.1,
 WP_031942865.1, 6D00_A, 6D00_B, 6D00_C, 6D00_D, 6D10_A, 6D10_B,
 6D10_C, 6D10_D, 6D10_E, 6D10_F, 6D10_G, 6D10_H, 6D3H_A, 6D3H_B,
 6D3H_I, 6D3H_M, 6D3I_A, 6D3I_D, 6D3I_G, 6D3I_J, 6D3J_A, 6D3M_A,
 6D3M_B, 6D3M_F, 6D3M_J
 xrefs (non-sequence databases): PDBsum:6D00, PDBsum:6D10,
 PDBsum:6D3H, PDBsum:6D3I, PDBsum:6D3J, PDBsum:6D3M, SMR:Q8KSC8,
 BioCyc:GCF_001598535:G1ES4-4015-MONOMER, BRENDA:1.14.11.44,
 UniPathway:UPA00348, GO:0051213, GO:0046872, GO:0019439,
 Gene3D:3.60.130.10, InterPro:IPR042098, InterPro:IPR003819,
 Pfam:PF02668

KEYWORDS 3D-structure; Aromatic hydrocarbons catabolism; Dioxygenase; Iron;
 Metal-binding; Oxidoreductase.

SOURCE Sphingobium herbicidovorans NBRC 16415

ORGANISM [Sphingobium herbicidovorans NBRC 16415](#)
 Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 Sphingomonadaceae; Sphingobium.

REFERENCE 1 (residues 1 to 295)

AUTHORS Kohler,H.P.

TITLE Sphingomonas herbicidovorans MH: a versatile phenoxyalkanoic acid
 herbicide degrader

JOURNAL J. Ind. Microbiol. Biotechnol. 23 (4-5), 336-340 (1999)

PUBMED [11423952](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.;
 STRAIN=ATCC 700291 / DSM 11019 / NBRC 16415 / MH

REFERENCE 2 (residues 1 to 295)

AUTHORS Schleinitz,K.M., Kleinsteuber,S., Vallaey,S. and Babel,W.

TITLE Localization and characterization of two novel genes encoding
 stereospecific dioxygenases catalyzing
 2(2,4-dichlorophenoxy)propionate cleavage in Delftia acidovorans
 MC1

JOURNAL Appl. Environ. Microbiol. 70 (9), 5357-5365 (2004)

PUBMED [15345423](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].;
 STRAIN=ATCC 700291 / DSM 11019 / NBRC 16415 / MH
 Erratum:[Appl Environ Microbiol. 2004 Nov;70(11):6948]

REFERENCE 3 (residues 1 to 295)

AUTHORS Muller,T.A., Byrde,S.M., Werlen,C., van der Meer,J.R. and
 Kohler,H.P.

TITLE Genetic analysis of phenoxyalkanoic acid degradation in
 Sphingomonas herbicidovorans MH

8/24/2020

RecName: Full=(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; S - Protein - NCBI

JOURNAL Appl. Environ. Microbiol. 70 (10), 6066-6075 (2004)
PUBMED ~~15466552~~
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].;
STRAIN=ATCC 700291 / DSM 11019 / NBRC 16415 / MH

REFERENCE 4 (residues 1 to 295)
AUTHORS Muller,T.A., Fleischmann,T., van der Meer,J.R. and Kohler,H.P.
TITLE Purification and characterization of two enantioselective
alpha-ketoglutarate-dependent dioxygenases, RdpA and SdpA, from
Sphingomonas herbicidovorans MH

JOURNAL Appl. Environ. Microbiol. 72 (7), 4853-4861 (2006)
PUBMED ~~16820480~~
REMARK FUNCTION, CATALYTIC ACTIVITY, BIOPHYSICOCHEMICAL PROPERTIES,
SUBUNIT, COFACTOR, SUBSTRATE SPECIFICITY, AND PATHWAY.

REFERENCE 5 (residues 1 to 295)
AUTHORS Muller,T.A., Zavodszky,M.I., Feig,M., Kuhn,L.A. and Hausinger,R.P.
TITLE Structural basis for the enantiospecificities of R- and S-specific
phenoxypropionate/alpha-ketoglutarate dioxygenases

JOURNAL Protein Sci. 15 (6), 1356-1368 (2006)
PUBMED ~~16731970~~
REMARK FUNCTION, CATALYTIC ACTIVITY, BIOPHYSICOCHEMICAL PROPERTIES, AND
MUTAGENESIS OF VAL-80; LEU-83; GLN-93; ILE-106; GLY-107; PHE-171;
TYR-221 AND ARG-285.

COMMENT [FUNCTION] Involved in the degradation of the phenoxypropionate
herbicides. Catalyzes the enantiospecific cleavage of the ether
bond in the herbicide R-dichlorprop
(R)-2-(2,4-dichlorophenoxy)propionate(R-2,4-DP) and R-mecoprop
(R)-2-(4-chloro-2-methylphenoxy)propionate(R-2,4-MCPP). It can
also accept (RS)-4-chlorophenoxypropanoate, however it can only
accept 2-oxoglutarate as oxygen acceptor.
{ECO:0000269|PubMed:16731970, ECO:0000269|PubMed:16820480,
ECO:0000303|PubMed:11423952}.
[CATALYTIC ACTIVITY]
Reaction=(R)-2-(4-chloro-2-methylphenoxy)propanoate +
2-oxoglutarate + O2 = 2-methyl-4-chlorophenol + CO2 + pyruvate +
succinate; Xref=Rhea:RHEA:37815, ChEBI:CHEBI:1800,
ChEBI:CHEBI:15361, ChEBI:CHEBI:15379, ChEBI:CHEBI:16526,
ChEBI:CHEBI:16810, ChEBI:CHEBI:30031, ChEBI:CHEBI:75284;
EC=1.14.11.44; Evidence={ECO:0000269|PubMed:16731970,
ECO:0000269|PubMed:16820480, ECO:0000303|PubMed:11423952}.
[CATALYTIC ACTIVITY] Reaction=(R)-(2,4-dichlorophenoxy)propanoate +
2-oxoglutarate + O2 = 2,4-dichlorophenol + CO2 + pyruvate +
succinate; Xref=Rhea:RHEA:37823, ChEBI:CHEBI:15361,
ChEBI:CHEBI:15379, ChEBI:CHEBI:16526, ChEBI:CHEBI:16738,
ChEBI:CHEBI:16810, ChEBI:CHEBI:30031, ChEBI:CHEBI:75288;
EC=1.14.11.44; Evidence={ECO:0000269|PubMed:16731970,
ECO:0000269|PubMed:16820480}.
[COFACTOR] Name=Fe cation; Xref=ChEBI:CHEBI:24875;
Evidence={ECO:0000269|PubMed:16820480}.
[COFACTOR] Name=L-ascorbate; Xref=ChEBI:CHEBI:38290;
Evidence={ECO:0000250|UniProtKB:Q67FR0}.
[BIOPHYSICOCHEMICAL PROPERTIES] Kinetic parameters: KM=2.8 uM for
alpha-ketoglutarate (at pH 6.75 and 30 degrees Celsius)
{ECO:0000269|PubMed:16820480}; KM=98.8 uM for R-2,4-MCPP (at pH
6.75 and 30 degrees Celsius) {ECO:0000269|PubMed:16820480};
KM=163.7 uM for R-2,4-DP (at pH 6.75 and 30 degrees Celsius)
{ECO:0000269|PubMed:16820480}; KM=262.4 uM for
(RS)-4-chlorophenoxypropanoate (at pH 6.75 and 30 degrees Celsius)
{ECO:0000269|PubMed:16820480}; KM=380 uM for R-2,4-MCPP (at pH 6.75
and 30 degrees Celsius) {ECO:0000269|PubMed:16731970}; Note=Kcat is
114.2 min(-1) for dioxygenase activity with R-2,4-MCPP (at pH 6.75
and 30 degrees Celsius). Kcat is 135.6 min(-1) for dioxygenase
activity with alpha-ketoglutarate (at pH 6.75 and 30 degrees
Celsius). Kcat is 170.1 min(-1) for dioxygenase activity with
R-2,4-DP (at pH 6.75 and 30 degrees Celsius). Kcat is 241.9 min(-1)
for dioxygenase activity with (RS)-4-chlorophenoxypropanoate (at pH
6.75 and 30 degrees Celsius). Kcat is 252 min(-1) for dioxygenase
activity with R-2,4-MCPP (at pH 6.75 and 30 degrees Celsius).
{ECO:0000269|PubMed:16731970, ECO:0000269|PubMed:16820480}; pH
dependence: Optimum pH is about 6.5. {ECO:0000269|PubMed:16820480};
Temperature dependence: Optimum temperature is between 35 and 40
degrees Celsius. {ECO:0000269|PubMed:16820480}.
[PATHWAY] Xenobiotic degradation; 2-(2,4-dichlorophenoxy)propanoate
degradation. {ECO:0000305|PubMed:16820480}.
[SUBUNIT] Homotrimer. {ECO:0000269|PubMed:16820480}.
[SIMILARITY] Belongs to the TfdA dioxygenase family. {ECO:0000305}.

FEATURES
source Location/Qualifiers
1..295
/organism="Sphingobium herbicidovorans NBRC 16415"
/db_xref="taxon:1213045"
gene 1..295
/gene="rdpA"

<https://www.ncbi.nlm.nih.gov/protein/Q8KSC8.2>

2/5

COR-AAD1-00003392

Protein 1..295
 /product="(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase"
 /EC_number="1.14.11.44"
 /note="RdpA; (R)-dichlorprop/(R)-mecoprop dioxygenase; Alpha-ketoglutarate-dependent dioxygenase; Dichlorprop/alpha-ketoglutarate-dioxygenase; Mecoprop/alpha-ketoglutarate-dioxygenase"
 /UniProtKB_evidence="Evidence at protein level"

Region 1..295
 /region_name="Mature chain"
 /note="(R)-phenoxypropionate/alpha-ketoglutarate-dioxygenase. /id=PRO_0000430761."

Region 13..293
 /region_name="TauD"
 /note="Taurine dioxygenase, alpha-ketoglutarate-dependent [Secondary metabolites biosynthesis, transport and catabolism]; COG2175"
 /db_xref="CDD:225085"

Region 13..24
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Region 17..287
 /region_name="TauD"
 /note="Taurine catabolism dioxygenase TauD, TfdA family; pfam02668"
 /db_xref="CDD:280777"

Region 26..30
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Region 39..52
 /region_name="Helical region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Region 53..59
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Region 64..72
 /region_name="Helical region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Site 80
 /site_type="mutagenized"
 /note="V->A: The dioxygenase activity with R-2,4-MCPP is 60% of the wild-type. 6-fold decrease of the affinity binding for R-2,4-MCPP.
 /evidence=ECO:0000269|PubMed:16731970."

Region 81..83
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Site 83
 /site_type="mutagenized"
 /note="L->A: The dioxygenase activity with R-2,4-MCPP is 5% of the wild-type.
 /evidence=ECO:0000269|PubMed:16731970."

Region 89..97
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."

Site 93
 /site_type="mutagenized"
 /note="Q->A: The dioxygenase activity with R-2,4-MCPP is 10% of the wild-type. 7-fold decrease of the affinity binding for R-2,4-MCPP.
 /evidence=ECO:0000269|PubMed:16731970."

Region 101..103
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D10."

Site 106
 /site_type="mutagenized"
 /note="I->A: The dioxygenase activity with R-2,4-MCPP is 30% of the wild-type. 20-fold decrease of the affinity binding for R-2,4-MCPP. Loss of the dioxygenase activity; when associated with I-107. The dioxygenase activity with R-2,4-MCPP is 10% of the wild-type; when associated with N-107. /evidence=ECO:0000269|PubMed:16731970."

Site 107
 /site_type="mutagenized"
 /note="G->I: Loss of the dioxygenase activity; when associated with A-106.
 /evidence=ECO:0000269|PubMed:16731970."

Site 107
 /site_type="mutagenized"
 /note="G->N: The dioxygenase activity with R-2,4-MCPP is

10% of the wild-type; when associated with A-106.
 /evidence=ECO:0000269|PubMed:16731970."
 109..111
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Site
 111
 /site_type="metal-binding"
 /note="Iron; catalytic."
 /evidence=ECO:0000250|UniProtKB:P37610."
 Region
 113..116
 /region_name="Hydrogen bonded turn"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Site
 113
 /site_type="metal-binding"
 /note="Iron; catalytic."
 /evidence=ECO:0000250|UniProtKB:P37610."
 Region
 117..119
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 122..130
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 133..135
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3I."
 Region
 138..142
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Site
 138
 /site_type="binding"
 /note="2-oxoglutarate."
 /evidence=ECO:0000250|UniProtKB:P37610."
 Region
 143..148
 /region_name="Helical region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 152..158
 /region_name="Helical region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 162..165
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 168..171
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 /note="/evidence=ECO:0000244|PDB:6D3H."
 Site
 171
 /site_type="mutagenized"
 /note="F->A: The dioxygenase activity with R-2,4-MCPP is 60% of the wild-type. 4-fold increase of the affinity binding for R-2,4-MCPP."
 /evidence=ECO:0000269|PubMed:16731970."
 Site
 171
 /site_type="mutagenized"
 /note="F->Q: The dioxygenase activity with R-2,4-MCPP is 60% of the wild-type and the affinity binding R-2,4-MCPP is similar to the wild-type."
 /evidence=ECO:0000269|PubMed:16731970."
 Region
 173..177
 /region_name="Helical region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 178..180
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3I."
 Region
 184..186
 /region_name="Hydrogen bonded turn"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 192..196
 /region_name="Helical region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 199..206
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 208..210
 /region_name="Hydrogen bonded turn"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 213..215
 /region_name="Beta-strand region"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Region
 219..221
 /region_name="Hydrogen bonded turn"
 /note="/evidence=ECO:0000244|PDB:6D3H."
 Site
 221

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/site_type="other"
/note="Contributes to enantiospecificity.
/evidence=ECO:0000303|PubMed:16731970."
221
/site_type="mutagenized"
/note="Y->A: The dioxygenase activity with R-2,4-MCPP is
5% of the wild-type.
/evidence=ECO:0000269|PubMed:16731970."
222..225
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
230..244
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
247..249
/region_name="Helical region"
/note="/evidence=ECO:0000244|PDB:6D3H."
250..253
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
255
/site_type="binding"
/note="2-oxoglutarate.
/evidence=ECO:0000250|UniProtKB:P37610."
260..264
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
265..267
/region_name="Hydrogen bonded turn"
/note="/evidence=ECO:0000244|PDB:6D3H."
268..272
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
270
/site_type="metal-binding"
/note="Iron; catalytic.
/evidence=ECO:0000250|UniProtKB:P37610."
275..278
/region_name="Hydrogen bonded turn"
/note="/evidence=ECO:0000244|PDB:6D3I."
281..288
/region_name="Beta-strand region"
/note="/evidence=ECO:0000244|PDB:6D3H."
281
/site_type="binding"
/note="2-oxoglutarate.
/evidence=ECO:0000250|UniProtKB:P37610."
285
/site_type="other"
/note="Contributes to enantiospecificity.
/evidence=ECO:0000303|PubMed:16731970."
285
/site_type="mutagenized"
/note="R->A: The dioxygenase activity with R-2,4-MCPP is
10% of the wild-type. 4-fold decrease of the affinity
binding for R-2,4-MCPP.
/evidence=ECO:0000269|PubMed:16731970."

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ORIGIN

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61 aitneqhiat srrfcpvdpv plksiegyp evqmirrean esgrvigddw htdstfldap
121 paavvmraid vpehgdtgfl lsmytawetl sptmqatieg lnnvhsatrv fgslyqaqnr
181 rfsntsvkvm dvdagdretv hplvvthpgs grkglyvnqv ycqriegmtd aeskplllqfl
241 yehatrfdft crvrwkkdqv lwvdlctmh ravpdyagkf ryltrttvgg vrpar

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//