Phyre^2

Email	l.a.kelley@imperial.ac.uk
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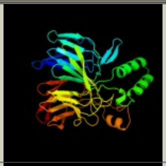
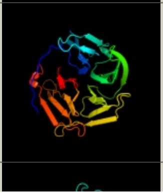
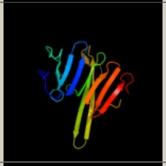
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2uvkB_	Alignment		100.0	99	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**yjht; **PDBTitle:** structure of yjht
2	c2zwaA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 2; **PDBTitle:** crystal structure of trna wybutosine synthesizing enzyme2 tyw4
3	d1k3ia3	Alignment		100.0	12	**Fold:**7-bladed beta-propeller **Superfamily:**Galactose oxidase, central domain **Family:**Galactose oxidase, central domain
4	c2wozA_	Alignment		100.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**kelch repeat and btb domain-containing protein **PDBTitle:** the novel beta-propeller of the btb-kelch protein krp12 provides the binding site for lasp-1 that is necessary for3 pseudopodia extension
5	c3ii7A_	Alignment		100.0	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**kelch-like protein 7; **PDBTitle:** crystal structure of the kelch domain of human klhl7
6	d1zgka1	Alignment		100.0	16	**Fold:**6-bladed beta-propeller **Superfamily:**Kelch motif **Family:**Kelch motif
7	c2vz1A_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**galactose oxidase; **PDBTitle:** premat-galactose oxidase
8	c1x2rA_	Alignment		100.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**kelch-like ech-associated protein 1; **PDBTitle:** structural basis for the defects of human lung cancer2 somatic mutations in the repression activity of keap1 on3 nrf2
9	c2vpjA_	Alignment		100.0	15	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**kelch-like protein 12; **PDBTitle:** crystal structure of the kelch domain of human klhl12
10	c2xn4A_	Alignment		100.0	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**kelch-like protein 2; **PDBTitle:** crystal structure of the kelch domain of human klhl2 (mayven)
11	c3mbrX_	Alignment		98.2	13	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of the glutaminyl cyclase from xanthomonas2 campestris

12	c1kv9A_	Alignment		98.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type ii quinohemoprotein alcohol dehydrogenase; **PDBTitle:** structure at 1.9 a resolution of a quinohemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
13	c3nolA_	Alignment		97.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
14	d1qhua1	Alignment		97.0	18	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
15	c1qhuA_	Alignment		96.9	22	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (hemopexin); **PDBTitle:** mammalian blood serum haemopexin deglycosylated and in2 complex with its ligand haem
16	d2ad6a1	Alignment		96.7	14	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
17	c3bwsA_	Alignment		96.6	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
18	c3hfqB_	Alignment		96.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein lp_2219; **PDBTitle:** crystal structure of the lp_2219 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr118.
19	c3ba0A_	Alignment		96.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** crystal structure of full-length human mmp-12
20	d1fbla1	Alignment		96.2	21	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
21	d1su3a2	Alignment	not modelled	96.2	19	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
22	c1kb0A_	Alignment	not modelled	96.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** crystal structure of quinohemoprotein alcohol dehydrogenase from2 comamonas testosteroni
23	c1su3A_	Alignment	not modelled	96.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interstitial collagenase; **PDBTitle:** x-ray structure of human prommp-1: new insights into2 collagenase action
24	c1yiqA_	Alignment	not modelled	95.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein alcohol dehydrogenase; **PDBTitle:** molecular cloning and structural analysis of2 quinohemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. compariison to the other4 quinohemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
25	d1gena_	Alignment	not modelled	95.7	21	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
26	d1kb0a2	Alignment	not modelled	95.6	12	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
27	d1itva_	Alignment	not modelled	95.3	21	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
28	c1nnoA	Alignment	not modelled	95.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase;

		Alignment	not modelled			**PDBTitle:** conformational changes occurring upon no binding in nitrite2 reductase from pseudomonas aeruginosa
29	c3nokB_	Alignment	not modelled	95.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutaminyl cyclase; **PDBTitle:** crystal structure of myxococcus xanthus glutaminyl cyclase
30	d1flga_	Alignment	not modelled	94.9	16	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
31	c1gxdA_	Alignment	not modelled	94.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
32	c2jxyA_	Alignment	not modelled	94.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrophage metalloelastase; **PDBTitle:** solution structure of the hemopexin-like domain of mmp12
33	d1hxna_	Alignment	not modelled	94.4	21	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
34	d1pexa_	Alignment	not modelled	94.4	20	**Fold:**4-bladed beta-propeller **Superfamily:**Hemopexin-like domain **Family:**Hemopexin-like domain
35	c2hz6A_	Alignment	not modelled	94.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**endoplasmic reticulum to nucleus signalling 1 **PDBTitle:** the crystal structure of human ire1-alpha luminal domain
36	d1kv9a2	Alignment	not modelled	94.1	12	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
37	d1w6sa_	Alignment	not modelled	93.1	13	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
38	c2ghsA_	Alignment	not modelled	92.9	15	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**agr_c_1268p; **PDBTitle:** crystal structure of a calcium-binding protein, regucalcin2 (agr_c_1268) from agrobacterium tumefaciens str. c58 at 1.55 a3 resolution
39	d2ghsa1	Alignment	not modelled	92.9	15	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
40	c3p1lA_	Alignment	not modelled	92.9	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lipoprotein yfgl; **PDBTitle:** crystal structure of escherichia coli bamb, a lipoprotein component of2 the beta-barrel assembly machinery complex, native crystals.
41	c2iwaA_	Alignment	not modelled	92.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** unbound glutaminyl cyclotransferase from carica papaya.
42	c3c7xA_	Alignment	not modelled	92.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-14; **PDBTitle:** hemopexin-like domain of matrix metalloproteinase 14
43	c1gq1B_	Alignment	not modelled	92.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
44	c3lp9C_	Alignment	not modelled	91.2	20	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**ls-24; **PDBTitle:** crystal structure of ls24, a seed albumin from lathyrus2 sativus
45	c2cltB_	Alignment	not modelled	89.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interstitial collagenase; **PDBTitle:** crystal structure of the active form (full-length) of human2 fibroblast collagenase.
46	c3jroA_	Alignment	not modelled	88.7	12	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
47	d2bbkh_	Alignment	not modelled	87.7	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
48	c3dsmA_	Alignment	not modelled	87.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bacuni_02894; **PDBTitle:** crystal structure of the surface layer protein bacuni_02894 from2 bacteroides uniformis, northeast structural genomics consortium3 target btr193d.
49	c1nr0A_	Alignment	not modelled	85.0	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** two seven-bladed beta-propeller domains revealed by the2 structure of a c. elegans homologue of yeast actin3 interacting protein 1 (aip1).
50	c2xbgA_	Alignment	not modelled	82.0	13	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**ycf48-like protein; **PDBTitle:** crystal structure of ycf48 from thermosynechococcus2 elongatus
51	d1lrwa_	Alignment	not modelled	81.9	19	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
52	c3g4hB_	Alignment	not modelled	80.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**regucalcin; **PDBTitle:** crystal structure of human senescence marker protein-30 (zinc bound)
53	d2p4oa1	Alignment	not modelled	79.0	13	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**All0351-like

54	c3e5zA_	Alignment	not modelled	75.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
55	c3ottB_	Alignment	not modelled	74.4	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two-component system sensor histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative one2 component system bt4673 from b. thetaiotaomicron
56	c3oyoB_	Alignment	not modelled	72.3	17	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**hemopexin fold protein cp4; **PDBTitle:** crystal structure of hemopexin fold protein cp4 from cow pea
57	c3u4yA_	Alignment	not modelled	72.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein (dtox_1751)2 from desulfotomaculum acetoxidans dsm 771.
58	c1qniE_	Alignment	not modelled	67.4	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from2 pseudomonas nautica, at 2.4a resolution
59	c2j57J_	Alignment	not modelled	59.0	11	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** x-ray reduced paraccocus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
60	c3no2A_	Alignment	not modelled	57.6	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein of unknown function (baccac_01654) from2 bacteroides caccae at 1.35 a resolution
61	c2h47F_	Alignment	not modelled	56.4	9	**PDB header:**oxidoreductase/electron transport **Chain:** F: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
62	d1jmxb_	Alignment	not modelled	51.9	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
63	c3dr2A_	Alignment	not modelled	50.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exported gluconolactonase; **PDBTitle:** structural and functional analyses of xc5397 from2 xanthomonas campestris: a gluconolactonase important in3 glucose secondary metabolic pathways
64	d1pbyb_	Alignment	not modelled	49.6	14	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
65	c3lrvA_	Alignment	not modelled	48.3	8	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor 19; **PDBTitle:** the prp19 wd40 domain contains a conserved protein interaction region2 essential for its function.
66	d1n1ta2	Alignment	not modelled	48.1	13	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
67	d2madh_	Alignment	not modelled	47.2	11	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
68	c1pi6A_	Alignment	not modelled	45.3	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
69	d1k32a2	Alignment	not modelled	44.7	10	**Fold:**6-bladed beta-propeller **Superfamily:**Tricorn protease N-terminal domain **Family:**Tricorn protease N-terminal domain
70	d2otma1	Alignment	not modelled	42.6	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
71	c3c75J_	Alignment	not modelled	41.3	10	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
72	d2dg1a1	Alignment	not modelled	39.0	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
73	c3k0tA_	Alignment	not modelled	37.2	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**endoribonuclease l-psp, putative; **PDBTitle:** crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
74	c1xrgB_	Alignment	not modelled	36.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative translation initiation inhibitor, yjgf **PDBTitle:** conserved hypothetical protein from clostridium2 thermocellum cth-2968
75	d1qfma1	Alignment	not modelled	36.0	13	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Prolyl oligopeptidase, N-terminal domain
76	c3dm0A_	Alignment	not modelled	31.9	15	**PDB header:**sugar binding protein,signaling protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein fused with **PDBTitle:** maltose binding protein fusion with rack1 from a. thaliana
77	d1xrga_	Alignment	not modelled	29.8	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
78	d1qnia2	Alignment	not modelled	29.4	9	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain

79	d1qksa2	Alignment	not modelled	28.7	11	**Fold:**8-bladed beta-propeller **Superfamily:**C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase **Family:**C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
80	d2cvla1	Alignment	not modelled	28.0	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
81	c3vh0C_	Alignment	not modelled	27.8	11	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
82	c2ig8C_	Alignment	not modelled	27.6	15	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pa3499; **PDBTitle:** crystal structure of a protein of unknown function pa3499 from2 pseudomonas aeruginosa
83	d1mdah_	Alignment	not modelled	27.3	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
84	c3m4sC_	Alignment	not modelled	23.4	24	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**putative endoribonuclease l-psp; **PDBTitle:** crystal structure of a putative endoribonuclease l-psp from entamoeba2 histolytica, orthorhombic form
85	c3l7qD_	Alignment	not modelled	19.4	13	**PDB header:**translation **Chain:** D: **PDB Molecule:**putative translation initiation inhibitor, aldr regulator- **PDBTitle:** crystal structure of aldr from streptococcus mutans
86	c2i0tB_	Alignment	not modelled	19.4	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
87	c3fgbB_	Alignment	not modelled	18.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein q89zh8_bactn; **PDBTitle:** crystal structure of the q89zh8_bactn protein from2 bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr289b.
88	d2b33a1	Alignment	not modelled	18.5	4	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
89	d1npea_	Alignment	not modelled	18.1	10	**Fold:**6-bladed beta-propeller **Superfamily:**YWTD domain **Family:**YWTD domain
90	d1qu9a_	Alignment	not modelled	18.1	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
91	d1qd9a_	Alignment	not modelled	17.2	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**YjgF/L-PSP
92	c2w18A_	Alignment	not modelled	17.2	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**partner and localizer of brca2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of human2 palb2
93	c2ivzD_	Alignment	not modelled	17.0	11	**PDB header:**protein transport/hydrolase **Chain:** D: **PDB Molecule:**protein tolb; **PDBTitle:** structure of tolb in complex with a peptide of the colicin2 e9 t-domain
94	c1l0qC_	Alignment	not modelled	16.9	12	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**surface layer protein; **PDBTitle:** tandem yvtn beta-propeller and pkd domains from an archaeal surface2 layer protein
95	c2cn2C_	Alignment	not modelled	16.6	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-1,4-xyloglucan hydrolase; **PDBTitle:** crystal structures of clostridium thermocellum2 xyloglucanase
96	c3hxjA_	Alignment	not modelled	15.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrrolo-quinoline quinone; **PDBTitle:** crystal structure of pyrrolo-quinoline quinone (pqq_dh) from2 methanococcus maripaludis, northeast structural genomics consortium3 target mrr86
97	d1v0ea1	Alignment	not modelled	14.7	16	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Endo-alpha-sialidase
98	d1nr0a1	Alignment	not modelled	12.5	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
99	c3pe7A_	Alignment	not modelled	12.4	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**oligogalacturonate lyase; **PDBTitle:** oligogalacturonate lyase in complex with manganese