



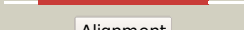

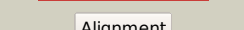









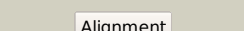

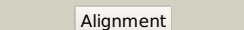





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2135c (-)_2395309_2396019
Date	Mon Aug 5 13:25:25 BST 2019
Unique Job ID	fcaab546e95e25bf

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ij5B_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: phosphoserine phosphatase 1; PDBTitle: crystal structure of a novel-type phosphoserine phosphatase from <i>hydrogenobacter thermophilus</i> tk-6
2	d1e58a_	 Alignment		100.0	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
3	c4embD_	 Alignment		100.0	17	PDB header: isomerase Chain: D: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpma from <i>borrelia burgdorferi</i> b31
4	c5zkkA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from <i>entamoeba histolytica</i>
5	c4pz9B_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: glucosyl-3-phosphoglycerate phosphatase; PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
6	c3ll4B_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
7	c6e4bC_	 Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: adenosylcobalamin/alpha-ribazole phosphatase; PDBTitle: the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from <i>escherichia coli</i> str. k-12 substr. mg1655
8	c3f3kA_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from <i>saccharomyces cerevisiae</i> .
9	c1yxjD_	 Alignment		100.0	20	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
10	d1xq9a_	 Alignment		100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
11	c5vveA_	 Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from <i>naegleria fowleri</i>

12	d1h2ea_	Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
13	c3r7aA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
14	c2a6pA_	Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: possible phosphoglycerate mutase gpm2; PDBTitle: structure solution to 2.2 angstrom and functional characterisation of 2 the open reading frame rv3214 from mycobacterium tuberculosis
15	c2yn0A_	Alignment		100.0	18	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain
16	c3eznB_	Alignment		100.0	22	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
17	c5um0A_	Alignment		100.0	20	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of 2,3-bisphosphoglycerate-dependent2 phosphoglycerate mutase from neisseria gonorrhoeae
18	d1qhfa_	Alignment		100.0	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
19	d1riia_	Alignment		100.0	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
20	c3dcyA_	Alignment		100.0	20	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
21	c3e9eB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
22	d2hhja1	Alignment	not modelled	100.0	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
23	c2yn2A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
24	d1bifa2	Alignment	not modelled	100.0	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
25	c3hjbB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-ribazole-5'-phosphate phosphatase cobc; PDBTitle: crystal structure of putative alpha-ribazole-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
26	c3d8hB_	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
27	c4eo9A_	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
						PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-

28	c1k6mA_	Alignment	not modelled	100.0	18	PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
29	c2i1vB_	Alignment	not modelled	100.0	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
30	d1fzta_	Alignment	not modelled	100.0	19	PDB header: bifunctional enzyme Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; PDBTitle: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
31	c1bifA_	Alignment	not modelled	100.0	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
32	d1tipa_	Alignment	not modelled	100.0	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
33	d1k6ma2	Alignment	not modelled	100.0	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
34	d3pgma_	Alignment	not modelled	100.0	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
35	c2qniA_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
36	c3mxoB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
37	c3d4iD_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
38	c2ikqA_	Alignment	not modelled	100.0	15	PDB header: signaling protein, immune system Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: crystal structure of mouse sts-1 pgm domain in complex with phosphate
39	d1v37a_	Alignment	not modelled	100.0	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
40	c3c7tB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
41	c3eozB_	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
42	c1ujcA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
43	c5gg7A_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family protein; PDBTitle: crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
44	c2rfiB_	Alignment	not modelled	100.0	19	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
45	c3f2iD_	Alignment	not modelled	99.9	10	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr0221 protein; PDBTitle: crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
46	c3fjyB_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
47	c4hbzA_	Alignment	not modelled	99.9	21	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartitia.
48	c2gicA_	Alignment	not modelled	98.1	24	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: structure of francisella tularensis histidine acid phosphatase bound2 to orthovanadate
49	c5cdhE_	Alignment	not modelled	98.1	19	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: major acid phosphatase; PDBTitle: structure of legionella pneumophila histidine acid phosphatase2 complexed with l(+)-tartrate
50	c4jodA_	Alignment	not modelled	98.0	24	PDB header: hydrolase Chain: A: PDB Molecule: lysophosphatidic acid phosphatase type 6; PDBTitle: crystal structure of human lysophosphatidic acid phosphatase type 62 complexed with tris
51	d1rpaA_	Alignment	not modelled	98.0	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
52	d1nd6a_	Alignment	not modelled	97.9	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
						Fold: Phosphoglycerate mutase-like

53	d1hpa_	Alignment	not modelled	97.9	21	Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
54	c4arvB_	Alignment	not modelled	97.9	22	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: yersinia kristensenii phytase apo form
55	c3zhcB_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
56	c4aruA_	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: hafnia alvei phytase in complex with tartrate
57	c2wniC_	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
58	c4fdtB_	Alignment	not modelled	97.6	17	PDB header: hydrolase Chain: B: PDB Molecule: putative multiple inositol polyphosphate histidine PDBTitle: crystal structure of a multiple inositol polyphosphate phosphatase
59	d1dkla_	Alignment	not modelled	97.5	28	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
60	d1nt4a_	Alignment	not modelled	97.5	13	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
61	d1qwoa_	Alignment	not modelled	97.4	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
62	d1qfxa_	Alignment	not modelled	97.3	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
63	c2qfIB_	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
64	d2hrca1	Alignment	not modelled	52.5	11	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
65	d1lbqa_	Alignment	not modelled	51.2	11	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
66	c3hbjA_	Alignment	not modelled	29.2	13	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
67	d2vcha1	Alignment	not modelled	29.2	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
68	c5v2kA_	Alignment	not modelled	28.8	21	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
69	c2o6IA_	Alignment	not modelled	26.2	21	PDB header: transferase Chain: A: PDB Molecule: udp-glucuronosyltransferase 2b7; PDBTitle: crystal structure of the human drug metabolizing udp-glucuronosyltransferase3 2b7
70	d2acva1	Alignment	not modelled	25.9	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
71	c6o86A_	Alignment	not modelled	25.3	13	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 76g1; PDBTitle: crystal structure of semet udp-dependent glucosyltransferases (ugt)2 from stevia rebaudiana in complex with udp
72	c2jzcA_	Alignment	not modelled	22.9	14	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of 2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
73	d2c1xa1	Alignment	not modelled	22.9	21	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
74	c5tmdA_	Alignment	not modelled	22.2	16	PDB header: transferase Chain: A: PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and 2 trichothecene.
75	c3wc4A_	Alignment	not modelled	21.8	13	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:anthocyanidin 3-o-glucosyltransferase; PDBTitle: crystal structure of udp-glucose: anthocyanidin 3-o-2 glucosyltransferase from clitoria ternatea
76	c6jtdB_	Alignment	not modelled	21.6	8	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccg1 in complex with udp
77	c2ashB_	Alignment	not modelled	21.3	13	PDB header: transferase Chain: B: PDB Molecule: queine trna-ribosyltransferase; PDBTitle: crystal structure of queine trna-ribosyltransferase (ec 2.4.2.29)2 (trna-guanine (tm1561) from thermotoga maritima at 1.90 a resolution
78	c3yuaA_	Alignment	not modelled	20.8	12	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3);

78	c3u0eA_	Alignment	not modelled	20.8	12	PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa PDB header: transferase
79	c5nlmB_	Alignment	not modelled	20.5	17	Chain: B: PDB Molecule: indoxyl udp-glucosyltransferase; PDBTitle: complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
80	d2pq6a1	Alignment	not modelled	20.2	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
81	c5gw8A_	Alignment	not modelled	19.3	12	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
82	c4r1dA_	Alignment	not modelled	17.9	9	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tie4-tli4 complex
83	c5xk2A_	Alignment	not modelled	17.0	19	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
84	c5e68A_	Alignment	not modelled	15.9	25	PDB header: lyase Chain: A: PDB Molecule: s-ribosylhomocysteine lyase; PDBTitle: high resolution crystal structure of luxs - quorum sensor molecular2 complex from salmonella typhi at 1.58 angstroms
85	d1efpb_	Alignment	not modelled	14.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
86	c5zcrB_	Alignment	not modelled	14.3	19	PDB header: hydrolase Chain: B: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
87	c3o0dF_	Alignment	not modelled	13.9	7	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
88	d1jl3a_	Alignment	not modelled	13.6	10	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
89	d3tgla_	Alignment	not modelled	13.5	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
90	d1tiba_	Alignment	not modelled	13.3	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
91	d1tiaa_	Alignment	not modelled	13.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
92	d1gpmal	Alignment	not modelled	11.5	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
93	c2p10D_	Alignment	not modelled	11.4	18	PDB header: hydrolase Chain: D: PDB Molecule: mll9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
94	c2wmyH_	Alignment	not modelled	10.8	15	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
95	d3b48a1	Alignment	not modelled	10.2	20	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
96	c2ijoA_	Alignment	not modelled	10.0	28	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: polyprotein; PDBTitle: crystal structure of the west Nile virus ns2b-ns3 protease2 complexed with bovine pancreatic trypsin inhibitor
97	c3e90C_	Alignment	not modelled	9.7	28	PDB header: hydrolase Chain: C: PDB Molecule: ns2b cofactor; PDBTitle: west Nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
98	c3ngmB_	Alignment	not modelled	9.6	14	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
99	d1qgoa_	Alignment	not modelled	8.8	15	Fold: Chelatase-like Superfamily: Chelatase Family: Cobalt chelatase CbiK