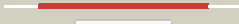



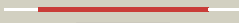



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3390_(lpqD)_3805045_3805755
Date	Fri Aug 9 18:20:05 BST 2019
Unique Job ID	ac1808f8964b73dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1e58a_</a>	 Alignment		100.0	16	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
2	<a href="#">c4ij5B_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoserine phosphatase 1; <b>PDBTitle:</b> crystal structure of a novel-type phosphoserine phosphatase from <i>hydrogenobacter thermophilus</i> tk-6
3	<a href="#">c4pz9B_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glucosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
4	<a href="#">d1h2ea_</a>	 Alignment		100.0	15	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
5	<a href="#">c3f3ka_</a>	 Alignment		100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ykr043c; <b>PDBTitle:</b> the structure of uncharacterized protein ykr043c from <i>saccharomyces2 cerevisiae</i> .
6	<a href="#">c4embD_</a>	 Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of a phosphoglycerate mutase gpma from <i>borrelia2 burgdorferi</i> b31
7	<a href="#">c2i1vB_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6- <b>PDBTitle:</b> crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
8	<a href="#">c3ll4B_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ykr043c; <b>PDBTitle:</b> structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
9	<a href="#">c1k6mA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6- <b>PDBTitle:</b> crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
10	<a href="#">c6e4bC_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylcobalamin/alpha-ribazole <b>PDBTitle:</b> the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from <i>escherichia coli</i> str. k-12 substr. mg1655
11	<a href="#">c5vveA_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from <i>naegleria fowleri</i>

12	<a href="#">c1yxjD_</a>	Alignment		100.0	14	<b>PDB header:</b> isomerase, hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoglycerate mutase 1; <b>PDBTitle:</b> crystal structure of human b type phosphoglycerate mutase
13	<a href="#">d1xq9a_</a>	Alignment		100.0	16	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
14	<a href="#">c3dcyA_</a>	Alignment		100.0	18	<b>PDB header:</b> apoptosis regulator <b>Chain:</b> A: <b>PDB Molecule:</b> regulator protein; <b>PDBTitle:</b> crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
15	<a href="#">d1fzta_</a>	Alignment		100.0	13	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
16	<a href="#">c3e9eB_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zgc:56074; <b>PDBTitle:</b> structure of full-length h11a mutant form of tigar from danio rerio
17	<a href="#">d1riia_</a>	Alignment		100.0	17	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
18	<a href="#">c3r7aA_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate mutase, putative; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
19	<a href="#">d2hhja1</a>	Alignment		100.0	17	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
20	<a href="#">c1bifA_</a>	Alignment		100.0	18	<b>PDB header:</b> bifunctional enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; <b>PDBTitle:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
21	<a href="#">d1bifa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
22	<a href="#">d1qhfa_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
23	<a href="#">c2yn0A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor tau 55 kda subunit; <b>PDBTitle:</b> tau55 histidine phosphatase domain
24	<a href="#">c3hjbB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-ribazole-5'-phosphate phosphatase cobc; <b>PDBTitle:</b> crystal structure of putative alpha-ribazole-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
25	<a href="#">c3d4iD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sts-2 protein; <b>PDBTitle:</b> crystal structure of the 2h-phosphatase domain of sts-2
26	<a href="#">c5um0A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of 2,3-bisphosphoglycerate-dependent2 phosphoglycerate mutase from neisseria gonorrhoeae
27	<a href="#">c5zkkA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate mutase family protein, putative; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
28	<a href="#">c2ikaA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> signaling protein, immune system <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor of t-cell receptor signaling 1;

28	<a href="#">c2kqA</a>	Alignment	not modelled	100.0	17	<b>PDBTitle:</b> crystal structure of mouse sts-1 pgm domain in complex with phosphate <b>PDB header:</b> isomerase
29	<a href="#">c3eznB</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b <b>PDB header:</b> isomerase
30	<a href="#">c3d8hB</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> B: <b>PDB Molecule:</b> glycolytic phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270 <b>PDB header:</b> isomerase
31	<a href="#">c2a6pA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible phosphoglycerate mutase gpm2; <b>PDBTitle:</b> structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis
32	<a href="#">c4eo9A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
33	<a href="#">c2yn2A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ynl108c; <b>PDBTitle:</b> huf protein - paralogue of the tau55 histidine phosphatase domain
34	<a href="#">d1k6ma2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
35	<a href="#">d1tipa</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
36	<a href="#">c2qniA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu0299; <b>PDBTitle:</b> crystal structure of uncharacterized protein atu0299
37	<a href="#">d3pgma</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
38	<a href="#">c3c7tB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ecdysteroid-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
39	<a href="#">d1v37a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
40	<a href="#">c3mxoB</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein phosphatase pgam5, mitochondrial; <b>PDBTitle:</b> crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
41	<a href="#">c3eozB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
42	<a href="#">c1ujcA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohistidine phosphatase sixa; <b>PDBTitle:</b> structure of the protein histidine phosphatase sixa2 complexed with tungstate
43	<a href="#">c2rf1B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase, isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphohistidine phosphatase sixa; <b>PDBTitle:</b> crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
44	<a href="#">c5gg7A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family protein; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
45	<a href="#">c3fjyB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable mutt1 protein; <b>PDBTitle:</b> crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
46	<a href="#">c3f2iD</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr0221 protein; <b>PDBTitle:</b> crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
47	<a href="#">c4hbzA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphohistidine phosphatase, sixa; <b>PDBTitle:</b> the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartita.
48	<a href="#">c2qlcA</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine acid phosphatase; <b>PDBTitle:</b> structure of francisella tularensis histidine acid phosphatase bound2 to orthovanadate
49	<a href="#">c4arvB</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> yersinia kristensenii phytase apo form
50	<a href="#">d1ihpa</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
51	<a href="#">d1nd6a</a>	Alignment	not modelled	97.6	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
52	<a href="#">c5cdhE</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> major acid phosphatase; <b>PDBTitle:</b> structure of legionella pneumophila histidine acid phosphatase2 complexed with l(+)-tartrate <b>PDB header:</b> hydrolase

53	<a href="#">c4jodA_</a>	Alignment	not modelled	97.6	18	<b>Chain:</b> A: <b>PDB Molecule:</b> lysophosphatidic acid phosphatase type 6; <b>PDBTitle:</b> crystal structure of human lysophosphatidic acid phosphatase type 62 complexed with tris
54	<a href="#">c2wniC_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-phytase; <b>PDBTitle:</b> crystal structure analysis of klebsiella sp asr1 phytase
55	<a href="#">c4aruA_</a>	Alignment	not modelled	97.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine acid phosphatase; <b>PDBTitle:</b> hafnia alvei phytase in complex with tartrate
56	<a href="#">d1rpaA_</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
57	<a href="#">c3zhcB_</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
58	<a href="#">d1dkla_</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
59	<a href="#">c4fdtB_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative multiple inositol polyphosphate histidine <b>PDBTitle:</b> crystal structure of a multiple inositol polyphosphate phosphatase
60	<a href="#">d1nt4a_</a>	Alignment	not modelled	97.2	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
61	<a href="#">d1qwoa_</a>	Alignment	not modelled	97.2	13	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
62	<a href="#">d1qfxa_</a>	Alignment	not modelled	97.2	15	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
63	<a href="#">c2gfiB_</a>	Alignment	not modelled	94.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> crystal structure of the phytase from d. castellii at 2.3 a
64	<a href="#">c5zcrB_</a>	Alignment	not modelled	36.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> maltooligosyl trehalose synthase; <b>PDBTitle:</b> dsm5389 glycosyltrehalose synthase
65	<a href="#">c5e68A_</a>	Alignment	not modelled	34.9	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> s-ribosylhomocysteine lyase; <b>PDBTitle:</b> high resolution crystal structure of luxs - quorum sensor molecular2 complex from salmonella typhi at 1.58 angstroms
66	<a href="#">c5oltA_</a>	Alignment	not modelled	28.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose biosynthesis protein bcsG; <b>PDBTitle:</b> crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsG from salmonella typhimurium
67	<a href="#">d1efpb_</a>	Alignment	not modelled	22.8	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
68	<a href="#">d1j98a_</a>	Alignment	not modelled	22.4	16	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> Autoinducer-2 production protein LuxS
69	<a href="#">c3hjeA_</a>	Alignment	not modelled	21.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 704aa long hypothetical glycosyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
70	<a href="#">d1iv8a2</a>	Alignment	not modelled	21.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
71	<a href="#">c4zmmB_</a>	Alignment	not modelled	18.5	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> ggdef domain of dcsbis complexed with c-di-gmp
72	<a href="#">d1vjea_</a>	Alignment	not modelled	17.3	17	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> Autoinducer-2 production protein LuxS
73	<a href="#">d1nlfa_</a>	Alignment	not modelled	16.8	9	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
74	<a href="#">c4r1dA_</a>	Alignment	not modelled	16.2	10	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of tie4-tli4 complex
75	<a href="#">c3ozxA_</a>	Alignment	not modelled	15.8	8	<b>PDB header:</b> hydrolase, translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
76	<a href="#">c3bk7A_</a>	Alignment	not modelled	15.8	23	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnaase-I inhibitor protein from2 pyrococcus abyssi
77	<a href="#">c1yqtA_</a>	Alignment	not modelled	15.1	23	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
78	<a href="#">c5xavB_</a>	Alignment	not modelled	14.4	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> intracellular polyhydroxyalkanoate synthase; <b>PDBTitle:</b> structure of phac from chromobacterium sp. usm2
79	<a href="#">c4u0pB_</a>	Alignment	not modelled	13.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoyl synthase 2; <b>PDBTitle:</b> the crystal structure of lipoyl synthase in complex with s-

						adenosyl2 homocysteine
80	<a href="#">c4x96B_</a>	Alignment	not modelled	13.3	5	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylcholine-sterol acyltransferase; <b>PDBTitle:</b> low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
81	<a href="#">c2zqeA_</a>	Alignment	not modelled	12.5	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mutS2 protein; <b>PDBTitle:</b> crystal structure of the smr domain of thermus thermophilus mutS2
82	<a href="#">c5ol2E_</a>	Alignment	not modelled	11.2	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
83	<a href="#">c3j16B_</a>	Alignment	not modelled	10.3	15	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> rli1p; <b>PDBTitle:</b> models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
84	<a href="#">d1efvb_</a>	Alignment	not modelled	9.9	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
85	<a href="#">c2nq2C_</a>	Alignment	not modelled	9.6	11	<b>PDB header:</b> metal transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical abc transporter atp-binding protein <b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.
86	<a href="#">c4s3jC_</a>	Alignment	not modelled	9.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cortical-lytic enzyme; <b>PDBTitle:</b> crystal structure of the bacillus cereus spore cortex-lytic enzyme2 sle1
87	<a href="#">c5cviB_</a>	Alignment	not modelled	9.1	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
88	<a href="#">d1o94c_</a>	Alignment	not modelled	8.9	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
89	<a href="#">d3b48a1</a>	Alignment	not modelled	8.9	10	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> DhaM-like
90	<a href="#">c6aikB_</a>	Alignment	not modelled	8.7	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantothenate--cysteine ligase cab2; <b>PDBTitle:</b> cab2 mutant h337a complex with phosphopantothenoyl-cmp
91	<a href="#">c3ux8A_</a>	Alignment	not modelled	8.5	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc, a subunit; <b>PDBTitle:</b> crystal structure of uvra
92	<a href="#">d3clsc1</a>	Alignment	not modelled	8.3	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
93	<a href="#">c2mc3A_</a>	Alignment	not modelled	8.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mus81 endonuclease homolog (yeast), isoform cra_b; <b>PDBTitle:</b> nmr solution structure of the winged-helix domain from mus812 structure-specific endonuclease
94	<a href="#">c2yyzA_</a>	Alignment	not modelled	8.2	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of sugar abc transporter, atp-binding protein
95	<a href="#">c5d3mA_</a>	Alignment	not modelled	8.2	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
96	<a href="#">c3quaA_</a>	Alignment	not modelled	8.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis
97	<a href="#">c4huqB_</a>	Alignment	not modelled	7.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein ecfA <b>PDBTitle:</b> crystal structure of a transporter
98	<a href="#">c3d31B_</a>	Alignment	not modelled	7.5	4	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding protein; <b>PDBTitle:</b> modbc from methanosarcina acetivorans
99	<a href="#">c4ochA_</a>	Alignment	not modelled	7.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease mutS2; <b>PDBTitle:</b> apo structure of smr domain of mutS2 from deinococcus radiodurans