Phyre2

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Description	P0A6L7
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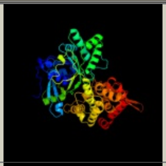
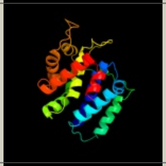
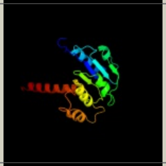
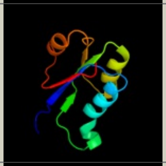
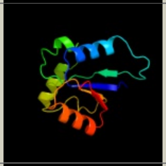
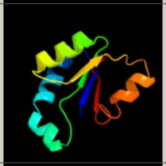
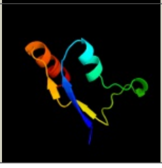
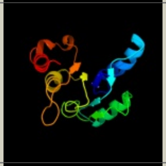
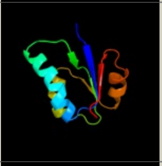
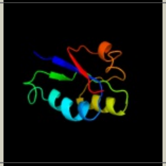
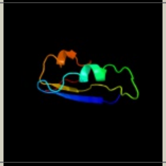
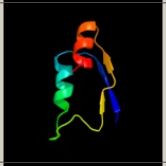
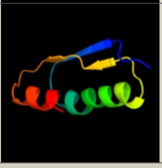
Unique Job ID	6b91f8be9c202a87

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m2wA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol dehydrogenase; **PDBTitle:** pseudomonas fluorescens mannitol 2-dehydrogenase ternary complex with2 nad and d-mannitol
2	c3h2zA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
3	d1lj8a4	Alignment		100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
4	d1lj8a3	Alignment		100.0	25	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Mannitol 2-dehydrogenase
5	c2ph5A_	Alignment		88.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
6	c3ceaA_	Alignment		87.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
7	c3mtjA_	Alignment		83.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
8	c3c7cB_	Alignment		78.2	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
9	c3euwB_	Alignment		77.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
10	c2axqA_	Alignment		66.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
11	c3q2kB_	Alignment		65.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca

12	c3ketA_	Alignment		64.7	15	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
13	c3e18A_	Alignment		60.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
14	c2q4eB_	Alignment		60.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
15	c1e5lA_	Alignment		58.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
16	c3fd8A_	Alignment		57.9	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
17	c3moiA_	Alignment		55.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
18	c3c1aB_	Alignment		50.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
19	c3db2C_	Alignment		48.6	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
20	c1ofgF_	Alignment		45.8	6	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
21	c1evjC_	Alignment	not modelled	45.4	6	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
22	c1zh8B_	Alignment	not modelled	41.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
23	c1h6dL_	Alignment	not modelled	40.8	8	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
24	c3ezyB_	Alignment	not modelled	39.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
25	c3nt5B_	Alignment	not modelled	38.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
26	d1q0qa2	Alignment	not modelled	38.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	d2nvwa1	Alignment	not modelled	38.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	d1zh8a1	Alignment	not modelled	37.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-

						terminal domain
29	d1ydwa1	Alignment	not modelled	36.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
30	d1k4ia_	Alignment	not modelled	36.3	20	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
31	d1gzsb_	Alignment	not modelled	34.9	18	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
32	c2ixaA_	Alignment	not modelled	30.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
33	c3rbvA_	Alignment	not modelled	29.8	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
34	d1snna_	Alignment	not modelled	29.2	29	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
35	d2dt5a2	Alignment	not modelled	27.9	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
36	c1z9bA_	Alignment	not modelled	27.8	11	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
37	c3mioA_	Alignment	not modelled	27.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
38	c3e9mC_	Alignment	not modelled	25.8	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
39	c2dt5A_	Alignment	not modelled	24.6	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
40	c1r0lD_	Alignment	not modelled	23.9	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
41	d1f06a1	Alignment	not modelled	23.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	c3dapB_	Alignment	not modelled	23.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
43	c2eghA_	Alignment	not modelled	22.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
44	d2o8ra3	Alignment	not modelled	22.3	33	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
45	d1yqga2	Alignment	not modelled	21.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
46	c3kuxA_	Alignment	not modelled	21.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
47	c2glxD_	Alignment	not modelled	20.6	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
48	c3ff6D_	Alignment	not modelled	20.5	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** human acc2 ct domain with cp-640186
49	c2ho3D_	Alignment	not modelled	18.8	8	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
50	c2nvwB_	Alignment	not modelled	18.3	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
51	c2o48X_	Alignment	not modelled	16.8	17	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
52	c3ec7C_	Alignment	not modelled	15.7	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase with nad(p)-

53	c3uuwB_	Alignment	not modelled	15.7	11	binding rossmann-fold **PDBTitle:** 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
54	c3updA_	Alignment	not modelled	15.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
55	d1v29a_	Alignment	not modelled	14.4	33	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
56	c1ceuA_	Alignment	not modelled	14.1	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
57	d1im8a_	Alignment	not modelled	13.9	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein HI0319 (YecO)
58	d1ebfa1	Alignment	not modelled	13.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
59	d1tlta1	Alignment	not modelled	13.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	c2ejwB_	Alignment	not modelled	13.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8
61	c3qyhG_	Alignment	not modelled	13.2	29	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
62	d2v0fa1	Alignment	not modelled	13.1	33	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
63	d1ugpa_	Alignment	not modelled	13.0	21	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
64	c3v5nA_	Alignment	not modelled	13.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
65	c3eywA_	Alignment	not modelled	12.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
66	c3btuD_	Alignment	not modelled	11.9	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
67	c3e82A_	Alignment	not modelled	11.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
68	c3m2tA_	Alignment	not modelled	11.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
69	d2qdya1	Alignment	not modelled	11.6	38	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
70	d1p32a_	Alignment	not modelled	11.4	14	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
71	d2py6a1	Alignment	not modelled	11.2	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**FkbM-like
72	c3qv0A_	Alignment	not modelled	11.2	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mitochondrial acidic protein mam33; **PDBTitle:** crystal structure of saccharomyces cerevisiae mam33
73	c3ogiC_	Alignment	not modelled	10.6	26	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative esat-6-like protein 6; **PDBTitle:** crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
74	c3tsuA_	Alignment	not modelled	10.6	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
75	d2atca2	Alignment	not modelled	10.6	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
76	c3gcgB_	Alignment	not modelled	10.5	21	**PDB header:**signaling protein/transcription **Chain:** B: **PDB Molecule:**l0028 (mitochondria associated protein); **PDBTitle:** crystal structure of map and cdc42 complex
77	c3ingA_	Alignment	not modelled	10.2	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
78	c3fggA	Alignment	not modelled	10.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bce2196;

78	c3lggA_	Alignment	not modelled	10.2	18	**PDBTitle:** crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
79	d1ekxa2	Alignment	not modelled	10.0	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
80	c3guzB_	Alignment	not modelled	9.5	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
81	c1iq5B_	Alignment	not modelled	9.4	57	**PDB header:**metal binding protein/protein binding **Chain:** B: **PDB Molecule:**ca2+/calmodulin dependent kinase kinase; **PDBTitle:** calmodulin/nematode ca2+/calmodulin dependent kinase kinase2 fragment
82	d1hcia1	Alignment	not modelled	9.2	19	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
83	d1yqfa1	Alignment	not modelled	9.0	15	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
84	c3jv1A_	Alignment	not modelled	8.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**p22 protein; **PDBTitle:** crystal structure of the trypanosoma brucei p22 protein
85	c2x24B_	Alignment	not modelled	8.6	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** bovine acc2 ct domain in complex with inhibitor
86	c3ip3D_	Alignment	not modelled	8.6	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
87	c3b20R_	Alignment	not modelled	8.5	17	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase (nadp+); **PDBTitle:** crystal structure analysis of dehydrogenase complexed with nad
88	d1mv8a2	Alignment	not modelled	8.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
89	c2dxbR_	Alignment	not modelled	8.1	25	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
90	d1xdpa3	Alignment	not modelled	8.0	50	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
91	c2z8jA_	Alignment	not modelled	7.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of escherichia coli gamma-2 glutamyltranspeptidase in complex with azaserine prepared3 in the dark
92	c2ew2B_	Alignment	not modelled	7.9	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative; **PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
93	c3d1lB_	Alignment	not modelled	7.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
94	d2ouxa1	Alignment	not modelled	7.8	17	**Fold:**alpha-alpha superhelix **Superfamily:**MgtE N-terminal domain-like **Family:**MgtE N-terminal domain-like
95	d1ryda1	Alignment	not modelled	7.8	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	c2jz1A_	Alignment	not modelled	7.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein doublesex; **PDBTitle:** dsx_long
97	d1g7sa3	Alignment	not modelled	7.7	7	**Fold:**Initiation factor IF2/eIF5b, domain 3 **Superfamily:**Initiation factor IF2/eIF5b, domain 3 **Family:**Initiation factor IF2/eIF5b, domain 3
98	c3pu6A_	Alignment	not modelled	7.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
99	d1ebda2	Alignment	not modelled	7.7	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains