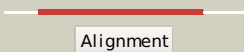

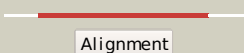

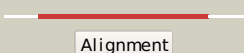

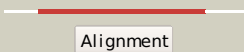

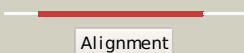

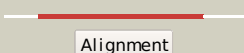

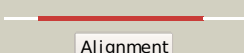

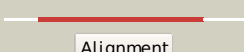

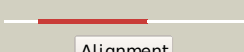

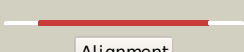

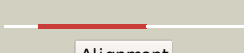












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2vawA_</a>	 Alignment		100.0	67	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz pseudomonas aeruginosa gdp
2	<a href="#">c1w59B_</a>	 Alignment		100.0	44	<b>PDB header:</b> cell division <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz homolog 1; <b>PDBTitle:</b> ftsz dimer, empty (m. jannaschii)
3	<a href="#">c2r6r1_</a>	 Alignment		100.0	46	<b>PDB header:</b> cell cycle <b>Chain:</b> 1: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> aquifex aeolicus ftsz
4	<a href="#">c1w5fA_</a>	 Alignment		100.0	47	<b>PDB header:</b> cell division <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz, t7 mutated, domain swapped (t. maritima)
5	<a href="#">c1ofuB_</a>	 Alignment		100.0	68	<b>PDB header:</b> bacterial cell division inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> crystal structure of sula:fts from pseudomonas aeruginosa
6	<a href="#">c2vxyA_</a>	 Alignment		100.0	54	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> the structure of ftsz from bacillus subtilis at 1.7a2 resolution
7	<a href="#">c2rhoB_</a>	 Alignment		100.0	54	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
8	<a href="#">c2q1yB_</a>	 Alignment		100.0	54	<b>PDB header:</b> cell cycle, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
9	<a href="#">d2vapa1</a>	 Alignment		100.0	48	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
10	<a href="#">c3m8kA_</a>	 Alignment		100.0	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> ftsztubulin-related protein; <b>PDBTitle:</b> protein structure of type iii plasmid segregation tubz
11	<a href="#">d1ofua1</a>	 Alignment		100.0	68	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain

12	<a href="#">d1rq2a1</a>	Alignment		100.0	56	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
13	<a href="#">d1w5fa1</a>	Alignment		100.0	54	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
14	<a href="#">d2vapa2</a>	Alignment		100.0	40	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
15	<a href="#">d1w5fa2</a>	Alignment		100.0	35	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
16	<a href="#">d1ofua2</a>	Alignment		100.0	69	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
17	<a href="#">d1rq2a2</a>	Alignment		100.0	47	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> Tubulin C-terminal domain-like <b>Family:</b> Tubulin, C-terminal domain
18	<a href="#">c3edlA</a>	Alignment		99.7	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-tubulin; <b>PDBTitle:</b> kinesin13-microtubule ring complex
19	<a href="#">c1z5wA</a>	Alignment		99.7	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin gamma-1 chain; <b>PDBTitle:</b> crystal structure of gamma-tubulin bound to gtp
20	<a href="#">c2btqB</a>	Alignment		99.6	19	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> tubulin btubb; <b>PDBTitle:</b> structure of btubb heterodimer from prosthecobacter2 dejongei
21	<a href="#">c2p4nB</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> tubulin beta chain; <b>PDBTitle:</b> human monomeric kinesin (1bg2) and bovine tubulin (1jff)2 docked into the 9-angstrom cryo-em map of nucleotide-free3 complexed to the microtubule
22	<a href="#">c2btoA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> cytoskeletal protein <b>Chain:</b> A: <b>PDB Molecule:</b> tubulin btuba; <b>PDBTitle:</b> structure of btuba from prosthecobacter dejongei
23	<a href="#">d1tubb1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
24	<a href="#">d1tuba1</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
25	<a href="#">d2btoa1</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
26	<a href="#">c1ez4B</a>	Alignment	not modelled	97.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
27	<a href="#">d1i10a1</a>	Alignment	not modelled	97.1	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
28	<a href="#">c1ldbA</a>	Alignment	not modelled	97.1	25	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase

29	<a href="#">d1ldna1</a>	Alignment	not modelled	97.0	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
30	<a href="#">c2v65A</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase a chain; <b>PDBTitle:</b> apo ldh from the psychrophile c. gunnari
31	<a href="#">d1llda1</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
32	<a href="#">c3d0oA</a>	Alignment	not modelled	97.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from2 staphylococcus aureus
33	<a href="#">c1lldA</a>	Alignment	not modelled	96.9	24	<b>PDB header:</b> oxidoreductase(choh (d)-nad (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
34	<a href="#">d1i0za1</a>	Alignment	not modelled	96.8	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
35	<a href="#">d1ldma1</a>	Alignment	not modelled	96.8	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
36	<a href="#">c3pqeD</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
37	<a href="#">d1u8xx1</a>	Alignment	not modelled	96.7	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
38	<a href="#">c3prjB</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
39	<a href="#">c1pzfD</a>	Alignment	not modelled	96.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> t.gondii ldh1 ternary complex with apad+ and oxalate
40	<a href="#">c2ldxA</a>	Alignment	not modelled	96.6	23	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-lactate dehydrogenase; <b>PDBTitle:</b> characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
41	<a href="#">d9ldta1</a>	Alignment	not modelled	96.5	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
42	<a href="#">c1a5zA</a>	Alignment	not modelled	96.5	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> lactate dehydrogenase from thermotoga maritima (tml dh)
43	<a href="#">c1ojuA</a>	Alignment	not modelled	96.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
44	<a href="#">c2e37B</a>	Alignment	not modelled	96.4	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> structure of tt0471 protein from thermus thermophilus
45	<a href="#">c1hyhA</a>	Alignment	not modelled	96.4	24	<b>PDB header:</b> oxidoreductase (choh(d)-nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
46	<a href="#">d1pzga1</a>	Alignment	not modelled	96.4	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
47	<a href="#">c1y6jA</a>	Alignment	not modelled	96.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> l-lactate dehydrogenase from clostridium thermocellum cth-1135
48	<a href="#">c1u4sA</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
49	<a href="#">d2ldxa1</a>	Alignment	not modelled	96.2	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
50	<a href="#">d1up7a1</a>	Alignment	not modelled	96.2	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
51	<a href="#">c8ldhA</a>	Alignment	not modelled	96.2	22	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
52	<a href="#">c3fefB</a>	Alignment	not modelled	96.1	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glucosidase lpld; <b>PDBTitle:</b> crystal structure of putative glucosidase lpld from2 bacillus subtilis
53	<a href="#">c3dl2A</a>	Alignment	not modelled	96.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 variant 3; <b>PDBTitle:</b> hexagonal structure of the ldh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
54	<a href="#">c3p7mC</a>	Alignment	not modelled	95.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4

55	<a href="#">d1ojua1</a>	Alignment	not modelled	95.9	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
56	<a href="#">c1hygA</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate/malate dehydrogenase; <b>PDBTitle:</b> crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
57	<a href="#">c2hjrK</a>	Alignment	not modelled	95.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum malate2 dehydrogenase
58	<a href="#">d1a5za1</a>	Alignment	not modelled	95.8	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
59	<a href="#">d2cmda1</a>	Alignment	not modelled	95.8	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
60	<a href="#">d1y6ja1</a>	Alignment	not modelled	95.7	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
61	<a href="#">c1obbB</a>	Alignment	not modelled	95.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
62	<a href="#">c2v6bB</a>	Alignment	not modelled	95.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
63	<a href="#">c2dfdD</a>	Alignment	not modelled	95.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of human malate dehydrogenase type 2
64	<a href="#">c3gucB</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 5; <b>PDBTitle:</b> human ubiquitin-activating enzyme 5 in complex with amppnp
65	<a href="#">c3h9gA</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> mccb protein; <b>PDBTitle:</b> crystal structure of e. coli mccb + mcca-n7isoasn
66	<a href="#">d1obba1</a>	Alignment	not modelled	95.6	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
67	<a href="#">c3gviB</a>	Alignment	not modelled	95.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
68	<a href="#">d1s6ya1</a>	Alignment	not modelled	95.5	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
69	<a href="#">c2pwzG</a>	Alignment	not modelled	95.4	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo form of e.coli malate dehydrogenase
70	<a href="#">c1u8xX</a>	Alignment	not modelled	95.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> maltose-6'-phosphate glucosidase; <b>PDBTitle:</b> crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
71	<a href="#">c3nepX</a>	Alignment	not modelled	95.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
72	<a href="#">d5ldha1</a>	Alignment	not modelled	95.2	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
73	<a href="#">d1hyha1</a>	Alignment	not modelled	95.2	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
74	<a href="#">d1gv0a1</a>	Alignment	not modelled	95.1	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
75	<a href="#">c1smkD</a>	Alignment	not modelled	95.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal; <b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
76	<a href="#">c1sevA</a>	Alignment	not modelled	95.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal precursor; <b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
77	<a href="#">c1up6F</a>	Alignment	not modelled	95.1	31	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> structure of the 6-phospho-beta glucosidase from thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal form3 with manganese, nad+ and glucose-6-phosphate
78	<a href="#">d7mdha1</a>	Alignment	not modelled	95.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
79	<a href="#">c3ic5A</a>	Alignment	not modelled	94.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
80	<a href="#">c1ev1D</a>	Alignment	not modelled	94.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase;

80	<a href="#">c1qv1D_</a>	Alignment	not modelled	94.9	23	<b>PDBTitle:</b> structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
81	<a href="#">d1y7ta1</a>	Alignment	not modelled	94.8	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
82	<a href="#">c1s6yA_</a>	Alignment	not modelled	94.8	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> 2.3a crystal structure of phospho-beta-glucosidase
83	<a href="#">d1guza1</a>	Alignment	not modelled	94.8	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
84	<a href="#">c2fnzA_</a>	Alignment	not modelled	94.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
85	<a href="#">c1ur5C_</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface
86	<a href="#">c1mldA_</a>	Alignment	not modelled	94.7	25	<b>PDB header:</b> oxidoreductase(nad(a)-choh(d)) <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
87	<a href="#">c1llcA_</a>	Alignment	not modelled	94.6	23	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution
88	<a href="#">d1jw9b_</a>	Alignment	not modelled	94.5	17	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Molybdenum cofactor biosynthesis protein MoeB
89	<a href="#">d1luxa1</a>	Alignment	not modelled	94.3	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
90	<a href="#">c3triB_</a>	Alignment	not modelled	94.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
91	<a href="#">d1o6za1</a>	Alignment	not modelled	94.2	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
92	<a href="#">c1b8vA_</a>	Alignment	not modelled	94.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> malate dehydrogenase from aquaspirillum arcticum
93	<a href="#">d1p3da1</a>	Alignment	not modelled	94.2	29	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
94	<a href="#">c3tt2A_</a>	Alignment	not modelled	93.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
95	<a href="#">c5mdhB_</a>	Alignment	not modelled	93.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution
96	<a href="#">c2nvuB_</a>	Alignment	not modelled	93.8	19	<b>PDB header:</b> protein turnover, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein/nedd8-activating enzyme <b>PDBTitle:</b> structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
97	<a href="#">d1ez4a1</a>	Alignment	not modelled	93.7	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
98	<a href="#">d1llca1</a>	Alignment	not modelled	93.6	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
99	<a href="#">c1y8qA_</a>	Alignment	not modelled	93.6	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like 1 activating enzyme e1a; <b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex
100	<a href="#">d1t2da1</a>	Alignment	not modelled	93.5	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
101	<a href="#">d1tk9a_</a>	Alignment	not modelled	93.4	20	<b>Fold:</b> SIS domain <b>Superfamily:</b> SIS domain <b>Family:</b> mono-SIS domain
102	<a href="#">c2axqA_</a>	Alignment	not modelled	93.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
103	<a href="#">c3kydB_</a>	Alignment	not modelled	93.2	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> sumo-activating enzyme subunit 2; <b>PDBTitle:</b> human sumo e1~sumo1-amp tetrahedral intermediate mimic
104	<a href="#">c1wziA_</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
105	<a href="#">d5mdha1</a>	Alignment	not modelled	93.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like



106	<a href="#">c2x3yA_</a>	Alignment	not modelled	93.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> crystal structure of gmha from burkholderia pseudomallei
107	<a href="#">c1txgA_</a>	Alignment	not modelled	93.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
108	<a href="#">c1y8qD_</a>	Alignment	not modelled	92.7	16	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like 2 activating enzyme e1b; <b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex
109	<a href="#">d1j6ua1</a>	Alignment	not modelled	92.6	16	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
110	<a href="#">d2jfga1</a>	Alignment	not modelled	92.6	24	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
111	<a href="#">c2q3eH_</a>	Alignment	not modelled	92.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
112	<a href="#">c1e5lA_</a>	Alignment	not modelled	92.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
113	<a href="#">c7mdhA_</a>	Alignment	not modelled	92.2	23	<b>PDB header:</b> chloroplastic malate dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> structural basis for light activation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
114	<a href="#">c2yvaB_</a>	Alignment	not modelled	92.0	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dnaa initiator-associating protein diaa; <b>PDBTitle:</b> crystal structure of escherichia coli diaa
115	<a href="#">d1pjqa1</a>	Alignment	not modelled	92.0	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
116	<a href="#">d1e5qa1</a>	Alignment	not modelled	91.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
117	<a href="#">d2hjsa1</a>	Alignment	not modelled	91.3	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
118	<a href="#">c1zfnA_</a>	Alignment	not modelled	91.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenyllyltransferase thif; <b>PDBTitle:</b> structural analysis of escherichia coli thif
119	<a href="#">d1b8pa1</a>	Alignment	not modelled	90.5	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
120	<a href="#">d1txga2</a>	Alignment	not modelled	90.3	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain