Phyre^2

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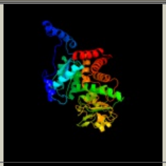
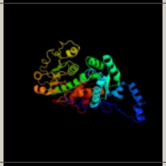
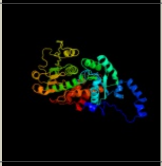
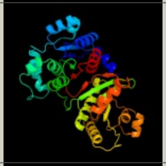
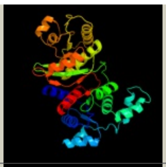
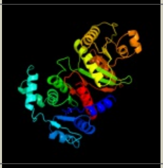
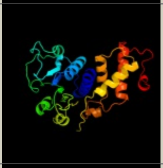
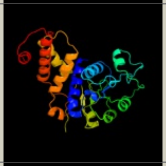
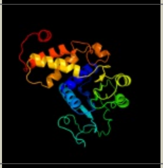
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ww8A_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate oxidoreductase; **PDBTitle:** crystal structure of malic enzyme from pyrococcus2 horikoshii ot3
2	c2a9fB_	Alignment		100.0	48	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative malic enzyme ((s)-malate:nad+ **PDBTitle:** crystal structure of a putative malic enzyme ((s)-2 malate:nad+ oxidoreductase (decarboxylating))
3	c3nv9A_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme; **PDBTitle:** crystal structure of entamoeba histolytica malic enzyme
4	c1vl6C_	Alignment		100.0	47	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate oxidoreductase; **PDBTitle:** crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
5	c1gz3B_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate
6	c1qr6A_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malic enzyme 2; **PDBTitle:** human mitochondrial nad(p)-dependent malic enzyme
7	c2aw5A_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp-dependent malic enzyme; **PDBTitle:** crystal structure of a human malic enzyme
8	c1o0sB_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent malic enzyme; **PDBTitle:** crystal structure of ascaris suum malic enzyme complexed with nadh
9	c1vmiA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphate acetyltransferase; **PDBTitle:** crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
10	d1vmia_	Alignment		100.0	33	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
11	d1xcoa_	Alignment		100.0	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase

12	d1r5ja_	Alignment		100.0	28	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
13	d2af4c1	Alignment		100.0	29	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
14	d1o0sa1	Alignment		100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
15	d1gq2a1	Alignment		100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
16	d1pj3a1	Alignment		100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
17	d1vl6a1	Alignment		100.0	43	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
18	c3tngA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lmo1369 protein; **PDBTitle:** the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
19	c1ycoA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**branched-chain phosphotransacylase; **PDBTitle:** crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
20	d1vl6a2	Alignment		100.0	53	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
21	d1pj3a2	Alignment	not modelled	100.0	32	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
22	d1gq2a2	Alignment	not modelled	100.0	31	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
23	d1vi1a_	Alignment	not modelled	100.0	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
24	d1o0sa2	Alignment	not modelled	100.0	27	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Malic enzyme N-domain
25	d1u7na_	Alignment	not modelled	100.0	23	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
26	d1ptma_	Alignment	not modelled	99.8	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
27	c1yxoB_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
28	d1r8ka_	Alignment	not modelled	99.4	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
						Fold:NAD(P)-binding Rossmann-fold domains

29	d1euza1	Alignment	not modelled	98.9	19	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
30	d1li4a1	Alignment	not modelled	98.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
31	c2hi1A_	Alignment	not modelled	98.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
32	d1v9la1	Alignment	not modelled	98.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
33	c3tozA_	Alignment	not modelled	98.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
34	c3d4oA_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
35	c2rirA_	Alignment	not modelled	98.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
36	d1v8ba1	Alignment	not modelled	98.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
37	c3dhyC_	Alignment	not modelled	98.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
38	c3gvpB_	Alignment	not modelled	98.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
39	c3n58D_	Alignment	not modelled	97.9	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
40	c3aoeC_	Alignment	not modelled	97.9	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
41	c1v8bA_	Alignment	not modelled	97.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
42	c1d4fD_	Alignment	not modelled	97.9	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
43	c3d64A_	Alignment	not modelled	97.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
44	c3oneA_	Alignment	not modelled	97.8	19	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
45	d1bvua1	Alignment	not modelled	97.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
46	d1vi2a1	Alignment	not modelled	97.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
47	c3aogA_	Alignment	not modelled	97.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
48	d1l7da1	Alignment	not modelled	97.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
49	c1gpjA_	Alignment	not modelled	97.7	21	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
50	c1v9lA_	Alignment	not modelled	97.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
51	d1b26a1	Alignment	not modelled	97.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
52	d1gpja2	Alignment	not modelled	97.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
53	c2bmaA_	Alignment	not modelled	97.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase (nadp+); **PDBTitle:** the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
54	d1gtma1	Alignment	not modelled	97.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain

55	c3k8zD_	Alignment	not modelled	97.5	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
56	c1bvuF_	Alignment	not modelled	97.4	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis
57	d1t2da1	Alignment	not modelled	97.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
58	d1hwxa1	Alignment	not modelled	97.3	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
59	d1bgva1	Alignment	not modelled	97.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
60	c1j4aA_	Alignment	not modelled	97.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
61	c2tmgD_	Alignment	not modelled	97.2	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
62	c3l07B_	Alignment	not modelled	97.2	21	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
63	d1pjca1	Alignment	not modelled	97.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
64	c2eklA_	Alignment	not modelled	97.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
65	c2j6iC_	Alignment	not modelled	97.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
66	c3p2yA_	Alignment	not modelled	96.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
67	d1ygya1	Alignment	not modelled	96.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
68	d1nyta1	Alignment	not modelled	96.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
69	c2eezG_	Alignment	not modelled	96.9	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
70	c1wwkA_	Alignment	not modelled	96.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
71	d1uxja1	Alignment	not modelled	96.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
72	d1a4ia1	Alignment	not modelled	96.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
73	c1bxgA_	Alignment	not modelled	96.8	20	**PDB header:**amino acid dehydrogenase **Chain:** A: **PDB Molecule:**phenylalanine dehydrogenase; **PDBTitle:** phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
74	d1gdha1	Alignment	not modelled	96.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
75	c3o8qB_	Alignment	not modelled	96.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
76	c1pjcA_	Alignment	not modelled	96.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
77	c4a5oB_	Alignment	not modelled	96.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
78	c3donA_	Alignment	not modelled	96.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
79	c1a4iB_	Alignment	not modelled	96.7	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
80	c3pgjB_	Alignment	not modelled	96.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str.

						n169613 in complex with shikimate
81	c2dbqA_	Alignment	not modelled	96.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
82	c3evtA_	Alignment	not modelled	96.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
83	d1b0aa1	Alignment	not modelled	96.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
84	c1p74B_	Alignment	not modelled	96.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
85	c3p2oB_	Alignment	not modelled	96.6	19	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
86	c1hrdA_	Alignment	not modelled	96.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** glutamate dehydrogenase
87	d1llda1	Alignment	not modelled	96.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
88	c2cukC_	Alignment	not modelled	96.5	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
89	c3p2oA_	Alignment	not modelled	96.5	19	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
90	d1pzga1	Alignment	not modelled	96.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
91	c1gdhA_	Alignment	not modelled	96.5	19	**PDB header:**oxidoreductase(choh (d)-nad(p)+ (a)) **Chain:** A: **PDB Molecule:**d-glycerate dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
92	c4a26B_	Alignment	not modelled	96.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
93	d2naca1	Alignment	not modelled	96.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
94	c2d0iC_	Alignment	not modelled	96.4	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
95	d1mx3a1	Alignment	not modelled	96.4	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
96	c2gcgB_	Alignment	not modelled	96.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
97	c2yfqA_	Alignment	not modelled	96.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
98	d1ez4a1	Alignment	not modelled	96.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
99	c3u62A_	Alignment	not modelled	96.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima
100	d1leha1	Alignment	not modelled	96.3	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
101	c1pzfD_	Alignment	not modelled	96.3	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** t.gondii ldh1 ternary complex with apad+ and oxalate
102	c1lehB_	Alignment	not modelled	96.2	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**leucine dehydrogenase; **PDBTitle:** leucine dehydrogenase from bacillus sphaericus
103	c3kboB_	Alignment	not modelled	96.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate/hydroxypyruvate reductase a; **PDBTitle:** 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
104	c3hg7A_	Alignment	not modelled	96.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-isomer specific 2-hydroxyacid dehydrogenase family **PDBTitle:** crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
105	c1l7eC_	Alignment	not modelled	96.1	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinamide nucleotide transhydrogenase,

							PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
106	c3oj0A_		Alignment	not modelled	96.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
107	c1b0aA_		Alignment	not modelled	96.1	17	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
108	c3fefB_		Alignment	not modelled	96.1	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
109	d1u8xx1		Alignment	not modelled	96.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
110	d1qp8a1		Alignment	not modelled	96.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
111	c2g76A_		Alignment	not modelled	96.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
112	c1vi2B_		Alignment	not modelled	96.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
113	c1xdwA_		Alignment	not modelled	96.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
114	c2fnzA_		Alignment	not modelled	96.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
115	c1nr1A_		Alignment	not modelled	96.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase 1; **PDBTitle:** crystal structure of the r463a mutant of human glutamate2 dehydrogenase
116	c1ur5C_		Alignment	not modelled	95.9	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface
117	c3oetF_		Alignment	not modelled	95.9	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
118	c2o4cB_		Alignment	not modelled	95.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
119	d9ldta1		Alignment	not modelled	95.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
120	c3n7uD_		Alignment	not modelled	95.7	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide