Phyre2

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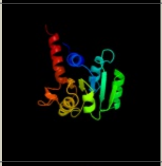
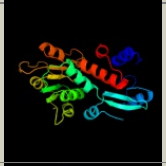
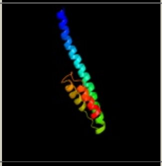
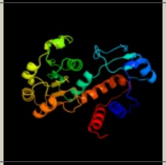
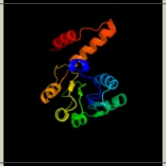
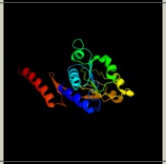
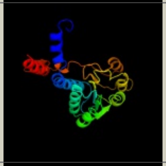
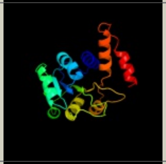
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gpjA_	Alignment		100.0	34	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
2	d1gpja3	Alignment		100.0	37	**Fold:**Ferredoxin-like **Superfamily:**Glutamyl tRNA-reductase catalytic, N-terminal domain **Family:**Glutamyl tRNA-reductase catalytic, N-terminal domain
3	d1gpja2	Alignment		100.0	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
4	c3oj0A_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
5	c1luaA_	Alignment		99.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methylene tetrahydromethanopterin dehydrogenase; **PDBTitle:** structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
6	c3pgjB_	Alignment		99.8	18	**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
7	c2nloA_	Alignment		99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
8	d1gpja1	Alignment		99.7	15	**Fold:**Glutamyl tRNA-reductase dimerization domain **Superfamily:**Glutamyl tRNA-reductase dimerization domain **Family:**Glutamyl tRNA-reductase dimerization domain
9	c3donA_	Alignment		99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
10	c2eggA_	Alignment		99.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
11	c3gvpB_	Alignment		99.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3

12	c1lehB_	Alignment		99.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**leucine dehydrogenase; **PDBTitle:** leucine dehydrogenase from bacillus sphaericus
13	c3o8qB_	Alignment		99.6	18	**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
14	d1nvta1	Alignment		99.6	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
15	c2rirA_	Alignment		99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
16	c2i99A_	Alignment		99.5	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mu-crystallin homolog; **PDBTitle:** crystal structure of human mu_crystallin at 2.6 angstrom
17	d1l7da1	Alignment		99.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
18	c3d4oA_	Alignment		99.5	17	**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
19	d1nyta1	Alignment		99.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
20	d1npya1	Alignment		99.4	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
21	d1vi2a1	Alignment	not modelled	99.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
22	d1pjca1	Alignment	not modelled	99.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
23	d1p77a1	Alignment	not modelled	99.4	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
24	d1x7da_	Alignment	not modelled	99.4	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Ornithine cyclodeaminase-like
25	c3pwzA_	Alignment	not modelled	99.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
26	c2eezG_	Alignment	not modelled	99.3	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
27	c2hk8B_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
28	d1omoa_	Alignment	not modelled	99.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Ornithine cyclodeaminase-like
29	c1nytA_	Alignment	not modelled	99.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5'-dehydrogenase;

29	c1nvtA_	Alignment	not modelled	99.3	25	**PDBTitle:** crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
30	c3u62A_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima
31	c1p74B_	Alignment	not modelled	99.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
32	c3tozA_	Alignment	not modelled	99.2	14	**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.
33	c1nytC_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** shikimate dehydrogenase aroe complexed with nadp+
34	c3dfzB_	Alignment	not modelled	99.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
35	c3hdjA_	Alignment	not modelled	99.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable ornithine cyclodeaminase; **PDBTitle:** the crystal structure of probable ornithine cyclodeaminase from2 bordetella pertussis tohama i
36	c1npyA_	Alignment	not modelled	99.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
37	c2o7qA_	Alignment	not modelled	99.1	26	**PDB header:**oxidoreductase,transferase **Chain:** A: **PDB Molecule:**bifunctional 3-dehydroquinate dehydratase/shikimate **PDBTitle:** crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
38	c2ev9B_	Alignment	not modelled	99.1	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
39	c1vi2B_	Alignment	not modelled	99.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
40	c3p2yA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
41	c1d4fD_	Alignment	not modelled	99.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
42	c4a26B_	Alignment	not modelled	99.0	18	**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
43	c2bruB_	Alignment	not modelled	99.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase subunit alpha; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
44	c3fbtB_	Alignment	not modelled	98.9	16	**PDB header:**oxidoreductase, lyase **Chain:** B: **PDB Molecule:**chorismate mutase and shikimate 5-dehydrogenase **PDBTitle:** crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
45	d1li4a1	Alignment	not modelled	98.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
46	d1a4ia1	Alignment	not modelled	98.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
47	c1pjcA_	Alignment	not modelled	98.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
48	d1leha1	Alignment	not modelled	98.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
49	c2axqA_	Alignment	not modelled	98.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
50	c1l7eC_	Alignment	not modelled	98.8	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinamide nucleotide transhydrogenase, **PDBTitle:** crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
51	c3n58D_	Alignment	not modelled	98.8	16	**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
52	c3l07B_	Alignment	not modelled	98.8	22	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
53	d1b0aa1	Alignment	not modelled	98.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Aminoacid dehydrogenase-like, C-terminal domain
54	c1v8bA_	Alignment	not modelled	98.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
55	c1e5lA_	Alignment	not modelled	98.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
56	c3dhyC_	Alignment	not modelled	98.7	16	**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
57	c3oneA_	Alignment	not modelled	98.7	20	**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
58	c1np3B_	Alignment	not modelled	98.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
59	c3triB_	Alignment	not modelled	98.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
60	d1v8ba1	Alignment	not modelled	98.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
61	c3d64A_	Alignment	not modelled	98.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
62	c3d1lB_	Alignment	not modelled	98.6	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
63	c4a5oB_	Alignment	not modelled	98.6	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
64	c1a4iB_	Alignment	not modelled	98.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
65	d1pjqa1	Alignment	not modelled	98.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
66	c3b1fA_	Alignment	not modelled	98.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans
67	c3cumA_	Alignment	not modelled	98.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
68	c3gt0A_	Alignment	not modelled	98.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
69	d1e5qa1	Alignment	not modelled	98.6	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	c3p2oB_	Alignment	not modelled	98.6	21	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
71	d1luaa1	Alignment	not modelled	98.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
72	c2f1kD_	Alignment	not modelled	98.6	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
73	c2g5cD_	Alignment	not modelled	98.6	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
74	c3p2oA_	Alignment	not modelled	98.6	21	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
75	c2ag8A_	Alignment	not modelled	98.5	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
76	d1gdha1	Alignment	not modelled	98.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
77	d1mx3a1	Alignment	not modelled	98.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
78	c2g76A_	Alignment	not modelled	98.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase

79	d1ygya1	Alignment	not modelled	98.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
80	c2ahrB_	Alignment	not modelled	98.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative pyrroline carboxylate reductase; **PDBTitle:** crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
81	c3dttA_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp oxidoreductase; **PDBTitle:** crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
82	d1c1da1	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
83	d2naca1	Alignment	not modelled	98.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
84	c2c2xB_	Alignment	not modelled	98.5	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
85	c1vpdA_	Alignment	not modelled	98.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
86	d1uxja1	Alignment	not modelled	98.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
87	c3dzbA_	Alignment	not modelled	98.5	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
88	c2eklA_	Alignment	not modelled	98.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
89	c3fwnB_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
90	d1np3a2	Alignment	not modelled	98.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
91	c1b0aA_	Alignment	not modelled	98.5	14	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
92	c3g0oA_	Alignment	not modelled	98.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
93	c3l6dB_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
94	d1bg6a2	Alignment	not modelled	98.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
95	c1gdhA_	Alignment	not modelled	98.4	16	**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
96	d1jaya_	Alignment	not modelled	98.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
97	c1wwkA_	Alignment	not modelled	98.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
98	c2iz1C_	Alignment	not modelled	98.4	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
99	c2uyyD_	Alignment	not modelled	98.4	16	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
100	c2vhyB_	Alignment	not modelled	98.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
101	d1yqga2	Alignment	not modelled	98.4	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
102	c3ggpA_	Alignment	not modelled	98.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
103	c1bxgA_	Alignment	not modelled	98.4	15	**PDB header:**amino acid dehydrogenase **Chain:** A: **PDB Molecule:**phenylalanine dehydrogenase; **PDBTitle:** phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate

104	d2pgda2	Alignment	not modelled	98.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
105	c3n7uD_	Alignment	not modelled	98.4	20	**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
106	d3cuma2	Alignment	not modelled	98.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
107	c2d0iC_	Alignment	not modelled	98.4	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
108	d1j4aa1	Alignment	not modelled	98.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
109	c1pgjA_	Alignment	not modelled	98.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
110	c2cvzD_	Alignment	not modelled	98.4	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
111	c1bg6A_	Alignment	not modelled	98.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; **PDBTitle:** crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
112	c3ktdC_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
113	c1edzA_	Alignment	not modelled	98.4	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate dehydrogenase; **PDBTitle:** structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
114	c2dbqA_	Alignment	not modelled	98.4	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)
115	d2dlda1	Alignment	not modelled	98.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
116	c2j6iC_	Alignment	not modelled	98.4	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
117	c3c24A_	Alignment	not modelled	98.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
118	d1dxya1	Alignment	not modelled	98.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
119	d2ahra2	Alignment	not modelled	98.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
120	c3gg9C_	Alignment	not modelled	98.3	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase oxidoreductase protein; **PDBTitle:** crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum