Phyre^2

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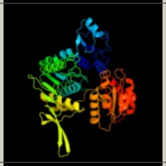
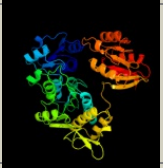
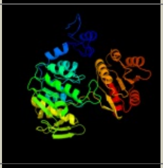
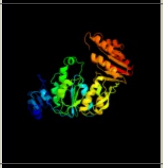
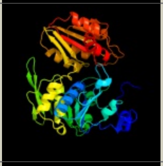
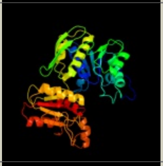
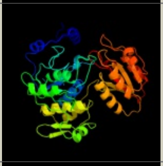
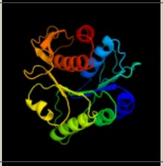
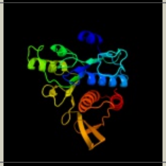
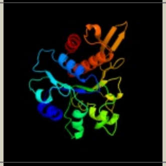
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f00A_	Alignment		100.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
2	c3hn7A_	Alignment		100.0	49	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
3	c1j6uA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
4	c1gqqA_	Alignment		100.0	26	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae
5	c3uagA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (udp-n-acetylmuramoyl-l-alanine:d- **PDBTitle:** udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
6	c3lk7A_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine--d-glutamate ligase; **PDBTitle:** the crystal structure of udp-n-acetylmuramoylalanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
7	c3eagA_	Alignment		100.0	59	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- **PDBTitle:** the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
8	c2am1A_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- **PDBTitle:** sp protein ligand 1
9	c1e8cB_	Alignment		100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamate--2,6- **PDBTitle:** structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
10	c1gg4A_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamyl-2,6- **PDBTitle:** crystal structure of escherichia coli udpmurnac-tripeptide2 d-alanyl-d-alanine-adding enzyme (murf) at 2.3 angstrom3 resolution
11	c2wtzC_	Alignment		100.0	24	**PDB header:**ligase **Chain:** C: **PDB Molecule:**udp-n-acetylmuramoyl-l-alanyl-d-glutamate- **PDBTitle:** mure ligase of mycobacterium tuberculosis

12	c2vosA_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
13	c1w78A_	Alignment		100.0	18	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
14	c2gc6A_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase; **PDBTitle:** s73a mutant of l. casei fpgs
15	c1o5zA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
16	c3n2aA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bifunctional folylpolyglutamate synthase/dihydrofolate **PDBTitle:** crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
17	d1p3da3	Alignment		100.0	29	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
18	d1j6ua3	Alignment		100.0	21	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
19	d2jfga3	Alignment		100.0	16	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
20	d2gc6a2	Alignment		100.0	15	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
21	d1e8ca3	Alignment	not modelled	100.0	18	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
22	d1gg4a4	Alignment	not modelled	100.0	22	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
23	d1o5za2	Alignment	not modelled	100.0	17	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
24	d1p3da2	Alignment	not modelled	99.9	25	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
25	d1j6ua1	Alignment	not modelled	99.8	28	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
26	c3mvnA_	Alignment	not modelled	99.8	55	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
27	d1p3da1	Alignment	not modelled	99.8	26	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
28	d1j6ua2	Alignment	not modelled	99.8	18	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain

29	d2jfga2	Alignment	not modelled	99.7	18	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
30	d1e8ca2	Alignment	not modelled	99.7	19	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
31	d1gg4a1	Alignment	not modelled	99.7	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
32	d2jfga1	Alignment	not modelled	99.7	16	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
33	d1o5za1	Alignment	not modelled	99.4	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
34	d2gc6a1	Alignment	not modelled	99.3	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
35	d1pjqa1	Alignment	not modelled	98.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
36	c3gg2B_	Alignment	not modelled	98.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose **PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
37	c1mv8A_	Alignment	not modelled	98.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gdp-mannose 6-dehydrogenase; **PDBTitle:** 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
38	c2y0dB_	Alignment	not modelled	98.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
39	c1i36A_	Alignment	not modelled	98.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth1747; **PDBTitle:** structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
40	d1i36a2	Alignment	not modelled	97.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
41	c3l6dB_	Alignment	not modelled	97.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
42	c3g0oA_	Alignment	not modelled	97.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
43	c2o3jC_	Alignment	not modelled	97.9	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase
44	d1mv8a2	Alignment	not modelled	97.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
45	c2f1kD_	Alignment	not modelled	97.8	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
46	c3qhaB_	Alignment	not modelled	97.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
47	c3ckyA_	Alignment	not modelled	97.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-hydroxymethyl glutarate dehydrogenase; **PDBTitle:** structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
48	c3d1lB_	Alignment	not modelled	97.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
49	c3d4oA_	Alignment	not modelled	97.8	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
50	c3plnA_	Alignment	not modelled	97.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
51	c1dliA_	Alignment	not modelled	97.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
52	c3cumA_	Alignment	not modelled	97.7	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
53	c2hk8B_	Alignment	not modelled	97.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
						PDB header:oxidoreductase

54	c3ojlA_	Alignment	not modelled	97.7	16	**Chain:** A: **PDB Molecule:**cap5o; **PDBTitle:** native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
55	c2izzE_	Alignment	not modelled	97.7	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyrroline-5-carboxylate reductase 1; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate2 reductase
56	c3ic5A_	Alignment	not modelled	97.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
57	d2f1ka2	Alignment	not modelled	97.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
58	c1vpdA_	Alignment	not modelled	97.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
59	d1vpda2	Alignment	not modelled	97.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
60	c2graA_	Alignment	not modelled	97.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase 1; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
61	c3ghyA_	Alignment	not modelled	97.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
62	c2q3eH_	Alignment	not modelled	97.5	12	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
63	c3prjB_	Alignment	not modelled	97.5	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
64	c3hn2A_	Alignment	not modelled	97.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
65	d1txga2	Alignment	not modelled	97.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
66	c2g5cD_	Alignment	not modelled	97.5	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
67	c3dojA_	Alignment	not modelled	97.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
68	d2ahra2	Alignment	not modelled	97.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
69	d1dlja2	Alignment	not modelled	97.5	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
70	c2uyyD_	Alignment	not modelled	97.4	19	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
71	c3ggpA_	Alignment	not modelled	97.4	15	**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+
72	c2ev9B_	Alignment	not modelled	97.4	18	**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
73	c3fwnB_	Alignment	not modelled	97.4	13	**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
74	c1xeaD_	Alignment	not modelled	97.4	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
75	d1uxja1	Alignment	not modelled	97.4	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
76	d1e5qa1	Alignment	not modelled	97.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	c1pgjA_	Alignment	not modelled	97.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
78	c3rbvA_	Alignment	not modelled	97.4	15	**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
						PDB header:oxidoreductase

79	c2gf2B_	Alignment	not modelled	97.3	16	**Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
80	c1nytC_	Alignment	not modelled	97.3	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** shikimate dehydrogenase aroe complexed with nadp+
81	d1nyta1	Alignment	not modelled	97.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
82	c2ahrB_	Alignment	not modelled	97.3	24	**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
83	c2rirA_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
84	c1e5lA_	Alignment	not modelled	97.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
85	c2p4qA_	Alignment	not modelled	97.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating 1; **PDBTitle:** crystal structure analysis of gnd1 in saccharomyces cerevisiae
86	c3hwrA_	Alignment	not modelled	97.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
87	c3qsgA_	Alignment	not modelled	97.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-binding phosphogluconate dehydrogenase-like protein; **PDBTitle:** crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
88	c3k96B_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
89	d3cuma2	Alignment	not modelled	97.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
90	c3g79A_	Alignment	not modelled	97.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; **PDBTitle:** crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
91	c3eywA_	Alignment	not modelled	97.3	22	**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
92	c1txgA_	Alignment	not modelled	97.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
93	c3triB_	Alignment	not modelled	97.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
94	d1guza1	Alignment	not modelled	97.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
95	c3ktdC_	Alignment	not modelled	97.2	15	**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
96	d1l7da1	Alignment	not modelled	97.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
97	c1np3B_	Alignment	not modelled	97.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
98	d1zh8a1	Alignment	not modelled	97.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	c2pv7B_	Alignment	not modelled	97.2	17	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
100	d1n1ea2	Alignment	not modelled	97.1	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
101	c1ks9A_	Alignment	not modelled	97.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
102	c3k30B_	Alignment	not modelled	97.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex

103	c1ps9A_	Alignment	not modelled	97.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
104	c1djnB_	Alignment	not modelled	97.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase; **PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
105	d1xeaa1	Alignment	not modelled	97.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
106	c2eggA_	Alignment	not modelled	97.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
107	c2ho3D_	Alignment	not modelled	97.1	9	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
108	c3euwB_	Alignment	not modelled	97.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
109	c1npyA_	Alignment	not modelled	97.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
110	d9ldta1	Alignment	not modelled	97.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
111	c3egoB_	Alignment	not modelled	97.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
112	c3ezyB_	Alignment	not modelled	97.0	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
113	c3c7cB_	Alignment	not modelled	97.0	16	**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)
114	d1ojua1	Alignment	not modelled	97.0	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
115	c3oc4A_	Alignment	not modelled	97.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, pyridine nucleotide-disulfide family; **PDBTitle:** crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
116	c1zh8B_	Alignment	not modelled	97.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
117	c3o8qB_	Alignment	not modelled	97.0	15	**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
118	d1t2da1	Alignment	not modelled	97.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
119	c3ceaA_	Alignment	not modelled	97.0	11	**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
120	d1np3a2	Alignment	not modelled	97.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain