Phyre^2

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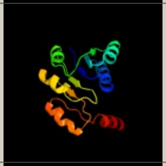
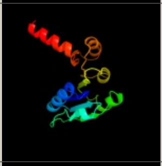
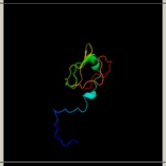
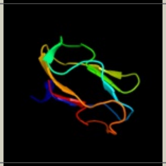
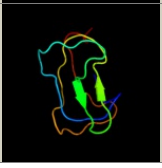
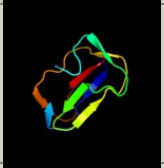
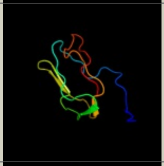
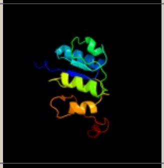
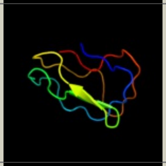
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2we7A_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
2	c3on5B_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bh1974 protein; **PDBTitle:** crystal structure of a xanthine dehydrogenase (bh1974) from bacillus2 halodurans at 2.80 a resolution
3	c3llvA_	Alignment		98.4	16	**PDB header:**nad(p) binding protein **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
4	c2g1uA_	Alignment		98.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
5	c2kccA_	Alignment		97.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
6	c2dn8A_	Alignment		97.7	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
7	c3fmcC_	Alignment		97.6	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
8	c3ic5A_	Alignment		97.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
9	d1lssa_	Alignment		97.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
10	c2qj8B_	Alignment		97.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
11	c2b8gA_	Alignment		97.4	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)

12	d2hmva1	Alignment		97.4	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
13	d2jfga1	Alignment		97.4	14	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
14	c3cdxB_	Alignment		97.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
15	d1bdoa_	Alignment		97.3	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
16	c3na6A_	Alignment		97.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
17	c3fwzA_	Alignment		97.3	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
18	c3k5iB_	Alignment		97.3	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
19	c2ejgD_	Alignment		97.3	34	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
20	c3eywA_	Alignment		97.2	12	**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
21	d1dcza_	Alignment	not modelled	97.2	38	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
22	d1o78a_	Alignment	not modelled	97.2	39	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	c3n6rK_	Alignment	not modelled	97.2	23	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
24	c3uvzB_	Alignment	not modelled	97.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
25	c3l4bG_	Alignment	not modelled	97.0	12	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
26	c3k5pA_	Alignment	not modelled	97.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
27	c2dbqA_	Alignment	not modelled	96.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
						PDB header:ligase

28	c2ejmA_	Alignment	not modelled	96.9	32	**Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
29	c2cukC_	Alignment	not modelled	96.8	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
30	c1dxyA_	Alignment	not modelled	96.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase
31	c3orqA_	Alignment	not modelled	96.7	16	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
32	c1ybaC_	Alignment	not modelled	96.7	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
33	d1kjqa2	Alignment	not modelled	96.7	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
34	c3evtA_	Alignment	not modelled	96.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
35	c1wwkA_	Alignment	not modelled	96.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
36	d1id1a_	Alignment	not modelled	96.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
37	c2gcgB_	Alignment	not modelled	96.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
38	c3kboB_	Alignment	not modelled	96.6	18	**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
39	c1xdwA_	Alignment	not modelled	96.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
40	c3hg7A_	Alignment	not modelled	96.6	13	**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
41	d2dlda1	Alignment	not modelled	96.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
42	d1sc6a1	Alignment	not modelled	96.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
43	d1e5qa1	Alignment	not modelled	96.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	c2z04A_	Alignment	not modelled	96.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
45	c2g76A_	Alignment	not modelled	96.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
46	c1j4aA_	Alignment	not modelled	96.5	15	**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
47	d1qp8a1	Alignment	not modelled	96.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
48	c1kjjA_	Alignment	not modelled	96.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
49	c3bazA_	Alignment	not modelled	96.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyphenylpyruvate reductase; **PDBTitle:** structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
50	c2eklA_	Alignment	not modelled	96.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
51	c3q2oB_	Alignment	not modelled	96.5	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole

						ribonucleotide2 synthetase
52	c2dwcB_	Alignment	not modelled	96.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
53	d1j4aa1	Alignment	not modelled	96.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
54	c1gdhA_	Alignment	not modelled	96.4	22	**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
55	c2omeA_	Alignment	not modelled	96.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
56	c3uagA_	Alignment	not modelled	96.4	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (udp-n-acetylmuramoyl-l-alanine:d- **PDBTitle:** udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
57	c1e5lA_	Alignment	not modelled	96.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
58	c2j6iC_	Alignment	not modelled	96.3	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
59	d1iyua_	Alignment	not modelled	96.3	30	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
60	c3n7uD_	Alignment	not modelled	96.3	15	**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
61	d1dxya1	Alignment	not modelled	96.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
62	c2pv7B_	Alignment	not modelled	96.3	15	**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
63	c3gg9C_	Alignment	not modelled	96.3	18	**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
64	c2d0iC_	Alignment	not modelled	96.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
65	c1qp8A_	Alignment	not modelled	96.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
66	c2pi1C_	Alignment	not modelled	96.2	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
67	d1ghja_	Alignment	not modelled	96.1	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
68	c2w2kB_	Alignment	not modelled	96.1	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-mandelate dehydrogenase; **PDBTitle:** crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
69	d2naca1	Alignment	not modelled	96.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
70	c3gvxA_	Alignment	not modelled	95.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerate dehydrogenase related protein; **PDBTitle:** crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
71	c2ahrB_	Alignment	not modelled	95.9	11	**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
72	d1ygya1	Alignment	not modelled	95.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
73	c3c85A_	Alignment	not modelled	95.8	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
74	d1p3da1	Alignment	not modelled	95.8	17	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
75	d1mx3a1	Alignment	not modelled	95.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
76	d1v8ba1	Alignment	not modelled	95.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Formate/glycerate dehydrogenases, NAD-domain
77	d1qjoa_	Alignment	not modelled	95.7	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
78	c2nacA_	Alignment	not modelled	95.7	19	**PDB header:**oxidoreductase(aldehyde(d),nad+(a)) **Chain:** A: **PDB Molecule:**nad-dependent formate dehydrogenase; **PDBTitle:** high resolution structures of holo and apo formate dehydrogenase
79	c1ygyA_	Alignment	not modelled	95.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
80	d1gdha1	Alignment	not modelled	95.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
81	d1li4a1	Alignment	not modelled	95.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
82	c3d4oA_	Alignment	not modelled	95.5	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
83	d1pjca1	Alignment	not modelled	95.5	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
84	c1d4fD_	Alignment	not modelled	95.5	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
85	c2l5tA_	Alignment	not modelled	95.4	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
86	d1l7da1	Alignment	not modelled	95.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
87	c2axqA_	Alignment	not modelled	95.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
88	d1k8ma_	Alignment	not modelled	95.4	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
89	c2q8iB_	Alignment	not modelled	95.3	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
90	c3ketA_	Alignment	not modelled	95.3	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
91	c2ew2B_	Alignment	not modelled	95.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative; **PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
92	d1pjqa1	Alignment	not modelled	95.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
93	d1pmra_	Alignment	not modelled	95.1	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
94	c2o4cB_	Alignment	not modelled	95.1	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
95	d2pv7a2	Alignment	not modelled	95.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c2f1kD_	Alignment	not modelled	95.0	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
97	c2rirA_	Alignment	not modelled	95.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
98	c2vouA_	Alignment	not modelled	95.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,6-dihydroxypyridine hydroxylase; **PDBTitle:** structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
99	c1v8bA_	Alignment	not modelled	94.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
100	c2bryA_	Alignment	not modelled	94.8	22	**PDB header:**transport **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
101	c3n58D_	Alignment	not modelled	94.8	21	**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
102	c3qhaB_	Alignment	not modelled	94.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
103	c3oetF_	Alignment	not modelled	94.8	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
104	d3c96a1	Alignment	not modelled	94.7	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
105	c3oneA_	Alignment	not modelled	94.7	15	**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
106	c2vhyB_	Alignment	not modelled	94.7	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
107	c2ep9A_	Alignment	not modelled	94.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase; **PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
108	c3dhyC_	Alignment	not modelled	94.5	19	**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
109	d1c1da1	Alignment	not modelled	94.5	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
110	d1gjxa_	Alignment	not modelled	94.5	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
111	d2voua1	Alignment	not modelled	94.5	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
112	d1reoa1	Alignment	not modelled	94.5	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
113	c3allA_	Alignment	not modelled	94.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
114	c2z2vA_	Alignment	not modelled	94.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
115	d2fy8a1	Alignment	not modelled	94.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
116	c2eezG_	Alignment	not modelled	94.4	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
117	d1laba_	Alignment	not modelled	94.4	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
118	c2dncA_	Alignment	not modelled	94.3	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
119	c3ew7A_	Alignment	not modelled	94.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo0794 protein; **PDBTitle:** crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
120	d1y8ob1	Alignment	not modelled	94.2	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains