Phyre^2

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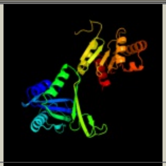
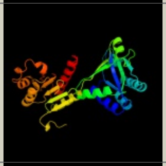
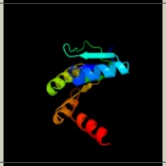
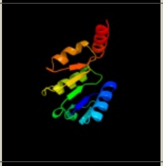
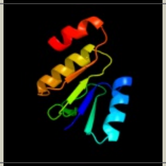
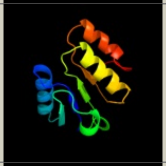
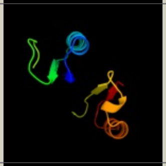
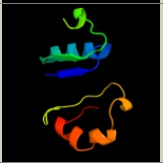
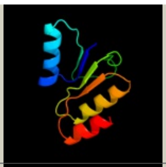
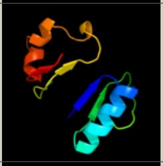
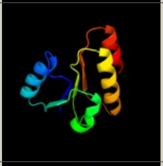
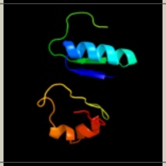
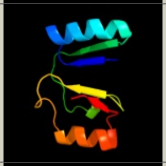
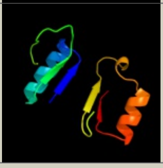
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2we7A_	Alignment		100.0	33	**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	22	**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		98.2	19	**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		97.7	21	**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	d1lssa_	Alignment		97.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
6	c3eywA_	Alignment		97.3	23	**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
7	c3l4bG_	Alignment		97.2	17	**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
8	c2dbqA_	Alignment		97.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
9	c2cukC_	Alignment		96.9	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
10	c2eklA_	Alignment		96.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
11	c1wwkA_	Alignment		96.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3

12	d2hmva1	Alignment		96.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
13	c3evtA_	Alignment		96.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
14	c3fwzA_	Alignment		96.8	14	**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
15	c1dxyA_	Alignment		96.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase
16	d2jfga1	Alignment		96.7	21	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
17	c3ic5A_	Alignment		96.7	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.
18	c3bazA_	Alignment		96.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyphenylpyruvate reductase; **PDBTitle:** structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
19	c1gdhA_	Alignment		96.5	28	**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
20	c3hg7A_	Alignment		96.5	17	**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
21	c2gcgB_	Alignment	not modelled	96.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
22	c1j4aA_	Alignment	not modelled	96.5	13	**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
23	d1dxya1	Alignment	not modelled	96.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
24	d1pjqa1	Alignment	not modelled	96.4	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
25	c1xdwA_	Alignment	not modelled	96.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
26	c2d0iC_	Alignment	not modelled	96.4	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
27	d1j4aa1	Alignment	not modelled	96.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
28	d1qp8a1	Alignment	not modelled	96.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain

29	c2pi1C_	Alignment	not modelled	96.3	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
30	c2g76A_	Alignment	not modelled	96.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
31	c1qp8A_	Alignment	not modelled	96.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
32	d1e5qa1	Alignment	not modelled	96.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
33	d1sc6a1	Alignment	not modelled	96.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
34	d2dlda1	Alignment	not modelled	96.2	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
35	c3k5pA_	Alignment	not modelled	96.2	14	**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
36	c3gg9C_	Alignment	not modelled	96.1	22	**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
37	c3kboB_	Alignment	not modelled	96.1	21	**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
38	c1ybaC_	Alignment	not modelled	96.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
39	d1kjqa2	Alignment	not modelled	96.0	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
40	c3gvxA_	Alignment	not modelled	96.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerate dehydrogenase related protein; **PDBTitle:** crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
41	c2vouA_	Alignment	not modelled	95.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,6-dihydroxypyridine hydroxylase; **PDBTitle:** structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
42	d1mx3a1	Alignment	not modelled	95.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
43	d1id1a_	Alignment	not modelled	95.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
44	d2naca1	Alignment	not modelled	95.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
45	c1kjjA_	Alignment	not modelled	95.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
46	d1ygya1	Alignment	not modelled	95.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
47	c2dwcB_	Alignment	not modelled	95.8	12	**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
48	c3uvzB_	Alignment	not modelled	95.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
49	c3oetF_	Alignment	not modelled	95.8	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
50	c3n7uD_	Alignment	not modelled	95.8	10	**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
51	c1ygyA_	Alignment	not modelled	95.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
52	c3q2oB_	Alignment	not modelled	95.7	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
						PDB header:oxidoreductase

53	c2j6iC_	Alignment	not modelled	95.6	17	**Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
54	c1e5lA_	Alignment	not modelled	95.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
55	c2o4cB_	Alignment	not modelled	95.6	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
56	c3k5iB_	Alignment	not modelled	95.6	9	**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
57	c2omeA_	Alignment	not modelled	95.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
58	c2w2kB_	Alignment	not modelled	95.5	18	**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.
59	c3d4oA_	Alignment	not modelled	95.5	20	**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
60	d1gdha1	Alignment	not modelled	95.4	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
61	c3orqA_	Alignment	not modelled	95.4	14	**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
62	d1pjca1	Alignment	not modelled	95.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
63	d2voua1	Alignment	not modelled	95.3	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
64	d3c96a1	Alignment	not modelled	95.3	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
65	c2bryA_	Alignment	not modelled	95.2	12	**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
66	c3etjB_	Alignment	not modelled	95.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
67	d1l7da1	Alignment	not modelled	95.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
68	d1reoa1	Alignment	not modelled	95.1	8	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
69	c3allA_	Alignment	not modelled	95.1	14	**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
70	c3gmbB_	Alignment	not modelled	95.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic2 acid oxygenase
71	d1p3da1	Alignment	not modelled	95.0	11	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
72	d1j6ua1	Alignment	not modelled	95.0	16	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
73	c3qhaB_	Alignment	not modelled	95.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
74	c2pv7B_	Alignment	not modelled	94.9	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
75	c2nacA_	Alignment	not modelled	94.9	15	**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
76	c2xdoC_	Alignment	not modelled	94.8	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
77	c2ew2B_	Alignment	not modelled	94.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative;

77	c2ew2B_	Alignment	not modelled	94.8	22	**PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
78	c2rgjA_	Alignment	not modelled	94.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** crystal structure of flavin-containing monooxygenase phzs
79	c2vhyB_	Alignment	not modelled	94.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
80	c2qa2A_	Alignment	not modelled	94.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyketide oxygenase cabe; **PDBTitle:** crystal structure of cabe, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
81	d1c1da1	Alignment	not modelled	94.7	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
82	d1li4a1	Alignment	not modelled	94.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
83	c2rirA_	Alignment	not modelled	94.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
84	d1k0ia1	Alignment	not modelled	94.4	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
85	c2z04A_	Alignment	not modelled	94.4	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
86	d1v8ba1	Alignment	not modelled	94.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
87	c1phhA_	Alignment	not modelled	94.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**p-hydroxybenzoate hydroxylase; **PDBTitle:** crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
88	c3ihmB_	Alignment	not modelled	94.3	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**styrene monooxygenase a; **PDBTitle:** structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
89	c3uagA_	Alignment	not modelled	94.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (udp-n-acetylmuramoyl-l-alanine:d- **PDBTitle:** udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
90	c2r0gB_	Alignment	not modelled	94.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rebc; **PDBTitle:** chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
91	d1djqa3	Alignment	not modelled	94.2	19	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
92	d1ps9a3	Alignment	not modelled	94.2	29	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
93	c1c0iA_	Alignment	not modelled	94.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** crystal structure of d-amino acid oxidase in complex with2 two anthranylate molecules
94	c1z82A_	Alignment	not modelled	94.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
95	c3d64A_	Alignment	not modelled	94.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
96	c3c4aA_	Alignment	not modelled	94.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable tryptophan hydroxylase viod; **PDBTitle:** crystal structure of viod hydroxylase in complex with fad2 from chromobacterium violaceum. northeast structural3 genomics consortium target cvr158
97	c3fmwC_	Alignment	not modelled	94.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxygenase; **PDBTitle:** the crystal structure of mtmoiv, a baeyer-villiger2 monooxygenase from the mithramycin biosynthetic pathway in3 streptomyces argillaceus.
98	c3cgvA_	Alignment	not modelled	94.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**geranylgeranyl reductase related protein; **PDBTitle:** crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
99	c3dfzB_	Alignment	not modelled	94.0	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
100	c1pjcA_	Alignment	not modelled	94.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
101	c3gvpB_	Alignment	not modelled	94.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
						PDB header:hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase;

102	c3n58D_	Alignment	not modelled	93.9	16	**PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
103	c3nrnA_	Alignment	not modelled	93.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf1083; **PDBTitle:** crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
104	c3ps9A_	Alignment	not modelled	93.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
105	c1d4fD_	Alignment	not modelled	93.8	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
106	c3kljA_	Alignment	not modelled	93.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-dependent dehydrogenase, nirb-family (n-terminal **PDBTitle:** crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
107	c3ihgA_	Alignment	not modelled	93.8	22	**PDB header:**flavoprotein, oxidoreductase **Chain:** A: **PDB Molecule:**rdme; **PDBTitle:** crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
108	c2eezG_	Alignment	not modelled	93.8	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
109	c3p2yA_	Alignment	not modelled	93.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
110	c3c85A_	Alignment	not modelled	93.7	16	**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
111	c1ps9A_	Alignment	not modelled	93.7	19	**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
112	d2iida1	Alignment	not modelled	93.7	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
113	c2dc1A_	Alignment	not modelled	93.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
114	c2v1dA_	Alignment	not modelled	93.6	16	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
115	c2xagA_	Alignment	not modelled	93.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
116	c2e1mA_	Alignment	not modelled	93.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
117	c3hn7A_	Alignment	not modelled	93.6	20	**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
118	d1b5qa1	Alignment	not modelled	93.5	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
119	d1t2da1	Alignment	not modelled	93.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
120	c2dkhA_	Alignment	not modelled	93.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxybenzoate hydroxylase; **PDBTitle:** crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate