Phyre^2

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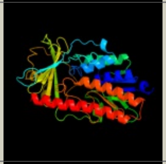
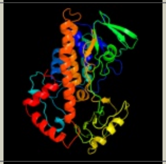
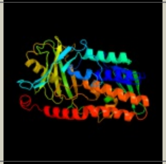
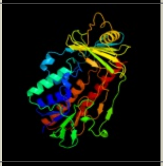
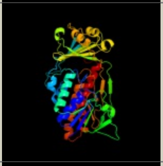
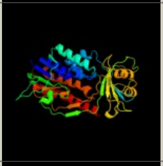
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qa2A_	Alignment		100.0	17	**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
2	c3i3lA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
3	c3fmwC_	Alignment		100.0	16	**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.
4	c3e1tA_	Alignment		100.0	14	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**halogenase; **PDBTitle:** structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
5	c3nixF_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**flavoprotein/dehydrogenase; **PDBTitle:** crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
6	c2dkhA_	Alignment		100.0	13	**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
7	c3atrA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
8	c3ihgA_	Alignment		100.0	19	**PDB header:**flavoprotein, oxidoreductase **Chain:** A: **PDB Molecule:**rdme; **PDBTitle:** crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
9	c3cgvA_	Alignment		100.0	20	**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
10	c1pn0A_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenol 2-monooxygenase; **PDBTitle:** phenol hydroxylase from trichosporon cutaneum
11	c2gmhA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone **PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone

12	c2x3nA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-dependent monooxygenase; **PDBTitle:** crystal structure of pqsl, a probable fad-dependent2 monooxygenase from pseudomonas aeruginosa
13	c1phhA_	Alignment		100.0	15	**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
14	c2rgjA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** crystal structure of flavin-containing monooxygenase phzs
15	c2r0gB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rebc; **PDBTitle:** chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
16	d2gmha1	Alignment		100.0	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
17	c3allA_	Alignment		100.0	17	**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
18	c3gmbB_	Alignment		100.0	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
19	c3c4aA_	Alignment		100.0	12	**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
20	c2vouA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,6-dihydroxypyridine hydroxylase; **PDBTitle:** structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
21	c2xdoC_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
22	d1k0ia1	Alignment	not modelled	99.9	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
23	c2bryA_	Alignment	not modelled	99.9	18	**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
24	d3c96a1	Alignment	not modelled	99.9	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
25	d1pn0a1	Alignment	not modelled	99.9	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
26	c3ihmB_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**styrene monooxygenase a; **PDBTitle:** structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
27	d2voua1	Alignment	not modelled	99.9	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
28	c2ardA_	Alignment	not modelled	99.9	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**tryptophan halogenase prna; **PDBTitle:** the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination

29	c2e4gB_	Alignment	not modelled	99.9	15	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
30	c2weuD_	Alignment	not modelled	99.9	14	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
31	c2pyxA_	Alignment	not modelled	99.9	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
32	c1yvvB_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase, flavin-containing; **PDBTitle:** x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
33	c1y56B_	Alignment	not modelled	99.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sarcosine oxidase; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
34	c2gahB_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**heterotetrameric sarcosine oxidase beta-subunit; **PDBTitle:** heterotetrameric sarcosine: structure of a diflavin2 metaloenzyme at 1.85 a resolution
35	c3bhkA_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monomeric sarcosine oxidase; **PDBTitle:** crystal structure of r49k mutant of monomeric sarcosine oxidase2 crystallized in phosphate as precipitant
36	c3nyeA_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
37	c2olnA_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nikd protein; **PDBTitle:** nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
38	c3nrnA_	Alignment	not modelled	99.7	18	**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
39	c3dmeB_	Alignment	not modelled	99.7	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved exported protein; **PDBTitle:** crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
40	c1pj6A_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
41	c1ryiB_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycine oxidase; **PDBTitle:** structure of glycine oxidase with bound inhibitor glycolate
42	c3djeA_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl amine: oxygen oxidoreductase; **PDBTitle:** crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
43	c3ps9A_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
44	c3da1A_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
45	c2rgoA_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
46	c2r4jA_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aerobic glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
47	d1kf6a2	Alignment	not modelled	99.6	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
48	d1neka2	Alignment	not modelled	99.6	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
49	c3pvcA_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
50	d2bs2a2	Alignment	not modelled	99.6	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
51	c2uzzD_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-methyl-l-tryptophan oxidase; **PDBTitle:** x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
52	c1c0iA_	Alignment	not modelled	99.6	16	**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
53	c3fbsB	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase;

		Alignment	not modelled			**PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
54	d1qo8a2	Alignment	not modelled	99.6	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
55	c3qj4A_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
56	c3f8rD_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**thioredoxin reductase (trxb-3); **PDBTitle:** crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
57	d2gf3a1	Alignment	not modelled	99.5	28	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
58	d1ryia1	Alignment	not modelled	99.5	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
59	d2gqfa1	Alignment	not modelled	99.5	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
60	d1d4ca2	Alignment	not modelled	99.5	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
61	c3ka7A_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
62	d1jnra2	Alignment	not modelled	99.5	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
63	c3i6dA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of ppo from bacillus subtilis with af
64	c2rghA_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
65	c2bs3A_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinol-fumarate reductase flavoprotein subunit a; **PDBTitle:** glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
66	c3r9uA_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** thioredoxin-disulfide reductase from campylobacter jejuni.
67	c3ab1B_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
68	c1s3bB_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amine oxidase [flavin-containing] b; **PDBTitle:** crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
69	c3p4rM_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**fumarate reductase flavoprotein subunit; **PDBTitle:** crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
70	c1kf6A_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase flavoprotein; **PDBTitle:** e. coli quinol-fumarate reductase with bound inhibitor hqno
71	c2vvlD_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**monoamine oxidase n; **PDBTitle:** the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
72	c1ltxR_	Alignment	not modelled	99.5	17	**PDB header:**transferase/protein binding **Chain:** R: **PDB Molecule:**rab escort protein 1; **PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
73	c2zbwA_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
74	c2zxiC_	Alignment	not modelled	99.4	15	**PDB header:**fad-binding protein **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal
75	c2ivdA_	Alignment	not modelled	99.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
76	c3lzxB_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase 2; **PDBTitle:** crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
77	d2ivda1	Alignment	not modelled	99.4	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
78	c2aczA_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase/electron transport **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with

						atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
79	c3rhaA_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
80	c2yg4B_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
81	c3g05B_	Alignment	not modelled	99.4	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of n-terminal domain (2-550) of e.coli mnmg
82	d1y0pa2	Alignment	not modelled	99.4	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
83	c2gqfA_	Alignment	not modelled	99.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0933; **PDBTitle:** crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
84	c3cesB_	Alignment	not modelled	99.4	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
85	c3ctyA_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of t. acidophilum thioredoxin reductase
86	c3o0hA_	Alignment	not modelled	99.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase from bartonella henselae
87	d1w4xa1	Alignment	not modelled	99.4	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
88	c1f6mF_	Alignment	not modelled	99.4	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
89	c3k7tB_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-hydroxy-l-nicotine oxidase; **PDBTitle:** crystal structure of apo-form 6-hydroxy-l-nicotine oxidase,2 crystal form p3121
90	c2q7vA_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of deinococcus radiodurans thioredoxin2 reductase
91	c1h83A_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase; **PDBTitle:** structure of polyamine oxidase in complex with2 1,8-diaminooctane
92	c3cp8C_	Alignment	not modelled	99.3	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
93	d1pj5a2	Alignment	not modelled	99.3	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
94	c3jskN_	Alignment	not modelled	99.3	24	**PDB header:**biosynthetic protein **Chain:** N: **PDB Molecule:**cypbp37 protein; **PDBTitle:** thiazole synthase from neurospora crassa
95	c3nlcA_	Alignment	not modelled	99.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vp0956; **PDBTitle:** crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
96	d2i0za1	Alignment	not modelled	99.3	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
97	d1rp0a1	Alignment	not modelled	99.3	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
98	c2a87A_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
99	c1kifE_	Alignment	not modelled	99.3	14	**PDB header:**flavoprotein **Chain:** E: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** d-amino acid oxidase from pig kidney
100	c1sezA_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase, mitochondrial; **PDBTitle:** crystal structure of protoporphyrinogen ix oxidase
101	c1yq4A_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
102	c3gwdA_	Alignment	not modelled	99.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase
103	c1fl2A_	Alignment	not modelled	99.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli

104	c1qo8A_	Alignment	not modelled	99.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
105	c1hyuA_	Alignment	not modelled	99.2	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
106	d2cula1	Alignment	not modelled	99.2	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GidA-like
107	c1w4xA_	Alignment	not modelled	99.2	20	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
108	c2eq7B_	Alignment	not modelled	99.2	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
109	c1jrxA_	Alignment	not modelled	99.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
110	d1d5ta1	Alignment	not modelled	99.2	28	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
111	d2bcgg1	Alignment	not modelled	99.2	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
112	c1chuA_	Alignment	not modelled	99.1	12	**PDB header:**flavoenzyme **Chain:** A: **PDB Molecule:**protein (l-aspartate oxidase); **PDBTitle:** structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reducatse family
113	d2gjca1	Alignment	not modelled	99.1	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
114	c1d4cB_	Alignment	not modelled	99.1	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**flavocytochrome c fumarate reductase; **PDBTitle:** crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
115	d1o5wa1	Alignment	not modelled	99.1	32	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
116	d1v59a1	Alignment	not modelled	99.1	32	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
117	c3hdql_	Alignment	not modelled	99.1	46	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
118	d1chua2	Alignment	not modelled	99.1	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
119	d3lada1	Alignment	not modelled	99.1	36	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
120	c1vdcA_	Alignment	not modelled	99.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dependent thioredoxin reductase; **PDBTitle:** structure of nadph dependent thioredoxin reductase