Phyre^2

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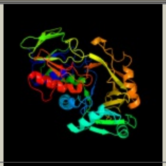
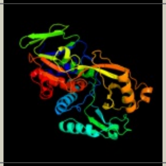
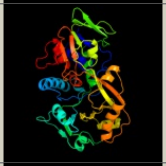
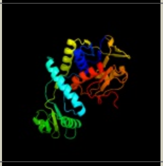
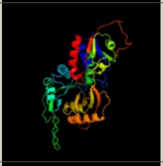
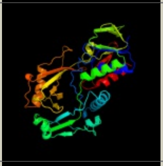
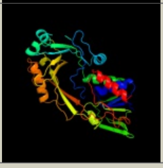
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2uzzD_	Alignment		100.0	99	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-methyl-l-tryptophan oxidase; **PDBTitle:** x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
2	c3bhkA_	Alignment		100.0	37	**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
3	c1pj6A_	Alignment		100.0	15	**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
4	c2olnA_	Alignment		100.0	22	**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
5	c2gahB_	Alignment		100.0	23	**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
6	c3ps9A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
7	c1y56B_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sarcosine oxidase; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
8	c3nyeA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
9	c3pvcA_	Alignment		100.0	17	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
10	c3djeA_	Alignment		100.0	17	**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
11	c1ryiB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycine oxidase; **PDBTitle:** structure of glycine oxidase with bound inhibitor glycolate

12	c3dmeB_	Alignment		100.0	16	**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
13	d2gf3a1	Alignment		100.0	44	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
14	c1kifE_	Alignment		100.0	14	**PDB header:**flavoprotein **Chain:** E: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** d-amino acid oxidase from pig kidney
15	d1ryia1	Alignment		100.0	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
16	c2r4jA_	Alignment		100.0	16	**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
17	c1c0iA_	Alignment		100.0	11	**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
18	c2rgoA_	Alignment		100.0	15	**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
19	c2rghA_	Alignment		100.0	14	**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
20	c3da1A_	Alignment		100.0	16	**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.
21	d1pj5a2	Alignment	not modelled	99.9	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
22	d1kifa1	Alignment	not modelled	99.8	16	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
23	d1c0pa1	Alignment	not modelled	99.8	14	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
24	c3i6dA_	Alignment	not modelled	99.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of ppo from bacillus subtilis with af
25	c3atrA_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
26	c1ltxR_	Alignment	not modelled	99.6	10	**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
27	d1o5wa1	Alignment	not modelled	99.6	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
28	c3e1tA_	Alignment	not modelled	99.5	12	**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
						PDB header:oxidoreductase

29	c2ivdA_	Alignment	not modelled	99.5	13	**Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
30	c2ardA_	Alignment	not modelled	99.5	11	**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
31	c3i3lA_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
32	c3ka7A_	Alignment	not modelled	99.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
33	c3cgvA_	Alignment	not modelled	99.5	17	**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
34	c3nixF_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**flavoprotein/dehydrogenase; **PDBTitle:** crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
35	c1s3bB_	Alignment	not modelled	99.4	13	**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
36	d2gqfa1	Alignment	not modelled	99.4	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
37	d2i0za1	Alignment	not modelled	99.4	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
38	c3rhaA_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
39	c1phhA_	Alignment	not modelled	99.4	11	**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
40	c1yvvB_	Alignment	not modelled	99.4	11	**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.
41	c2qa2A_	Alignment	not modelled	99.4	14	**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
42	d2v5za1	Alignment	not modelled	99.4	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
43	c3ihgA_	Alignment	not modelled	99.4	15	**PDB header:**flavoprotein, oxidoreductase **Chain:** A: **PDB Molecule:**rdme; **PDBTitle:** crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
44	c3nksA_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of human protoporphyrinogen ix oxidase
45	c2gmhA_	Alignment	not modelled	99.4	17	**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
46	c2i0zA_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-utilizing dehydrogenases; **PDBTitle:** crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
47	c2pyxA_	Alignment	not modelled	99.3	11	**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
48	c2aczA_	Alignment	not modelled	99.3	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
49	c3lovA_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
50	c1yq4A_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
51	c2xdoC_	Alignment	not modelled	99.3	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
52	c3allA_	Alignment	not modelled	99.3	13	**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

53	c3fmwC_	Alignment	not modelled	99.3	15	**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.
54	c2x3nA_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable fad-dependent monooxygenase; **PDBTitle:** crystal structure of pqsl, a probable fad-dependent2 monooxygenase from pseudomonas aeruginosa
55	c3qj4A_	Alignment	not modelled	99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
56	c2e4gB_	Alignment	not modelled	99.3	10	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
57	c2r0gB_	Alignment	not modelled	99.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rebc; **PDBTitle:** chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
58	c2weuD_	Alignment	not modelled	99.2	10	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
59	d1neka2	Alignment	not modelled	99.2	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
60	c2b9yA_	Alignment	not modelled	99.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
61	c2yg4B_	Alignment	not modelled	99.2	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
62	c3fbsB_	Alignment	not modelled	99.2	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
63	c2dkhA_	Alignment	not modelled	99.2	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
64	c3gmbB_	Alignment	not modelled	99.2	11	**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
65	c2bs3A_	Alignment	not modelled	99.2	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	c2zxiC_	Alignment	not modelled	99.2	16	**PDB header:**fad-binding protein **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal
67	c1jrxA_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
68	c1pn0A_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenol 2-monooxygenase; **PDBTitle:** phenol hydroxylase from trichosporon cutaneum
69	c3k7tB_	Alignment	not modelled	99.2	29	**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
70	d1y0pa2	Alignment	not modelled	99.2	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
71	c2vvlD_	Alignment	not modelled	99.2	29	**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	d1d5ta1	Alignment	not modelled	99.2	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
73	c1qo8A_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
74	d1qo8a2	Alignment	not modelled	99.2	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
75	c3hdqI_	Alignment	not modelled	99.1	21	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
76	d1kf6a2	Alignment	not modelled	99.1	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
77	c3o0hA_	Alignment	not modelled	99.1	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase from bartonella henselae
						PDB header:structural genomics, unknown function

78	c3nlcA_	Alignment	not modelled	99.1	17	**Chain:** A: **PDB Molecule:**uncharacterized protein vp0956; **PDBTitle:** crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
79	c2gqfA_	Alignment	not modelled	99.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0933; **PDBTitle:** crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
80	d2gmha1	Alignment	not modelled	99.1	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
81	c1d4cB_	Alignment	not modelled	99.1	20	**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
82	c1ebdB_	Alignment	not modelled	99.1	18	**PDB header:**complex (oxidoreductase/transferase) **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
83	d2bcgg1	Alignment	not modelled	99.1	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
84	c3l8kB_	Alignment	not modelled	99.1	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
85	c3p4rM_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**fumarate reductase flavoprotein subunit; **PDBTitle:** crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
86	d2bs2a2	Alignment	not modelled	99.1	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
87	c3ic9D_	Alignment	not modelled	99.1	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
88	c3v76A_	Alignment	not modelled	99.1	21	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavoprotein; **PDBTitle:** the crystal structure of a flavoprotein from sinorhizobium meliloti
89	c1i8tB_	Alignment	not modelled	99.1	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** strcuture of udp-galactopyranose mutase from e.coli
90	c3cp8C_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
91	c2eq8E_	Alignment	not modelled	99.1	44	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
92	c1zmcG_	Alignment	not modelled	99.0	23	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
93	c3ctyA_	Alignment	not modelled	99.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of t. acidophilum thioredoxin reductase
94	c3g05B_	Alignment	not modelled	99.0	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
95	c1v0jB_	Alignment	not modelled	99.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-galactopyranose mutase; **PDBTitle:** udp-galactopyranose mutase from mycobacterium tuberculosis
96	c3d8xB_	Alignment	not modelled	99.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
97	c1gndA_	Alignment	not modelled	99.0	24	**PDB header:**gtpase activation **Chain:** A: **PDB Molecule:**guanine nucleotide dissociation inhibitor; **PDBTitle:** guanine nucleotide dissociation inhibitor, alpha-isoform
98	d1ebda1	Alignment	not modelled	99.0	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
99	c1bwcA_	Alignment	not modelled	99.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (glutathione reductase); **PDBTitle:** structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
100	c3cpiH_	Alignment	not modelled	99.0	21	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**rab gdp-dissociation inhibitor; **PDBTitle:** crystal structure of yeast rab-gdi
101	d1k0ia1	Alignment	not modelled	99.0	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
102	c2hqmB_	Alignment	not modelled	99.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
103	c1zx9A_	Alignment	not modelled	99.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase;

						PDBTitle: crystal structure of tn501 mera
104	d1vg0a1	Alignment	not modelled	99.0	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
105	d3grsa1	Alignment	not modelled	99.0	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
106	c2qaeA_	Alignment	not modelled	99.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
107	c2q7vA_	Alignment	not modelled	99.0	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of deinococcus radiodurans thioredoxin2 reductase
108	c3bnuA_	Alignment	not modelled	99.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase fms1; **PDBTitle:** crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
109	c2a8xA_	Alignment	not modelled	99.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
110	c1geuA_	Alignment	not modelled	99.0	32	**PDB header:**oxidoreductase(flavoenzyme) **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** anatomy of an engineered nad-binding site
111	d1d4ca2	Alignment	not modelled	99.0	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
112	d1i8ta1	Alignment	not modelled	99.0	25	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**UDP-galactopyranose mutase, N-terminal domain
113	c3dgzA_	Alignment	not modelled	99.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2; **PDBTitle:** crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
114	c1lvlA_	Alignment	not modelled	99.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
115	c1ojtA_	Alignment	not modelled	99.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**surface protein; **PDBTitle:** structure of dihydrolipoamide dehydrogenase
116	c2r9zB_	Alignment	not modelled	99.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione amide reductase; **PDBTitle:** glutathione amide reductase from chromatium gracile
117	d1gesa1	Alignment	not modelled	99.0	32	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
118	c3c4aA_	Alignment	not modelled	99.0	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
119	d1jnra2	Alignment	not modelled	99.0	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
120	c1zkqA_	Alignment	not modelled	98.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2, mitochondrial; **PDBTitle:** crystal structure of mouse thioredoxin reductase type 2