Phyre2

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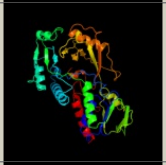
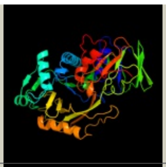
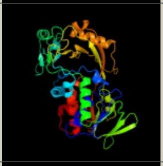
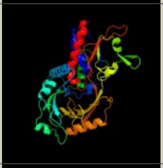
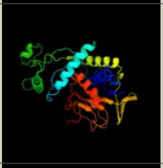
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pj6A_	Alignment		100.0	18	**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
2	c3dmeB_	Alignment		100.0	25	**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
3	c3ps9A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
4	c2gahB_	Alignment		100.0	18	**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
5	c3pvcA_	Alignment		100.0	18	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
6	c1y56B_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sarcosine oxidase; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
7	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
8	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
9	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
10	c2olnA_	Alignment		100.0	15	**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
11	c3nyeA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine

12	c3bhkA_	Alignment		100.0	17	**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
13	c2rghA_	Alignment		100.0	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
14	c2uzzD_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-methyl-l-tryptophan oxidase; **PDBTitle:** x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
15	c3da1A_	Alignment		100.0	17	**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.
16	c1ryiB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycine oxidase; **PDBTitle:** structure of glycine oxidase with bound inhibitor glycolate
17	c1kifE_	Alignment		100.0	15	**PDB header:**flavoprotein **Chain:** E: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** d-amino acid oxidase from pig kidney
18	d2gf3a1	Alignment		100.0	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
19	c1c0iA_	Alignment		100.0	14	**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
20	d1ryia1	Alignment		100.0	31	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
21	d1pj5a2	Alignment	not modelled	100.0	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
22	d1kifa1	Alignment	not modelled	99.9	18	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
23	d1c0pa1	Alignment	not modelled	99.9	19	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
24	c3ka7A_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
25	c3i6dA_	Alignment	not modelled	99.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of ppo from bacillus subtilis with af
26	c1ltxR_	Alignment	not modelled	99.8	12	**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	99.8	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
28	c2ardA_	Alignment	not modelled	99.8	14	**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
						PDB header:oxidoreductase

29	c3atrA_	Alignment	not modelled	99.8	18	**Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
30	c3i3lA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
31	c2ivdA_	Alignment	not modelled	99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
32	c2weuD_	Alignment	not modelled	99.8	14	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
33	c1yq4A_	Alignment	not modelled	99.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
34	d1d5ta1	Alignment	not modelled	99.7	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
35	c2e4gB_	Alignment	not modelled	99.7	14	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
36	d2gqfa1	Alignment	not modelled	99.7	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
37	c3k7tB_	Alignment	not modelled	99.7	16	**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
38	c2pyxA_	Alignment	not modelled	99.7	16	**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
39	c1s3bB_	Alignment	not modelled	99.7	15	**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
40	c3e1tA_	Alignment	not modelled	99.7	15	**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
41	c3cgvA_	Alignment	not modelled	99.7	13	**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
42	d2i0za1	Alignment	not modelled	99.7	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
43	c2aczA_	Alignment	not modelled	99.7	17	**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
44	c2zxiC_	Alignment	not modelled	99.7	20	**PDB header:**fad-binding protein **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal
45	d2bcgg1	Alignment	not modelled	99.7	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
46	c1qo8A_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
47	c3cp8C_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
48	c3nksA_	Alignment	not modelled	99.7	12	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of human protoporphyrinogen ix oxidase
49	c2bs3A_	Alignment	not modelled	99.7	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
50	c1jrxA_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
51	d1qo8a2	Alignment	not modelled	99.7	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
52	c2eq7B_	Alignment	not modelled	99.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
53	c2gmhA_	Alignment	not modelled	99.6	14	**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

54	d1y0pa2	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	c1d4cB_	Alignment	not modelled	99.6	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
56	c3cpiH_	Alignment	not modelled	99.6	15	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**rab gdp-dissociation inhibitor; **PDBTitle:** crystal structure of yeast rab-gdi
57	c3p4rM_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**fumarate reductase flavoprotein subunit; **PDBTitle:** crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
58	c3g05B_	Alignment	not modelled	99.6	19	**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
59	c1ndaD_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**trypanothione oxidoreductase; **PDBTitle:** the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
60	c1kf6A_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase flavoprotein; **PDBTitle:** e. coli quinol-fumarate reductase with bound inhibitor hqno
61	c1naaB_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cellobiose dehydrogenase; **PDBTitle:** cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
62	c3nixF_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**flavoprotein/dehydrogenase; **PDBTitle:** crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
63	c3cesB_	Alignment	not modelled	99.6	18	**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
64	d1kf6a2	Alignment	not modelled	99.6	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
65	d1neka2	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
66	c1h83A_	Alignment	not modelled	99.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase; **PDBTitle:** structure of polyamine oxidase in complex with2 1,8-diaminooctane
67	c2vvlD_	Alignment	not modelled	99.6	14	**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.
68	c1gndA_	Alignment	not modelled	99.6	16	**PDB header:**gtpase activation **Chain:** A: **PDB Molecule:**guanine nucleotide dissociation inhibitor; **PDBTitle:** guanine nucleotide dissociation inhibitor, alpha-isoform
69	c2gewA_	Alignment	not modelled	99.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
70	c1yvvB_	Alignment	not modelled	99.6	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.
71	c3lovA_	Alignment	not modelled	99.6	12	**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
72	d1vg0a1	Alignment	not modelled	99.6	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
73	c3o0hA_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase from bartonella henselae
74	d2bs2a2	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
75	d1w4xa1	Alignment	not modelled	99.6	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
76	d2v5za1	Alignment	not modelled	99.6	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
77	c3dgzA_	Alignment	not modelled	99.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2; **PDBTitle:** crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
						PDB header:oxidoreductase

78	c1zkqA_	Alignment	not modelled	99.6	11	**Chain:** A: **PDB Molecule:**thioredoxin reductase 2, mitochondrial; **PDBTitle:** crystal structure of mouse thioredoxin reductase type 2
79	c3jskN_	Alignment	not modelled	99.5	26	**PDB header:**biosynthetic protein **Chain:** N: **PDB Molecule:**cypbp37 protein; **PDBTitle:** thiazole synthase from neurospora crassa
80	c3v76A_	Alignment	not modelled	99.5	20	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavoprotein; **PDBTitle:** the crystal structure of a flavoprotein from sinorhizobium meliloti
81	c2qa2A_	Alignment	not modelled	99.5	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
82	d2gmha1	Alignment	not modelled	99.5	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
83	c2i0zA_	Alignment	not modelled	99.5	19	**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
84	c1xdiA_	Alignment	not modelled	99.5	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
85	c2yg4B_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putrescine oxidase; **PDBTitle:** structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
86	c1tytA_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase, oxidized form; **PDBTitle:** crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
87	c2jb1B_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
88	c3nrnA_	Alignment	not modelled	99.5	22	**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
89	c3qj4A_	Alignment	not modelled	99.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
90	c2jbvA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**choline oxidase; **PDBTitle:** crystal structure of choline oxidase reveals insights into2 the catalytic mechanism
91	c2w0hA_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase; **PDBTitle:** x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
92	c1coyA_	Alignment	not modelled	99.5	9	**PDB header:**oxidoreductase(oxygen receptor) **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase complexed with a2 steroid substrate. implications for fad dependent alcohol3 oxidases
93	c3rhaA_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
94	d1d4ca2	Alignment	not modelled	99.5	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
95	c3urhB_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
96	d1kdga1	Alignment	not modelled	99.5	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
97	c1geuA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase(flavoenzyme) **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** anatomy of an engineered nad-binding site
98	d1k0ia1	Alignment	not modelled	99.5	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
99	c1m6iA_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programmed cell death protein 8; **PDBTitle:** crystal structure of apoptosis inducing factor (aif)
100	c1phhA_	Alignment	not modelled	99.5	13	**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
101	c2gqfA_	Alignment	not modelled	99.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0933; **PDBTitle:** crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
102	c2qaeA_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
103	c1gv4A_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programed cell death protein 8; **PDBTitle:** murine apoptosis-inducing factor (aif)
104	c2nvkX	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**thioredoxin reductase;

104	c2nvkX_	Alignment	not modelled	99.5	14	**PDBTitle:** crystal structure of thioredoxin reductase from drosophila2 melanogaster
105	c2b9yA_	Alignment	not modelled	99.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
106	d3coxa1	Alignment	not modelled	99.5	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
107	c3nlcA_	Alignment	not modelled	99.5	15	**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
108	d1rp0a1	Alignment	not modelled	99.5	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
109	c2fjaC_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenylylsulfate reductase, subunit a; **PDBTitle:** adenosine 5'-phosphosulfate reductase in complex with2 substrate
110	c1f8sA_	Alignment	not modelled	99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
111	d2voua1	Alignment	not modelled	99.5	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
112	c2c3dB_	Alignment	not modelled	99.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxopropyl-com reductase; **PDBTitle:** 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
113	c2dkhA_	Alignment	not modelled	99.5	12	**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
114	c1w4xA_	Alignment	not modelled	99.4	18	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
115	c1zx9A_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** crystal structure of tn501 mera
116	c1ojtA_	Alignment	not modelled	99.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**surface protein; **PDBTitle:** structure of dihydrolipoamide dehydrogenase
117	c2cduB_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
118	c3gwdA_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase
119	d2cula1	Alignment	not modelled	99.4	23	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GidA-like
120	c2eq8E_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp