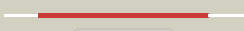
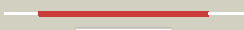


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rgoA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
2	c2rghA_	 Alignment		100.0	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
3	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.
4	c2r4jA_	 Alignment		100.0	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
5	c3dmeB_	 Alignment		100.0	12	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
6	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
7	c2gahB_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: heterotetrameric sarcosine oxidase beta-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
8	c3pvcA_	 Alignment		100.0	18	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mmc from yersinia pestis
9	c3ps9A_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mmc from e. coli
10	c3djeA_	 Alignment		100.0	11	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	c1y56B_	 Alignment		99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii

12	c2olnA_	Alignment		99.9	14	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
13	c3nyeA_	Alignment		99.9	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
14	d1pj5a2	Alignment		99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
15	c3bhkA_	Alignment		99.9	12	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
16	d1ryia1	Alignment		99.9	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
17	c2uzzD_	Alignment		99.9	15	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
18	d2gf3a1	Alignment		99.9	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
19	c1ryiB_	Alignment		99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
20	c2jbvA_	Alignment		99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into2 the catalytic mechanism
21	c1kifE_	Alignment	not modelled	99.8	13	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
22	c3fimB_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
23	c2igoG_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: G: PDB Molecule: pyranose oxidase; PDBTitle: crystal structure of pyranose 2-oxidase h167a mutant with 2-2 fluoro-2-deoxy-d-glucose
24	c2f5vA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose 2-oxidase; PDBTitle: reaction geometry and thermostability mutant of pyranose 2-oxidase2 from the white-rot fungus peniophora sp.
25	c1vq4A_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
26	d1kdga1	Alignment	not modelled	99.8	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
27	d1gpea1	Alignment	not modelled	99.8	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
28	c1cf3A_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger

29	c1gpeA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense
30	d1d5ta1	Alignment	not modelled	99.8	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
31	d3coxa1	Alignment	not modelled	99.8	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
32	c3q9tB_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase
33	d1ju2a1	Alignment	not modelled	99.8	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
34	c1naaB_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
35	c1coyA_	Alignment	not modelled	99.8	17	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
36	c3p4rM_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
37	c1jrxA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
38	d1kf6a2	Alignment	not modelled	99.7	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
39	c1kf6A_	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
40	d1n4wa1	Alignment	not modelled	99.7	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
41	d1cf3a1	Alignment	not modelled	99.7	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
42	c2gewA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
43	c1qo8A_	Alignment	not modelled	99.7	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
44	c2aczA_	Alignment	not modelled	99.7	13	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
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	c2bs3A_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
47	d1qo8a2	Alignment	not modelled	99.7	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
48	c1ju2A_	Alignment	not modelled	99.7	16	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
49	c1c0iA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-amino acid oxidase; PDBTitle: crystal structure of d-amino acid oxidase in complex with2 two anthranilate molecules
50	c1d4cB_	Alignment	not modelled	99.7	15	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
51	d1y0pa2	Alignment	not modelled	99.7	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
52	c1gndA_	Alignment	not modelled	99.7	12	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
53	c3ka7A_	Alignment	not modelled	99.7	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

54	c1zkqA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
55	c3dgzA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
56	c1ltxR_	Alignment	not modelled	99.7	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
57	c3cpiH_	Alignment	not modelled	99.6	9	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
58	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
59	d2gqfa1	Alignment	not modelled	99.6	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
60	c3gyxA_	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: adenyllysulfate reductase; PDBTitle: crystal structure of adenylysulfate reductase from2 desulfovibrio gigas
61	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
62	d2bs2a2	Alignment	not modelled	99.6	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
63	c2nvkX_	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
64	c2fjaC_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: C: PDB Molecule: adenyllysulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with2 substrate
65	c2zxiC_	Alignment	not modelled	99.6	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
66	c2ardA_	Alignment	not modelled	99.6	13	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
67	d2f5va1	Alignment	not modelled	99.6	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
68	c3i6dA_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
69	c2c3dB_	Alignment	not modelled	99.6	15	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
70	d1vg0a1	Alignment	not modelled	99.6	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
71	c2ivdA_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
72	d1d4ca2	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
73	c3jskN_	Alignment	not modelled	99.5	20	PDB header: biosynthetic protein Chain: N: PDB Molecule: cybbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
74	c2b9yA_	Alignment	not modelled	99.5	13	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
75	c3cp8C_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
76	c2dkhA_	Alignment	not modelled	99.5	14	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
77	c1zmcG_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
78	d2i0za1	Alignment	not modelled	99.5	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
79	c3cesB_	Alignment	not modelled	99.5	15	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

80	c3i3lA_	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
81	c3g05B_	Alignment	not modelled	99.5	16	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	c2vvld_	Alignment	not modelled	99.5	10	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.
83	c1tytA_	Alignment	not modelled	99.5	11	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
84	c2e4gB_	Alignment	not modelled	99.5	14	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
85	c3urhB_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
86	c2pyxA_	Alignment	not modelled	99.5	13	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
87	c2w0hA_	Alignment	not modelled	99.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
88	d1chua2	Alignment	not modelled	99.5	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
89	c1ndaD_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
90	c3atrA_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
91	c1geuA_	Alignment	not modelled	99.5	11	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
92	c3p1wA_	Alignment	not modelled	99.5	10	PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c
93	d1w4xa1	Alignment	not modelled	99.5	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
94	c3cgvA_	Alignment	not modelled	99.4	15	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
95	c1s3bB_	Alignment	not modelled	99.4	12	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
96	c2hqmB_	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
97	c2jb1B_	Alignment	not modelled	99.4	12	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
98	c2gmhA_	Alignment	not modelled	99.4	13	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
99	d1rp0a1	Alignment	not modelled	99.4	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
100	c3nlcA_	Alignment	not modelled	99.4	16	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
101	c2eq8E_	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
102	c2weuD_	Alignment	not modelled	99.4	13	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
103	d2gmha1	Alignment	not modelled	99.4	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
104	d1k0ia1	Alignment	not modelled	99.4	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain

105	c1v59B_	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
106	d2cula1	Alignment	not modelled	99.4	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GidA-like
107	c1dxlC_	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
108	c3k7tB_	Alignment	not modelled	99.4	13	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
109	c1f8sA_	Alignment	not modelled	99.4	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.
110	c1ebdB_	Alignment	not modelled	99.4	16	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
111	c2eq7B_	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
112	c1ojtA_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
113	c2qa2A_	Alignment	not modelled	99.4	19	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
114	c1v0jB_	Alignment	not modelled	99.4	11	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
115	c1hyuA_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
116	c1bwcA_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
117	c2cfyB_	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
118	c1vqwB_	Alignment	not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein with similarity to flavin-containing PDBTitle: crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
119	c3v76A_	Alignment	not modelled	99.4	14	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
120	c3nrrA_	Alignment	not modelled	99.4	11	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