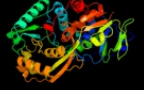
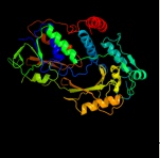
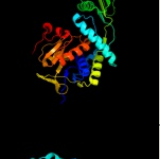
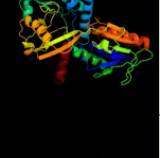
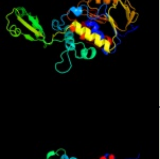
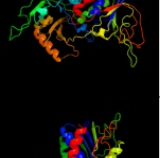
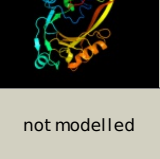
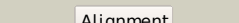
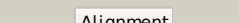
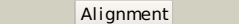
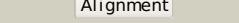
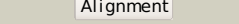
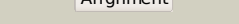
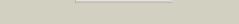
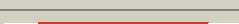
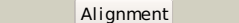
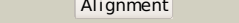
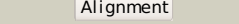


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gahB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: heterotetrameric sarcosine oxidase beta-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
2	c1pj6A_	 Alignment		100.0	16	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
3	c3ps9A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmC from e. coli
4	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
5	c1y56B_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
6	c3dmeB_	 Alignment		100.0	18	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
7	c3nyeA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
8	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
9	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
10	c2qlnA_	 Alignment		100.0	18	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	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)

12	c1ryiB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
13	c2r4jA_	Alignment		100.0	15	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
14	c2rgoA_	Alignment		100.0	13	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
15	c1kifE_	Alignment		100.0	16	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
16	d2gf3a1	Alignment		100.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
17	c2rghA_	Alignment		100.0	12	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
18	d1ryia1	Alignment		100.0	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
19	c1c0iA_	Alignment		100.0	13	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
20	c3da1A_	Alignment		100.0	15	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	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
22	d1c0pa1	Alignment	not modelled	99.9	16	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
23	d1kifa1	Alignment	not modelled	99.8	18	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
24	c1ltxR_	Alignment	not modelled	99.8	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
25	c3i6daA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
26	c3atrA_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
27	c3cgvA_	Alignment	not modelled	99.7	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
28	c3i3lA_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase

29	c3e1tA	 Alignment	not modelled	99.7	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
30	c2weuD	 Alignment	not modelled	99.7	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	c2ardA	 Alignment	not modelled	99.7	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
32	c2qa2A	 Alignment	not modelled	99.7	16	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
33	c3ka7A	 Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
34	c3nixF	 Alignment	not modelled	99.6	17	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	c1yq4A	 Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
36	d2gqfa1	 Alignment	not modelled	99.6	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
37	c2e4gB	 Alignment	not modelled	99.6	13	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
38	d1o5wa1	 Alignment	not modelled	99.6	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
39	c2pyxA	 Alignment	not modelled	99.6	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
40	c2aczA	 Alignment	not modelled	99.6	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
41	c2dkhA	 Alignment	not modelled	99.6	16	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
42	c2vv1D	 Alignment	not modelled	99.6	16	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.
43	c1phhA	 Alignment	not modelled	99.6	12	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
44	c2gmhA	 Alignment	not modelled	99.6	18	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
45	c2bs3A	 Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
46	d1y0pa2	 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
47	c2ivdA	 Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
48	c3ihgA	 Alignment	not modelled	99.6	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
49	d2i0za1	 Alignment	not modelled	99.6	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
50	d1qo8a2	 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
51	c1qo8A	 Alignment	not modelled	99.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
52	c3fmwC	 Alignment	not modelled	99.5	17	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.
		 Alignment				Fold: FAD/NAD(P)-binding domain

53	dlnka2	Alignment	not modelled	99.5	14	Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
54	c1jrxA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
55	d2bs2a2	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
56	c1pn0A	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
57	c1s3bB	Alignment	not modelled	99.5	18	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)-aminoinndan
58	d1kf6a2	Alignment	not modelled	99.5	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
59	c3k7tB	Alignment	not modelled	99.5	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
60	c1d4cB	Alignment	not modelled	99.5	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
61	c3lovA	Alignment	not modelled	99.5	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
62	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
63	d2gmha1	Alignment	not modelled	99.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
64	c1kf6A	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
65	c1yvvB	Alignment	not modelled	99.4	16	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.
66	c3nrnA	Alignment	not modelled	99.4	13	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
67	c3gmbB	Alignment	not modelled	99.4	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
68	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
69	c3allA	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
70	d1d4ca2	Alignment	not modelled	99.4	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
71	c2r0gB	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
72	c2x3nA	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-dependent monooxygenase; PDBTitle: crystal structure of pqs1, a probable fad-dependent2 monooxygenase from pseudomonas aeruginosa
73	c2zziC	Alignment	not modelled	99.3	22	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
74	c2xdoC	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
75	c3g05B	Alignment	not modelled	99.3	24	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
76	c2b9yA	Alignment	not modelled	99.3	15	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
77	c3cesB	Alignment	not modelled	99.3	24	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
78	c3c4aA_	Alignment	not modelled	99.3	13	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
79	c3v76A_	Alignment	not modelled	99.3	18	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
80	c2fjaC_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with2 substrate
81	c3gyxA_	Alignment	not modelled	99.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
82	c1h83A_	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase; PDBTitle: structure of polyamine oxidase in complex with2 1,8-diaminooctane
83	c3cp8C_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
84	c2e5vA_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
85	c3jskN_	Alignment	not modelled	99.3	18	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
86	d1rp0a1	Alignment	not modelled	99.2	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
87	c2i0zA_	Alignment	not modelled	99.2	20	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
88	c3nlcA_	Alignment	not modelled	99.2	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
89	d1chua2	Alignment	not modelled	99.2	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
90	c1x31A_	Alignment	not modelled	99.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
91	d1d5ta1	Alignment	not modelled	99.2	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
92	c2yg4B_	Alignment	not modelled	99.2	37	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
93	c2rgjA_	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
94	d1jnra2	Alignment	not modelled	99.2	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
95	d2bcgg1	Alignment	not modelled	99.2	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
96	c3rhaA_	Alignment	not modelled	99.2	40	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
97	c2vouA_	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorus
98	d1vg0a1	Alignment	not modelled	99.2	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
99	d3coxa1	Alignment	not modelled	99.2	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
100	d1k0ia1	Alignment	not modelled	99.2	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
101	c3hdql_	Alignment	not modelled	99.2	29	PDB header: isomerase Chain: I: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
102	c2gewA_	Alignment	not modelled	99.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
						PDB header: oxidoreductase

103	c3ihmB_	Alignment	not modelled	99.2	15	Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
104	c2q7vA_	Alignment	not modelled	99.1	30	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase
105	c3cpiH_	Alignment	not modelled	99.1	22	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
106	d2v5za1	Alignment	not modelled	99.1	46	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
107	c2bryA_	Alignment	not modelled	99.1	24	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
108	c1chuA_	Alignment	not modelled	99.1	23	PDB header: flavoenzyme Chain: A: PDB Molecule: protein (l-aspartate oxidase); PDBTitle: structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family
109	c1i8tB_	Alignment	not modelled	99.1	30	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli
110	c1gndA_	Alignment	not modelled	99.1	23	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
111	c1zmcG_	Alignment	not modelled	99.1	34	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
112	d2dw4a2	Alignment	not modelled	99.1	36	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
113	c3o0hA_	Alignment	not modelled	99.1	33	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
114	c1v0jB_	Alignment	not modelled	99.1	34	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
115	c3ctyA_	Alignment	not modelled	99.1	34	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
116	c3fbsB_	Alignment	not modelled	99.1	26	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
117	c1hyuA_	Alignment	not modelled	99.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
118	d2cula1	Alignment	not modelled	99.1	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GidA-like
119	c3bnuA_	Alignment	not modelled	99.1	33	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
120	c1f6mF_	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+