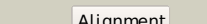
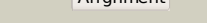
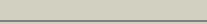
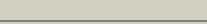


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pj6A_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
2	c3ps9A_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmC from e. coli
3	c2gahB_	 Alignment		100.0	22	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
4	c3pvcA_	 Alignment		100.0	16	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	23	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
6	c3djeA_	 Alignment		100.0	16	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
7	c3bhkA_	 Alignment		100.0	16	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
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	c2oInA_	 Alignment		100.0	17	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
10	c3dmeB_	 Alignment		100.0	22	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
11	c2uzzD_	 Alignment		100.0	16	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	20	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
13	c1kifE_	Alignment		100.0	18	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
14	c2r4jA_	Alignment		100.0	14	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
15	c2rgoA_	Alignment		100.0	18	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
16	d2gf3a1	Alignment		100.0	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
17	c1c0iA_	Alignment		100.0	19	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
18	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
19	d1rvia1	Alignment		100.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
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	c3ka7A_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
22	d1pj5a2	Alignment	not modelled	99.9	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
23	c3i6dA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
24	c2ivdA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
25	c1ltbR_	Alignment	not modelled	99.9	13	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
26	d1c0pa1	Alignment	not modelled	99.8	20	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
27	d1kifa1	Alignment	not modelled	99.8	23	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
28	c3k7tB_	Alignment	not modelled	99.8	11	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

29	c3nksA	Alignment	not modelled	99.8	14	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of human protoporphyrinogen ix oxidase
30	c1h83A	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase; PDBTitle: structure of polyamine oxidase in complex with2 1,8-diaminooctane
31	d1o5wa1	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	d1d5ta1	Alignment	not modelled	99.8	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
33	c1gndA	Alignment	not modelled	99.8	14	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
34	c2vv1D	Alignment	not modelled	99.8	11	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.
35	c3lovA	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exigubacterium sp. 255-15 at 2.06 a resolution
36	c1s3bB	Alignment	not modelled	99.7	11	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
37	c2b9yA	Alignment	not modelled	99.7	11	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
38	c1sezA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase
39	c2jb1B	Alignment	not modelled	99.7	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
40	c1f8sA	Alignment	not modelled	99.7	12	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.
41	c2yg4B	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
42	d2bcgg1	Alignment	not modelled	99.7	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
43	d2v5za1	Alignment	not modelled	99.7	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
44	c3rhaA	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
45	c3cpiH	Alignment	not modelled	99.7	15	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
46	c2v1dA	Alignment	not modelled	99.6	16	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
47	c2hkoA	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1
48	c2xagA	Alignment	not modelled	99.6	14	PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
49	c3nrnA	Alignment	not modelled	99.6	14	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
50	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
51	c2weuD	Alignment	not modelled	99.6	13	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
52	d2ivda1	Alignment	not modelled	99.6	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
53	c3p1wA	Alignment	not modelled	99.6	16	PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falci parum, pfl2060c
54	c3i3lA	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase

55	c1yvvB	 Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structure of p. syringae q888a4 oxidoreductase at 2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
56	c2gmhA	 Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complex with ubiquinone
57	c3bnuA	 Alignment	not modelled	99.5	13	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
58	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
59	d1vg0a1	 Alignment	not modelled	99.5	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
60	c3hdqL	 Alignment	not modelled	99.5	13	PDB header: isomerase Chain: I: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
61	c2e4gB	 Alignment	not modelled	99.5	12	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
62	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
63	c2bi8A	 Alignment	not modelled	99.5	14	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad
64	c3qj4A	 Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
65	c3cgvA	 Alignment	not modelled	99.5	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
66	d2gqfa1	 Alignment	not modelled	99.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
67	c3nixF	 Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
68	c2pyxA	 Alignment	not modelled	99.5	12	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
69	c3e1tA	 Alignment	not modelled	99.5	18	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
70	c1yq4A	 Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
71	c1phhA	 Alignment	not modelled	99.4	18	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
72	d1b5qa1	 Alignment	not modelled	99.4	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
73	c2e1mA	 Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
74	d2i0za1	 Alignment	not modelled	99.4	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
75	c2cduB	 Alignment	not modelled	99.4	10	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
76	c3allA	 Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
77	c1jrxA	 Alignment	not modelled	99.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
78	c2aczA	 Alignment	not modelled	99.4	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

79	c1qo8A	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
80	d2dw4a2	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
81	c1d4cB	Alignment	not modelled	99.3	28	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the open conformation of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
82	c1zx9A	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
83	c2xdoC	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
84	d2bs2a2	Alignment	not modelled	99.3	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
85	c3fmwC	Alignment	not modelled	99.3	14	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.
86	c1ps9A	Alignment	not modelled	99.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
87	c3nlcA	Alignment	not modelled	99.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956; PDBTitle: crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
88	c3gmbB	Alignment	not modelled	99.3	18	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
89	c1v0jB	Alignment	not modelled	99.3	16	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
90	c2bs3A	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunita; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolfinella succinogenes
91	c2eq7B	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
92	c1i8tB	Alignment	not modelled	99.3	24	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli
93	c1nhqA	Alignment	not modelled	99.3	12	PDB header: oxidoreductase (h2o2(a)) Chain: A: PDB Molecule: nadh peroxidase; PDBTitle: crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
94	d1qo8a2	Alignment	not modelled	99.2	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
95	d1y0pa2	Alignment	not modelled	99.2	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
96	c1zkqA	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
97	c3dgzA	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
98	c2zziC	Alignment	not modelled	99.2	19	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
99	c2dkhA	Alignment	not modelled	99.2	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
100	c2i0zA	Alignment	not modelled	99.2	21	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
101	d1neka2	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
102	c1tytA	Alignment	not modelled	99.2	17	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
						PDB header: oxidoreductase

103	c3k30B_	Alignment	not modelled	99.2	13	Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioles simplex
104	d1kf6a2	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
105	c3p4rM_	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
106	c3ihgA_	Alignment	not modelled	99.2	13	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
107	c3o0hA_	Alignment	not modelled	99.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
108	c1geuA_	Alignment	not modelled	99.2	11	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
109	c2vouA_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
110	c3urhB_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
111	c1ndaD_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
112	c2eq8E_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
113	c2w0hA_	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
114	c2bcpA_	Alignment	not modelled	99.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
115	c3ihmB_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
116	c3v76A_	Alignment	not modelled	99.2	23	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
117	c2nvkX_	Alignment	not modelled	99.2	11	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
118	c2e5vA_	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
119	d1w4xa1	Alignment	not modelled	99.1	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
120	c1kf6A_	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno