



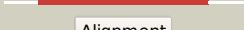

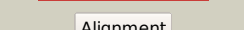

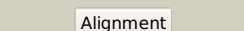







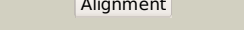

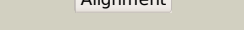

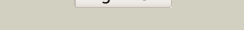




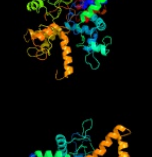

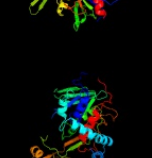
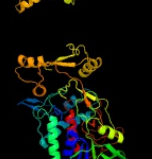

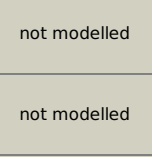


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1817_(-)_2059602_2061065
Date	Fri Aug 2 13:30:42 BST 2019
Unique Job ID	132a95520de0ef9e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qo8A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
2	c1d4cB_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the flavocytochrome c2 fumarate reductase of shewanella putrefaciens strain mr-1
3	c1jrxA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
4	c4at2A_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketosteroid-delta4-5alpha-dehydrogenase; PDBTitle: the crystal structure of 3-ketosteroid-delta4-(5alpha)-2 dehydrogenase from rhodococcus jostii rha1 in complex3 with 4-androstene-3,17- dione
5	c4c3yF_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-ketosteroid dehydrogenase; PDBTitle: crystal structure of 3-ketosteroid delta1-dehydrogenase from2 rhodococcus erythropolis sq1 in complex with 1,4-androstadiene-3,17-3 dione
6	c1yq4A_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
7	c3vr8E_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
8	c2aczA_	 Alignment		100.0	26	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
9	c2bs3A_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes
10	c5xmjE_	 Alignment		100.0	21	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
11	c1kf6A_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno

12	c3p4rM	Alignment		100.0	22	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
13	c5glgA	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase 2; PDBTitle: the novel function of osm1 under anaerobic condition in the er was2 revealed by crystal structure of osm1, a soluble fumarate reductase3 in yeast
14	c6n56A	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavo protein subunit; PDBTitle: crystal structure of fumarate reductase, flavo protein subunit, from2 helicobacter pylori g27
15	c3gyxA	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
16	c2fjaC	Alignment		100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
17	c3cirM	Alignment		100.0	24	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
18	c1chuA	Alignment		100.0	22	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
19	c2e5vA	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
20	c2gqfA	Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
21	c2i0zA	Alignment	not modelled	100.0	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
22	c3v76A	Alignment	not modelled	100.0	19	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
23	d1qo8a2	Alignment	not modelled	100.0	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
24	d1chua2	Alignment	not modelled	100.0	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
25	d1y0pa2	Alignment	not modelled	100.0	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
26	c4cnjD	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: l-amino acid oxidase; PDBTitle: l-aminoacetone oxidase from streptococcus oligofermentans2 belongs to a new 3-domain family of bacterial flavoproteins
27	d1d4ca2	Alignment	not modelled	100.0	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
28	d2gqfa1	Alignment	not modelled	100.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like

29	d1kf6a2	Alignment	not modelled	99.9	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
30	d1neka2	Alignment	not modelled	99.9	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
31	c3cesB	Alignment	not modelled	99.9	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
32	c3g05B	Alignment	not modelled	99.9	17	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
33	d2bs2a2	Alignment	not modelled	99.9	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
34	c3nlcA	Alignment	not modelled	99.9	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
35	d1jnra2	Alignment	not modelled	99.9	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
36	c3cp8C	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
37	c2zxiC	Alignment	not modelled	99.9	19	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
38	c3cp2A	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
39	d2i0za1	Alignment	not modelled	99.8	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
40	c2r4jA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted glycerol-3-2 phosphate dehydrogenase in complex with dhap
41	c1zkaA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
42	c3dqzA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
43	c5nccB	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and2 palmitic acid
44	c2c3dB	Alignment	not modelled	99.7	19	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
45	c5mogB	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
46	c2rghA	Alignment	not modelled	99.7	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
47	c2rgoA	Alignment	not modelled	99.7	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
48	c3da1A	Alignment	not modelled	99.7	20	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.
49	c1ojtA	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydroipoamide dehydrogenase
50	c2zbwA	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
51	c2f5vA	Alignment	not modelled	99.7	12	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.
52	c5odeA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: gll2934 protein; PDBTitle: structure of a novel oxidoreductase from gloeobacter violaceus

53	c2eq8E_	Alignment	not modelled	99.7	27	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
54	c6aonB_	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad
55	c5hxfF_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
56	c4p9sA_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
57	c4j56A_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
58	c2cfyB_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
59	c5g3sB_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase viao; PDBTitle: the structure of the l-tryptophan oxidase viao from chromobacterium2 violaceum - samarium derivative
60	c1tytA_	Alignment	not modelled	99.7	20	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
61	c1zmcG_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
62	c2w0hA_	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
63	c1v59B_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
64	c4b1bB_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom
65	c3dmeB_	Alignment	not modelled	99.7	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from bordetella2 pertussis. northeast structural genomics target ber141
66	d1ryia1	Alignment	not modelled	99.7	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
67	c3o0hA_	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
68	c1geuA_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
69	c4ntdA_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of hlmi
70	c2gahB_	Alignment	not modelled	99.7	18	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
71	c3axbA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix
72	c5jriA_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
73	c1ndaD_	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
74	c4migC_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
75	c1pj6A_	Alignment	not modelled	99.7	22	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
76	d1cf3a1	Alignment	not modelled	99.7	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
77	c6du7C_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae
						PDB header: oxidoreductase

78	c3r9uA	Alignment	not modelled	99.6	18	Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
79	c4dnaA	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: probable glutathione reductase; PDBTitle: crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
80	c2a8xA	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydropolyl dehydrogenase; PDBTitle: crystal structure of lipamide dehydrogenase from2 mycobacterium tuberculosis
81	c6bz0C	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydropolyl dehydrogenase; PDBTitle: 1.83 angstrom resolution crystal structure of dihydropolyl2 dehydrogenase from acinetobacter baumannii in complex with fad.
82	c6b4oB	Alignment	not modelled	99.6	23	PDB header: hydrolase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad
83	c1hyuA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
84	c4repA	Alignment	not modelled	99.6	11	PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
85	c6bwtD	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase; PDBTitle: 2.45 angstrom resolution crystal structure thioredoxin reductase from2 francisella tularensis.
86	c2eq7B	Alignment	not modelled	99.6	27	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
87	c2hqmB	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
88	c1bwcA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
89	c5v36A	Alignment	not modelled	99.6	24	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: 1.88 angstrom resolution crystal structure of glutathione reductase2 from streptococcus mutans ua159 in complex with fad
90	c5fjnB	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: B: PDB Molecule: l-amino acid deaminase; PDBTitle: structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate
91	c1ju2A	Alignment	not modelled	99.6	16	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
92	d2gf3a1	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
93	c4gcmB	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
94	c1lpfB	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydropolamide dehydrogenase; PDBTitle: three-dimensional structure of lipamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
95	c1s3bB	Alignment	not modelled	99.6	17	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	c6garB	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
97	c2yg4B	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
98	c5xhuA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ycgf from bacillus subtilis
99	c6a2uD	Alignment	not modelled	99.6	20	PDB header: signaling protein/oxidoreductase Chain: D: PDB Molecule: glucose dehydrogenase; PDBTitle: crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
100	c1naaB	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
101	c1zx9A	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
102	c1f6mF	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin reductase,2 thioredoxin, and the nadp+ analog, aadp+
103	c2v6oA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-

						glutathione2 reductase (smtgr) PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase
104	c1onfA_	Alignment	not modelled	99.6	22	
105	d3coxa1	Alignment	not modelled	99.6	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
106	c2q7vA_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin reductase
107	c4x9mA_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
108	c4qi6A_	Alignment	not modelled	99.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcus thermophilum, mtcdh
109	c3fbsB_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
110	c5w1jA_	Alignment	not modelled	99.6	17	PDB header: signaling protein Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: echinococcus granulosus thioredoxin glutathione reductase (egtgr)
111	c1ltxR_	Alignment	not modelled	99.6	19	PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
112	c2gewA_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
113	c6gncA_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a ferredoxin-flavin thioredoxin reductase from2 clostridium acetobutylicum at 1.64 a resolution
114	c5uwvA_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005
115	c3ab1B_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
116	c1gpeA_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense
117	d2gmha1	Alignment	not modelled	99.6	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
118	c5twcA_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
119	c1coyA_	Alignment	not modelled	99.6	19	PDB header: oxidoreductase(oxygen receptor) Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase complexed with a steroid2 substrate. implications for fad dependent alcohol oxidases
120	c4z24A_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702)