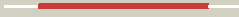
































Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0248c_(sdhA)_298863_300803
Date	Tue Jul 23 14:50:31 BST 2019
Unique Job ID	a5bde36e428502c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3vr8E_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquoinol-fumarate reductase from the parasitic2 nematode ascaris suum
2	c1yq4A_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
3	c5xmjE_	 Alignment		100.0	33	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
4	c2bs3A_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes
5	c1kf6A_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
6	c3p4rM_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
7	c2aczA_	 Alignment		100.0	38	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
8	c6n56A_	 Alignment		100.0	31	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
9	c2fjaC_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
10	c3cirM_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
11	c3gyxA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas

12	c1chuA	Alignment		100.0	34	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
13	c2e5vA	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
14	c1qo8A	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
15	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
16	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
17	c4c3yF	Alignment		100.0	18	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
18	c4at2A	Alignment		100.0	19	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
19	c5glgA	Alignment		100.0	25	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
20	d1chua2	Alignment		100.0	38	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
21	d1kf6a2	Alignment	not modelled	100.0	39	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
22	d1qo8a2	Alignment	not modelled	100.0	33	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
23	d1y0pa2	Alignment	not modelled	100.0	34	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
24	c3v76A	Alignment	not modelled	100.0	20	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
25	d1neka2	Alignment	not modelled	100.0	39	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
26	c2i0zA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-utilizing dehydrogenases; PDBTitle: crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
27	c2gqfA	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
28	d2bs2a2	Alignment	not modelled	100.0	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain

29	d1jnra2	Alignment	not modelled	100.0	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
30	d1d4ca2	Alignment	not modelled	100.0	35	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
31	c4cniD	Alignment	not modelled	100.0	18	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
32	d1neka1	Alignment	not modelled	100.0	28	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
33	d2bs2a1	Alignment	not modelled	100.0	30	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
34	c3cesB	Alignment	not modelled	100.0	16	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
35	c3g05B	Alignment	not modelled	100.0	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
36	d1kf6a1	Alignment	not modelled	100.0	28	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
37	d1jnra1	Alignment	not modelled	100.0	22	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
38	c3nlcA	Alignment	not modelled	99.9	17	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
39	c3cp2A	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
40	c3cp8C	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
41	c2zxiC	Alignment	not modelled	99.9	14	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
42	d2gqfa1	Alignment	not modelled	99.9	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
43	d1chua1	Alignment	not modelled	99.9	26	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
44	d1chua3	Alignment	not modelled	99.8	41	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
45	d1neka3	Alignment	not modelled	99.8	45	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
46	d2bs2a3	Alignment	not modelled	99.8	41	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
47	d2i0za1	Alignment	not modelled	99.8	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
48	d1kf6a3	Alignment	not modelled	99.8	39	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
49	c3dgzA	Alignment	not modelled	99.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
50	c1zkqA	Alignment	not modelled	99.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2

51	c3atrA	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfobolus acidocaldarius co-2 crystallized with its ligand
52	c2v6oA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
53	c2rgoA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
54	c1zmcG	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
55	c5w1jA	Alignment	not modelled	99.7	18	PDB header: signaling protein Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: echinococcus granulosus thioredoxin glutathione reductase (egtgr)
56	c2rghA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
57	c3da1A	Alignment	not modelled	99.7	14	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.
58	c2nvkX	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
59	c1hyuA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
60	c5odeA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: gl2934 protein; PDBTitle: structure of a novel oxidoreductase from gloeobacter violaceus
61	c2cfyB	Alignment	not modelled	99.7	31	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
62	c2c3dB	Alignment	not modelled	99.7	24	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
63	c2gmhA	Alignment	not modelled	99.7	17	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
64	c5w4cA	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
65	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
66	c4y4nE	Alignment	not modelled	99.7	24	PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus
67	c1v59B	Alignment	not modelled	99.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
68	c6bwtD	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase; PDBTitle: 2.45 angstrom resolution crystal structure thioredoxin reductase from2 francisella tularensis.
69	c3jskN	Alignment	not modelled	99.7	22	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
70	c3o0hA	Alignment	not modelled	99.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
71	d2gmha1	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
72	c5yggB	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris
73	c1oijtA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
74	c2r4jA	Alignment	not modelled	99.7	17	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
75	d1rp0a1	Alianment	not modelled	99.7	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

						Family:Thi4-like
76	c2a8xA	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
77	c5jriA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
78	c1tytA	Alignment	not modelled	99.7	18	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
79	c3urhB	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
80	c5twcA	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
81	c2zbwA	Alignment	not modelled	99.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
82	c4ntdA	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of hlmi
83	c4jmqA	Alignment	not modelled	99.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a thioredoxin reductase from brucella mellitensis
84	c5wgyA	Alignment	not modelled	99.6	16	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex
85	c6garB	Alignment	not modelled	99.6	14	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
86	c2w0hA	Alignment	not modelled	99.6	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
87	c1gthD	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
88	c1geuA	Alignment	not modelled	99.6	24	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
89	c5xhuA	Alignment	not modelled	99.6	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ycgf from bacillus subtilis
90	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
91	c6aonB	Alignment	not modelled	99.6	23	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
92	c4gcmB	Alignment	not modelled	99.6	25	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
93	c1vdCA	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
94	c5v36A	Alignment	not modelled	99.6	22	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
95	c3r9uA	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
96	c5g3sB	Alignment	not modelled	99.6	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
97	c1ndaD	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
98	c1bwcA	Alignment	not modelled	99.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
99	c4repA	Alignment	not modelled	99.6	10	PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
100	c5x1yC	Alignment	not modelled	99.6	23	PDB header: oxidoreductase Chain: C: PDB Molecule: mercuric reductase; PDBTitle: structure of mercuric reductase from lysinibacillus sphaericus
						PDB header: oxidoreductase

101	c6du7C_	Alignment	not modelled	99.6	23	Chain: C: PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae
102	c3ic9D_	Alignment	not modelled	99.6	26	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
103	c1f6mF_	Alignment	not modelled	99.6	21	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+
104	c6bz0C_	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: 1.83 angstrom resolution crystal structure of dihydrolipoyl2 dehydrogenase from acinetobacter baumannii in complex with fad.
105	c4a5lB_	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of the thioredoxin reductase from entamoeba2 histolytica
106	c5dbjA_	Alignment	not modelled	99.6	16	PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
107	c4j56A_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
108	c4ntcA_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glit; PDBTitle: crystal structure of glit
109	c2qaeA_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
110	d1h6va1	Alignment	not modelled	99.6	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
111	c5mogB_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
112	c3l8kB_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from sulfolobus2 solfataricus
113	c3dmeB_	Alignment	not modelled	99.6	14	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
114	c1lpfB_	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
115	d1ryia1	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
116	c2q0lA_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
117	d3grsa1	Alignment	not modelled	99.6	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
118	c2hqmB_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
119	c1onfA_	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase
120	c5uwvA_	Alignment	not modelled	99.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005