

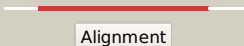



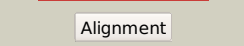





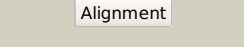

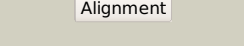
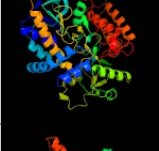
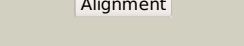

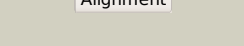

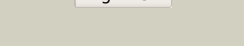




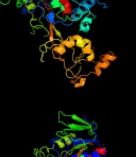




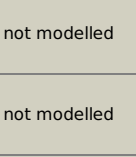


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1595_(nadB)_1795812_1797395
 Date Fri Aug 2 13:30:18 BST 2019
 Unique Job ID d758961e108199f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yq4A_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
2	c3vr8E_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhodoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
3	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
4	c5xmjE_	 Alignment		100.0	29	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
5	c2bs3A_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes
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	c2ac2A_	 Alignment		100.0	32	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	30	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	c2e5vA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
10	c1chuA_	 Alignment		100.0	36	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
11	c2fjaC_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate

12	c3cirM	Alignment		100.0	33	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
13	c3gyxA	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
14	c1qo8A	Alignment		100.0	31	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	34	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	32	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	24	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	d1chua2	Alignment		100.0	42	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
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	c4at2A	Alignment		100.0	24	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
21	d1kf6a2	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
22	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
23	d1qo8a2	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	d1d4ca2	Alignment	not modelled	100.0	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
25	d1neka2	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
26	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
27	d2bs2a2	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	c2i0zA	Alignment	not modelled	100.0	22	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

29	d1jnra2	Alignment	not modelled	100.0	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
30	c2gqfA	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
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	99.9	23	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
33	c3cesB	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 e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
34	c3g05B	Alignment	not modelled	99.9	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
35	d2bs2a1	Alignment	not modelled	99.9	19	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
36	d1kf6a1	Alignment	not modelled	99.9	24	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	99.9	20	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
38	c3cp2A	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
39	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
40	d1chua1	Alignment	not modelled	99.9	22	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
41	c2zxiC	Alignment	not modelled	99.9	21	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	c3nlcA	Alignment	not modelled	99.9	19	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
44	c5w1jA	Alignment	not modelled	99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: echinococcus granulosus thioredoxin glutathione reductas (egtgr)
45	c2v60A	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
46	d1chua3	Alignment	not modelled	99.9	43	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	c1hyuA	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
48	d2i0za1	Alignment	not modelled	99.9	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
49	c1oijtA	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydroliipoamide dehydrogenase
50	c5twcA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
51	c5w4cA	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
52	c5rdaA	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: gll2934 protein;

52	c300aA	Alignment	not modelled	99.8	17	PDBTitle: structure of a novel oxidoreductase from gloebacter violaceus PDB header: oxidoreductase
53	c3dgzA	Alignment	not modelled	99.8	19	Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
54	c1tytA	Alignment	not modelled	99.8	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
55	c2c3dB	Alignment	not modelled	99.8	21	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
56	c6garB	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of oxidised ferredoxin/ferredoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
57	c3o0hA	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
58	c2cfyB	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
59	c1zkgA	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
60	c2nvkX	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
61	d2bs2a3	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
62	c4gcmB	Alignment	not modelled	99.8	23	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
63	c1ndaD	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
64	c2qaeA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
65	c4ntdA	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of hlmi
66	c4jdrB	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
67	c2w0hA	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
68	d1neka3	Alignment	not modelled	99.8	42	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
69	c2eq8E	Alignment	not modelled	99.8	33	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
70	c3l8kB	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from sulfobolus2 solfataricus
71	c2a8xA	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
72	c5yggB	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris
73	c1zmcG	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
74	c1geuA	Alignment	not modelled	99.8	25	PDB header: oxidoreductase (flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
75	c3urhB	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
76	c6aonB	Alignment	not modelled	99.8	18	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
77	c5jriA_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
78	c6b4oB_	Alignment	not modelled	99.8	28	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
79	c2hqmB_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
80	c1dxlC_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
81	c2eq7B_	Alignment	not modelled	99.8	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
82	c4fk1D_	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: D: PDB Molecule: putative thioredoxin reductase; PDBTitle: crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis
83	c3r9uA_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
84	c1gthD_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
85	d3lada1	Alignment	not modelled	99.8	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
86	c1onfA_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase
87	c4dnaA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable glutathione reductase; PDBTitle: crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
88	c6bz0C_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: 1.83 angstrom resolution crystal structure of dihydrolipoamide dehydrogenase from acinetobacter baumannii in complex with fad.
89	c4b1bB_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom
90	c5j60B_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: structure of a thioredoxin reductase from gloeobacter violaceus
91	c3fbsB_	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
92	c4ntcA_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glit; PDBTitle: crystal structure of glit
93	c6gncA_	Alignment	not modelled	99.7	21	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
94	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+
95	d3grsa1	Alignment	not modelled	99.7	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
96	d1lpfa1	Alignment	not modelled	99.7	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
97	c4j56A_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
98	c1bwcA_	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
99	c2r9zB_	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from chromatium gracile
100	c5uwya_	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: the crystal structure of thioredoxin reductase from streptococcus2 pyogenes2 mgas5005
101	c1ebdB_	Alignment	not modelled	99.7	18	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase

102	c2zbwA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
103	d1h6va1	Alignment	not modelled	99.7	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
104	c4jnaA	Alignment	not modelled	99.7	22	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: deph; PDBTitle: crystal structure of the deph complex with dimethyl-fk228
105	c4a9wB	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: monooxygenase; PDBTitle: flavin-containing monooxygenase from stentrophomonas maltophilia
106	c3f8rD	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
107	c2q0lA	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
108	c2q7vA	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin reductase
109	d1dxa1	Alignment	not modelled	99.7	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
110	c3atrA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
111	c1lvA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
112	c5v36A	Alignment	not modelled	99.7	18	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
113	c5xhuA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ycg7 from bacillus subtilis
114	c1lpfB	Alignment	not modelled	99.7	19	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	c6du7C	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae
116	c5mjkC	Alignment	not modelled	99.7	26	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of lactococcus lactis thioredoxin reductase (fo2 conformation)
117	c3ic9D	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
118	c1yqzA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
119	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.
120	c3ntaA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase