

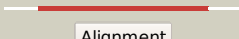

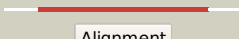



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0785 (-)_879343_881043
Date	Fri Jul 26 01:50:36 BST 2019
Unique Job ID	2759738a4198803d

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qo8A_	 Alignment		100.0	24	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	24	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	24	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
4	c4c3yF_	 Alignment		100.0	23	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
5	c1yq4A_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
6	c3vr8E_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquoinol-fumarate reductase from the parasitic2 nematode ascaris suum
7	c1kf6A_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
8	c3p4rM_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
9	c2aczA_	 Alignment		100.0	22	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
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	c2bs3A_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes

12	c5qlgA_	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
13	c4at2A_	Alignment		100.0	23	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
14	c6n56A_	Alignment		100.0	22	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	15	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
16	c2fjaC_	Alignment		100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
17	c2e5vA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
18	c3cirM_	Alignment		100.0	25	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
19	c1chuA_	Alignment		100.0	25	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
20	c3v76A_	Alignment		100.0	18	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
21	c2i0zA_	Alignment	not modelled	100.0	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
22	d1chua2	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	d1qo8a2	Alignment	not modelled	100.0	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
24	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
25	c2qqfA_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
26	c4cnjD_	Alignment	not modelled	100.0	15	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	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
28	d1kf6a2	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
						Fold: FAD/NAD(P)-binding domain

29	d2bs2a2	Alignment	not modelled	100.0	25	Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
30	d1neka2	Alignment	not modelled	100.0	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
31	c3nlcA_	Alignment	not modelled	100.0	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
32	d1jnra2	Alignment	not modelled	100.0	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
33	d2qqfa1	Alignment	not modelled	99.9	29	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
34	c3cesB_	Alignment	not modelled	99.9	20	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	99.9	20	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	c3cp8C_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
37	c3cp2A_	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
38	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
39	d1qo8a3	Alignment	not modelled	99.9	21	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
40	d1d4ca3	Alignment	not modelled	99.8	19	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
41	c6a2uD_	Alignment	not modelled	99.8	14	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
42	d1y0pa3	Alignment	not modelled	99.8	17	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
43	d2i0za1	Alignment	not modelled	99.8	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
44	c1ju2A_	Alignment	not modelled	99.8	16	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
45	c4qi6A_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcus thermophilum, mtc dh
46	c2lfcA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavoprotein subunit; PDBTitle: solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
47	d3coxa1	Alignment	not modelled	99.8	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
48	c4qi7A_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdh
49	c4qi4A_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcus thermophilum cellobiose2 dehydrogenase, mtdh
50	c1coyA_	Alignment	not modelled	99.8	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
51	c2f5vA_	Alignment	not modelled	99.8	14	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	c2gewA_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)

53	c1naaB	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
54	d1kdga1	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
55	d1pj5a2	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
56	c4z24A	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702)
57	d1n4wa1	Alignment	not modelled	99.7	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
58	c5nccB	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and2 palmitic acid
59	c2rghA	Alignment	not modelled	99.7	15	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
60	c1pj6A	Alignment	not modelled	99.7	19	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
61	c6h3gC	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol oxidase; PDBTitle: alcohol oxidase from phanerochaete chrysosporium
62	c3t37A	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of pyridoxine 4-oxidase from mesorhium loti
63	c4udpA	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-methanol-choline oxidoreductase; PDBTitle: crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
64	c1hyuA	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
65	c2rgoA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
66	c5hxwF	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
67	c1gpeA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense
68	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
69	c4yntA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose oxidase, putative; PDBTitle: crystal structure of aspergillus flavus fad glucose dehydrogenase
70	c4y4nE	Alignment	not modelled	99.7	19	PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus
71	c3dmeB	Alignment	not modelled	99.7	13	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
72	d1rp0a1	Alignment	not modelled	99.7	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
73	c3da1A	Alignment	not modelled	99.7	18	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.
74	c2jbvA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into the2 catalytic mechanism
75	c4p9sA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgh
76	c1cf3A	Alignment	not modelled	99.6	19	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger
77	c2r4jA	Alignment	not modelled	99.6	16	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
						PDB header: oxidoreductase

78	c5hsaG	Alignment	not modelled	99.6	22	Chain: G: PDB Molecule: alcohol oxidase 1; PDBTitle: alcohol oxidase aox1 from pichia pastoris
79	c5ygaB	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris
80	c3jskN	Alignment	not modelled	99.6	21	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
81	c6aonB	Alignment	not modelled	99.6	25	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
82	d2gf3a1	Alignment	not modelled	99.6	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
83	d1cf3a1	Alignment	not modelled	99.6	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
84	d1gpea1	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
85	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
86	d1ju2a1	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
87	c2igoG	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: G: PDB Molecule: pyranose oxidase; PDBTitle: crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose
88	c1tytA	Alignment	not modelled	99.6	22	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
89	c3q9tB	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase
90	c5w1jA	Alignment	not modelled	99.6	22	PDB header: signaling protein Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: echinococcus granulosus thioredoxin glutathione reductas (egtgr)
91	c5mogB	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
92	c2eq7B	Alignment	not modelled	99.6	32	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
93	d2gmha1	Alignment	not modelled	99.6	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
94	c4ntdA	Alignment	not modelled	99.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of hlmi
95	c3fimB	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
96	c5twcA	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
97	c4migC	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
98	c6gncA	Alignment	not modelled	99.6	22	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
99	c4h7uA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose dehydrogenase; PDBTitle: crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype
100	c2gahB	Alignment	not modelled	99.6	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
101	c4gcmB	Alignment	not modelled	99.6	22	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
102	c5jcaL	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
103	c5wgyA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide

					b complex
104	c1gthD_	Alignment	not modelled	99.5	21 PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dhd) from pig, ternary complex with 2 nadph and 5-iodouracil
105	c5odeA_	Alignment	not modelled	99.5	19 PDB header: oxidoreductase Chain: A: PDB Molecule: gll2934 protein; PDBTitle: structure of a novel oxidoreductase from gloeobacter violaceus
106	c4x9mA_	Alignment	not modelled	99.5	13 PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
107	c3axbA_	Alignment	not modelled	99.5	17 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
108	c5dbjA_	Alignment	not modelled	99.5	15 PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
109	d1ryia1	Alignment	not modelled	99.5	15 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
110	c4xwzA_	Alignment	not modelled	99.5	17 PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
111	d2cula1	Alignment	not modelled	99.5	30 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GidA-like
112	c6garB_	Alignment	not modelled	99.5	23 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
113	c2zbwA_	Alignment	not modelled	99.5	19 PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
114	c4rsIA_	Alignment	not modelled	99.5	16 PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
115	d1d5ta1	Alignment	not modelled	99.5	20 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
116	c3i6dA_	Alignment	not modelled	99.5	19 PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
117	c2gmbA_	Alignment	not modelled	99.5	18 PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
118	c3djeA_	Alignment	not modelled	99.5	17 PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine: oxygen oxidoreductase; PDBTitle: crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
119	c1y56B_	Alignment	not modelled	99.5	16 PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
120	c4fk1D_	Alignment	not modelled	99.5	20 PDB header: oxidoreductase Chain: D: PDB Molecule: putative thioredoxin reductase; PDBTitle: crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis