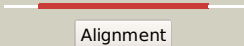

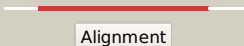

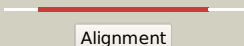







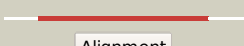






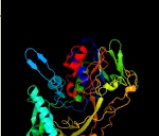




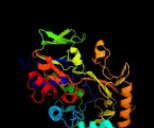








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2852c_(mqo)_3160590_3162071
Date	Wed Aug 7 12:50:52 BST 2019
Unique Job ID	add934bb0368fa08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rgoA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
2	c2rghA_	 Alignment		100.0	16	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
3	c2r4jA_	 Alignment		100.0	11	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
4	c3da1A_	 Alignment		100.0	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.
5	c3dmeB_	 Alignment		100.0	17	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
6	c4x9mA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
7	c4p9sA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmghd
8	c1pj6A_	 Alignment		100.0	16	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
9	c3axbA_	 Alignment		100.0	15	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
10	c4rslA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
11	c4xwzA_	 Alignment		100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine

12	c2gahB_	Alignment		100.0	14	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
13	c5fjnB_	Alignment		100.0	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
14	c3djeA_	Alignment		100.0	12	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
15	c3ps9A_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmc from e. coli
16	c3pvcA_	Alignment		100.0	18	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmc from yersinia pestis
17	c1y56B_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
18	c2olnA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomyacin biosynthesis: closed form at 1.15 a resolution
19	c5hxfF_	Alignment		100.0	16	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
20	c3nyeA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
21	c4yshA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus
22	c6j39A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: fad-dependent glycine oxydase; PDBTitle: crystal structure of cmis2 with inhibitor
23	c6gg2A_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: amino acid oxidase fmpa; PDBTitle: the structure of fsqb from aspergillus fumigatus, a flavoenzyme of the2 amine oxidase family
24	c3bhkA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: monomeric sarcosine oxidase; PDBTitle: crystal structure of r49k mutant of monomeric sarcosine oxidase2 crystallized in phosphate as precipitant
25	c2uzzD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
26	c1ryiB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
27	c5ez7A_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
28	d1pj5a2	Alignment	not modelled	99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
29	d1ryia1	Alignment	not modelled	99.9	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain

30	c1kifE_	Alignment	not modelled	99.9	13	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
31	d2gf3a1	Alignment	not modelled	99.9	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
32	c1c0iA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-amino acid oxidase; PDBTitle: crystal structure of d-amino acid oxidase in complex with two2 anthranilate molecules
33	d3coxa1	Alignment	not modelled	99.8	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
34	c6a2uD_	Alignment	not modelled	99.8	13	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
35	c3vr8E_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
36	c1yq4A_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
37	c1qo8A_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
38	c2aczA_	Alignment	not modelled	99.8	15	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
39	c2jbvA_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into the2 catalytic mechanism
40	c1jrxA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
41	c5hsaG_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: G: PDB Molecule: alcohol oxidase 1; PDBTitle: alcohol oxidase aox1 from pichia pastoris
42	d1d5ta1	Alignment	not modelled	99.8	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
43	c2bs3A_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
44	c1d4cB_	Alignment	not modelled	99.8	17	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
45	c4at2A_	Alignment	not modelled	99.8	15	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
46	d1y0pa2	Alignment	not modelled	99.8	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
47	c6h3gC_	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol oxidase; PDBTitle: alcohol oxidase from phanerochaete chrysosporium
48	c2igoG_	Alignment	not modelled	99.8	12	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
49	d1qo8a2	Alignment	not modelled	99.8	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
50	c2f5vA_	Alignment	not modelled	99.8	9	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.
51	c5xmjE_	Alignment	not modelled	99.8	14	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
52	c3fimB_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
53	c3q9tB_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase
54	c2dcaA_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2;

54	c3ug2A	Alignment	not modelled	99.8	10	PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
55	d1kdga1	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
56	c3p4rM	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
57	c4qi4A	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh
58	d1neka2	Alignment	not modelled	99.8	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
59	c4yntA	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose oxidase, putative; PDBTitle: crystal structure of aspergillus flavus fad glucose dehydrogenase
60	c1zkgA	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
61	c1coyA	Alignment	not modelled	99.8	15	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
62	c4qi7A	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdhn
63	c4h7uA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose dehydrogenase; PDBTitle: crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype
64	c2gewA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
65	c6n56A	Alignment	not modelled	99.7	13	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
66	c4qi6A	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcum thermophilum, mtcdh
67	d1ju2a1	Alignment	not modelled	99.7	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
68	d1n4wa1	Alignment	not modelled	99.7	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
69	d1kf6a2	Alignment	not modelled	99.7	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
70	c1naaB	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
71	c4migC	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
72	d2bcgg1	Alignment	not modelled	99.7	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
73	d2bs2a2	Alignment	not modelled	99.7	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
74	c4udpA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-methanol-choline oxidoreductase; PDBTitle: crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
75	c1gpeA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense
76	c1cf3A	Alignment	not modelled	99.7	17	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger
77	c5nccB	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and2 palmitic acid
78	c1kf6A	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
79	c3t37A	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of pyridoxine 4-oxidase from mesorbium loti
80	d2gqfa1	Alignment	not modelled	99.7	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like

81	c3ka7A	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
82	c2nvkX	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
83	c5g3sB	Alignment	not modelled	99.7	12	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
84	c3cirM	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
85	c2zxiC	Alignment	not modelled	99.7	15	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
86	c1gndA	Alignment	not modelled	99.7	12	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
87	c1ju2A	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
88	c1txR	Alignment	not modelled	99.7	13	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
89	c6c87A	Alignment	not modelled	99.7	14	PDB header: protein transport Chain: A: PDB Molecule: rab gdp dissociation inhibitor alpha; PDBTitle: crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri
90	c4dgaA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crt1 from pantoea ananatis
91	d1d4ca2	Alignment	not modelled	99.7	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
92	c4repA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
93	d1gpea1	Alignment	not modelled	99.7	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
94	c3i6dA	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
95	c3i3IA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
96	c2eq8E	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
97	c5glgA	Alignment	not modelled	99.7	13	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
98	c3cpiH	Alignment	not modelled	99.7	12	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
99	c5uaoA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
100	c2c3dB	Alignment	not modelled	99.7	13	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
101	c1zmcG	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
102	d2i0za1	Alignment	not modelled	99.6	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
103	c3uteB	Alignment	not modelled	99.6	11	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
104	c1tytA	Alignment	not modelled	99.6	16	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
105	c6mp5B	Alignment	not modelled	99.6	10	PDB header: membrane protein, oxidoreductase Chain: B: PDB Molecule: sulfide:quinone oxidoreductase, mitochondrial; PDBTitle: crystal structure of native human sulfide:quinone oxidoreductase

106	c6du7C_	Alignment	not modelled	99.6	10	PDB header: oxidoreductase Chain: C: PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae
107	c4z24A_	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702)
108	c1geuA_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
109	c2fjaC_	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
110	c3atrA_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
111	c3cp2A_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
112	c1bwcA_	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
113	c6b4oB_	Alignment	not modelled	99.6	14	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
114	c3cesB_	Alignment	not modelled	99.6	15	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
115	c4cnjD_	Alignment	not modelled	99.6	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
116	c1v59B_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
117	c3urhB_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
118	c2b9yA_	Alignment	not modelled	99.6	17	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
119	c4c3yF_	Alignment	not modelled	99.6	13	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
120	c5v36A_	Alignment	not modelled	99.6	11	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