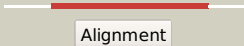

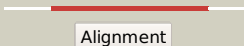

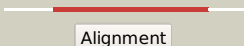







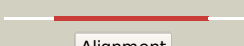











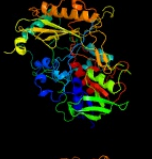
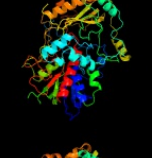
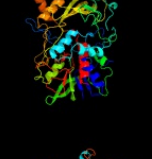






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0492c_(-)_581492_583381
Date	Fri Jul 26 01:50:03 BST 2019
Unique Job ID	51ce3d25221386ff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5nccB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and 2 palmitic acid
2	c1cf3A_	 Alignment		100.0	19	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from aspergillus niger
3	c4yntA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose oxidase, putative; PDBTitle: crystal structure of aspergillus flavus fad glucose dehydrogenase
4	c1gpeA_	 Alignment		100.0	18	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense
5	c4qi7A_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdh
6	c4qi6A_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcum thermophilum, mtc dh
7	c3t37A_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of pyridoxine 4-oxidase from mesorium loti
8	c6h3gC_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol oxidase; PDBTitle: alcohol oxidase from phanerochaete chrysosporium
9	c3fimB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
10	c5hsaG_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: G: PDB Molecule: alcohol oxidase 1; PDBTitle: alcohol oxidase aox1 from pichia pastoris
11	c1naaB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with 2 cellobionolactam

12	c2jbvA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into the2 catalytic mechanism
13	c4qi4A_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh
14	c3q9tB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase
15	c4h7uA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose dehydrogenase; PDBTitle: crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype
16	c4udpA_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-methanol-choline oxidoreductase; PDBTitle: crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
17	c1ju2A_	Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
18	c6a2uD_	Alignment		100.0	23	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
19	c2gewA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
20	c1coyA_	Alignment		100.0	22	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
21	c4z24A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702)
22	c4migC_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
23	d1cf3a1	Alignment	not modelled	100.0	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
24	c2f5vA_	Alignment	not modelled	100.0	17	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.
25	c2igoG_	Alignment	not modelled	100.0	16	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
26	d1kdga1	Alignment	not modelled	100.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
27	d1gpea1	Alignment	not modelled	100.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
28	d1n4wa1	Alignment	not modelled	100.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
						Fold: FAD/NAD(P)-binding domain

29	d3coxa1	Alignment	not modelled	100.0	27	Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
30	d2f5va1	Alignment	not modelled	100.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
31	d1ju2a1	Alignment	not modelled	100.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
32	c5glgA	Alignment	not modelled	99.9	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
33	c4at2A	Alignment	not modelled	99.9	14	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
34	c4repA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase, flavoprotein Chain: A; PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
35	c3p4rM	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: M; PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
36	c1kf6A	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A; PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
37	c5xmjE	Alignment	not modelled	99.7	14	PDB header: electron transport Chain: E; PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
38	c2aczA	Alignment	not modelled	99.7	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	c1yq4A	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A; PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
40	c1qo8A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A; PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
41	c1jrxA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A; PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
42	c3vr8E	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: E; PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
43	c4c3yF	Alignment	not modelled	99.7	14	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
44	d1d5ta1	Alignment	not modelled	99.6	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
45	c1d4cB	Alignment	not modelled	99.6	23	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
46	c6n56A	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: A; PDB Molecule: fumarate reductase, flavo protein subunit; PDBTitle: crystal structure of fumarate reductase, flavo protein subunit, from2 helicobacter pylori g27
47	c2bs3A	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A; PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
48	d1y0pa2	Alignment	not modelled	99.6	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
49	d1qo8a2	Alignment	not modelled	99.6	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
50	c2fjaC	Alignment	not modelled	99.5	21	PDB header: oxidoreductase Chain: C; PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
51	c3cirM	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: M; PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
52	c4p9sA	Alignment	not modelled	99.5	23	PDB header: oxidoreductase Chain: A; PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmghd
53	c3nc9A	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A; PDB Molecule: trna 5-methylaminomethyl-2-thiouridine

53	cyps2A	Alignment	not modelled	99.5	12	biosynthesis PDB header: crystal structure of mnmc from e. coli PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase;
54	c2rghA	Alignment	not modelled	99.5	19	PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase;
55	c2rgoA	Alignment	not modelled	99.5	17	PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis
56	c3pvcA	Alignment	not modelled	99.5	12	PDBTitle: crystal structure of apo mnmc from yersinia pestis PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1;
57	c1txR	Alignment	not modelled	99.5	10	PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
58	d1kf6a2	Alignment	not modelled	99.5	20	Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956;
59	c3nlcA	Alignment	not modelled	99.5	16	PDBTitle: crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
60	d2bcgg1	Alignment	not modelled	99.5	11	Family: GDI-like N domain PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase;
61	c3ka7A	Alignment	not modelled	99.5	15	PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208 PDB header: hydrolase Chain: B: PDB Molecule: l-amino acid deaminase;
62	c5fjnB	Alignment	not modelled	99.5	22	PDBTitle: structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase;
63	c5hxwF	Alignment	not modelled	99.5	22	PDBTitle: l-amino acid deaminase from proteus vulgaris Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
64	d1d4ca2	Alignment	not modelled	99.5	26	Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain PDB header: oxidoreductase Chain: A: PDB Molecule: n,n-dimethylglycine oxidase;
65	c1pj6A	Alignment	not modelled	99.4	18	PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
66	d1pj5a2	Alignment	not modelled	99.4	21	Family: FAD-linked reductases, N-terminal domain PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein;
67	c3dmeB	Alignment	not modelled	99.4	20	PDBTitle: crystal structure of conserved exported protein from bordetella2 pertussis. northeast structural genomics target ber141 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
68	d2bs2a2	Alignment	not modelled	99.4	18	Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
69	d2gf3a1	Alignment	not modelled	99.4	18	Family: FAD-linked reductases, N-terminal domain PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase;
70	c3da1A	Alignment	not modelled	99.4	27	PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167. Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
71	d1vg0a1	Alignment	not modelled	99.4	10	Family: GDI-like N domain PDB header: oxidoreductase Chain: A: PDB Molecule: adenylylsulfate reductase;
72	c3gyxA	Alignment	not modelled	99.4	17	PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor;
73	c1gndA	Alignment	not modelled	99.4	12	PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase;
74	c2r4jA	Alignment	not modelled	99.4	17	PDBTitle: crystal structure of escherichia coli semet substituted glycerol-3-2 phosphate dehydrogenase in complex with dhap PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase;
75	c3axbA	Alignment	not modelled	99.4	18	PDBTitle: structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
76	d2gqfa1	Alignment	not modelled	99.4	16	Family: HI0933 N-terminal domain-like Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain
77	d1neka2	Alignment	not modelled	99.4	18	Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain PDB header: oxidoreductase

78	c5mogB_	Alignment	not modelled	99.4	12	Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
79	c2c3dB_	Alignment	not modelled	99.4	18	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
80	c4x9mA_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
81	d1ryia1	Alignment	not modelled	99.4	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
82	c4xwzA_	Alignment	not modelled	99.3	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
83	c3cpiH_	Alignment	not modelled	99.3	12	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
84	c3dgzA_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
85	d2i0za1	Alignment	not modelled	99.3	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
86	c1zkqA_	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
87	c2zxiC_	Alignment	not modelled	99.3	20	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
88	c6c87A_	Alignment	not modelled	99.3	11	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
89	c2nvkX_	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
90	c3djeA_	Alignment	not modelled	99.3	16	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
91	c1zmcG_	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
92	c3g05B_	Alignment	not modelled	99.3	22	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
93	c4dggA_	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis
94	c2ivdA_	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
95	c6gg2A_	Alignment	not modelled	99.3	15	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
96	c5g3sB_	Alignment	not modelled	99.3	13	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	c2olnA_	Alignment	not modelled	99.2	23	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
98	c2gahB_	Alignment	not modelled	99.2	19	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
99	c3cesB_	Alignment	not modelled	99.2	22	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
100	c4y4nE_	Alignment	not modelled	99.2	25	PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus
101	c3jskN_	Alignment	not modelled	99.2	22	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
102	d1chua2	Alignment	not modelled	99.2	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/flavinate reductase flavoprotein

						N-terminal domain
103	c2e5vA_	Alignment	not modelled	99.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
104	c3v76A_	Alignment	not modelled	99.2	23	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
105	c6qkgB_	Alignment	not modelled	99.2	19	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
106	c3urhB_	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
107	c2eq8E_	Alignment	not modelled	99.2	24	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
108	c1v59B_	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
109	c1ojtA_	Alignment	not modelled	99.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
110	c3cp2A_	Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
111	c6bz0C_	Alignment	not modelled	99.1	23	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.
112	c4dnaA_	Alignment	not modelled	99.1	24	PDB header: oxidoreductase Chain: A: PDB Molecule: probable glutathione reductase; PDBTitle: crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
113	c3o0hA_	Alignment	not modelled	99.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
114	c1geuA_	Alignment	not modelled	99.1	17	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
115	c4rsIA_	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
116	c1dxIC_	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pismus sativum
117	c3p1wA_	Alignment	not modelled	99.1	12	PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c
118	c6b4oB_	Alignment	not modelled	99.1	20	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
119	d1o5wa1	Alignment	not modelled	99.1	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
120	c1m6iA_	Alignment	not modelled	99.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: crystal structure of apoptosis inducing factor (aif)