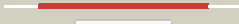



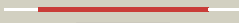




















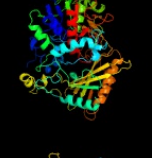


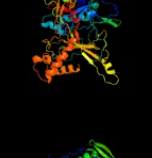
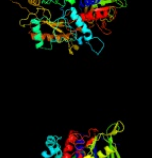
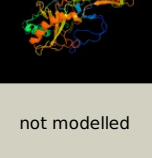


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1279_(-)_1430068_1431654
Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	d5a142e42e0233f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4yntA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose oxidase, putative; PDBTitle: crystal structure of aspergillus flavus fad glucose dehydrogenase
2	c5nccB_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and 2 palmitic acid
3	c3fimB_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
4	c2jbvA_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into the 2 catalytic mechanism
5	c5hsaG_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: G: PDB Molecule: alcohol oxidase 1; PDBTitle: alcohol oxidase aox1 from pichia pastoris
6	c4h7uA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose dehydrogenase; PDBTitle: crystal structure of pyranose dehydrogenase from agaricus meleagris, 2 wildtype
7	c3t37A_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of pyridoxine 4-oxidase from mesorhizobium loti
8	c6h3gC_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol oxidase; PDBTitle: alcohol oxidase from phanerochaete chrysosporium
9	c1cf3A_	 Alignment		100.0	26	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from aspergillus niger
10	c3q9tB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase
11	c1gpeA_	 Alignment		100.0	23	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense

12	c4udpA	Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-methanol-choline oxidoreductase; PDBTitle: crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
13	c4qi4A	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh
14	c4qi7A	Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdh
15	c4qi6A	Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcum thermophilum, mtdh
16	c1naaB	Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
17	c1ju2A	Alignment		100.0	24	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
18	c4z24A	Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702)
19	c6a2uD	Alignment		100.0	20	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
20	c1coyA	Alignment		100.0	18	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	c2gewA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
22	d1cf3a1	Alignment	not modelled	100.0	34	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
23	c4migC	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
24	c2igoG	Alignment	not modelled	100.0	17	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
25	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.
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	32	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	22	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	20	Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
30	d2f5va1	Alignment	not modelled	100.0	27	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	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
32	c5glgA	Alignment	not modelled	99.8	15	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	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
34	c4at2A	Alignment	not modelled	99.7	17	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
35	c4c3yF	Alignment	not modelled	99.6	15	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
36	c3vr8E	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
37	c1yq4A	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
38	c1jrxA	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
39	d1d5ta1	Alignment	not modelled	99.6	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
40	c1qo8A	Alignment	not modelled	99.6	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
41	c1d4cB	Alignment	not modelled	99.6	16	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
42	c3p4rM	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
43	d1y0pa2	Alignment	not modelled	99.6	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
44	c1kf6A	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
45	d2bcgg1	Alignment	not modelled	99.5	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
46	d1gpea2	Alignment	not modelled	99.5	12	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
47	c3cirM	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
48	c2aczA	Alignment	not modelled	99.5	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
49	d1cf3a2	Alignment	not modelled	99.5	16	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
50	d1qo8a2	Alignment	not modelled	99.5	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
51	c5xmjE	Alignment	not modelled	99.5	13	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
52	c2bs3A	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinnella succinogenes
53	c2fjaC	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with

						substrate
54	c2rghA	Alignment	not modelled	99.4	14	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
55	c6n56A	Alignment	not modelled	99.4	14	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
56	d1kf6a2	Alignment	not modelled	99.4	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
57	c1gndA	Alignment	not modelled	99.4	12	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
58	c2rgoA	Alignment	not modelled	99.4	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
59	d1d4ca2	Alignment	not modelled	99.4	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
60	d2gf3a1	Alignment	not modelled	99.4	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
61	d2bs2a2	Alignment	not modelled	99.4	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
62	d1pj5a2	Alignment	not modelled	99.4	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
63	d1ryia1	Alignment	not modelled	99.4	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
64	c2r4jA	Alignment	not modelled	99.3	19	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
65	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
66	c4p9sA	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
67	c6c87A	Alignment	not modelled	99.3	12	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
68	c1pj6A	Alignment	not modelled	99.3	20	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
69	c5hxwF	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
70	c3da1A	Alignment	not modelled	99.3	17	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.
71	c5fjnB	Alignment	not modelled	99.3	19	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
72	c3dmeB	Alignment	not modelled	99.3	16	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
73	c1zkgA	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
74	c3dqzA	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
75	d2gqfa1	Alignment	not modelled	99.2	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
76	c3gyxA	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
77	d1chua2	Alignment	not modelled	99.2	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
78	c4x9mA	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound PDB header: oxidoreductase

79	c3axbA	Alignment	not modelled	99.2	21	Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix
80	d1neka2	Alignment	not modelled	99.2	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
81	d2i0za1	Alignment	not modelled	99.2	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
82	c3g05B	Alignment	not modelled	99.2	21	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
83	c2c3dB	Alignment	not modelled	99.2	16	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
84	d1ju2a2	Alignment	not modelled	99.2	18	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GMC oxidoreductases
85	c2gahB	Alignment	not modelled	99.2	21	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
86	c4xwzA	Alignment	not modelled	99.2	19	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
87	c4dgaA	Alignment	not modelled	99.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crt1 from pantoea ananatis
88	c2zxiC	Alignment	not modelled	99.2	18	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
89	c2olnA	Alignment	not modelled	99.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
90	c2nvkX	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
91	c3djeA	Alignment	not modelled	99.1	15	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
92	c1chuA	Alignment	not modelled	99.1	28	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
93	c1hyuA	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
94	c3cesB	Alignment	not modelled	99.1	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
95	c3cp8C	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
96	c1zmcG	Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
97	c3jskN	Alignment	not modelled	99.1	26	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
98	c2e5vA	Alignment	not modelled	99.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
99	c1y56B	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
100	d1jnra2	Alignment	not modelled	99.0	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
101	c2eq8E	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
102	c3cp2A	Alignment	not modelled	99.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
103	d1rp0a1	Alianment	not modelled	99.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

						Family: Thi4-like
104	c3urhB_	Alignment	not modelled	99.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
105	c4rslA_	Alignment	not modelled	99.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
106	c3ka7A_	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
107	d2cula1	Alignment	not modelled	99.0	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GidA-like
108	c3nyeA_	Alignment	not modelled	98.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
109	c3nlcA_	Alignment	not modelled	98.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956; PDBTitle: crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
110	c4y4nE_	Alignment	not modelled	98.9	24	PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus
111	c1ltxR_	Alignment	not modelled	98.9	21	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
112	c6gg2A_	Alignment	not modelled	98.9	14	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
113	c5g3sB_	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase vioa; PDBTitle: the structure of the l-tryptophan oxidase vioa from chromobacterium2 violaceum - samarium derivative
114	c5iriA_	Alignment	not modelled	98.9	30	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
115	c5mogB_	Alignment	not modelled	98.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
116	c6qkgB_	Alignment	not modelled	98.9	21	PDB header: flavoprotein Chain: B: PDB Molecule: ncr a; PDBTitle: 2-naphthoyl-coa reductase(ncr)
117	c4cnjD_	Alignment	not modelled	98.8	27	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
118	c1gv4A_	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: programed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif)
119	c6c6rA_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad
120	c4ap3A_	Alignment	not modelled	98.8	30	PDB header: oxidoreductase Chain: A: PDB Molecule: steroid monooxygenase; PDBTitle: oxidized steroid monooxygenase bound to nadp