

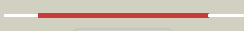












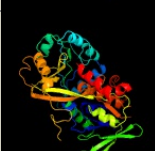

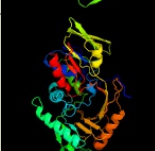















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3302c_glpD2_3687682_3689439
Date	Thu Aug 8 16:20:51 BST 2019
Unique Job ID	ac4faf15c462709c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rgoA_	 Alignment		100.0	30	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	29	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	c3da1A_	 Alignment		100.0	32	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.
4	c2r4jA_	 Alignment		100.0	32	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
5	c3dmeB_	 Alignment		100.0	20	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	19	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	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
8	c1pj6A_	 Alignment		100.0	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
9	c5fjnB_	 Alignment		100.0	17	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
10	c3axbA_	 Alignment		100.0	19	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
11	c2gahB_	 Alignment		100.0	13	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

12	c4yshA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus
13	c4xwzA_	Alignment		100.0	14	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
14	c1y56B_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
15	c5hxfF_	Alignment		100.0	18	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
16	c6j39A_	Alignment		100.0	20	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: fad-dependent glycine oxidase; PDBTitle: crystal structure of cmis2 with inhibitor
17	c3nyeA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
18	c4rslA_	Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
19	c2olnA_	Alignment		100.0	18	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
20	c3ps9A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmc from e. coli
21	c3djeA_	Alignment	not modelled	100.0	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
22	c3pvcA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmc from yersinia pestis
23	c1ryiB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
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	c5ez7A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
26	c6gg2A_	Alignment	not modelled	100.0	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
27	c1kifE_	Alignment	not modelled	100.0	17	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
28	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 (mtx)

29	c1c0iA	Alignment	not modelled	99.9	20	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
30	d1ryia1	Alignment	not modelled	99.9	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
31	d1pj5a2	Alignment	not modelled	99.9	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
32	d2gf3a1	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
33	c1x31A	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
34	c1yq4A	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
35	c3vr8E	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquoinol-fumarate reductase from the parasitic2 nematode ascaris suum
36	c1jrxA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
37	c1qo8A	Alignment	not modelled	99.8	16	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	14	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	c2bs3A	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
40	c1d4cB	Alignment	not modelled	99.8	15	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
41	d1qo8a2	Alignment	not modelled	99.8	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
42	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
43	c5xmjE	Alignment	not modelled	99.8	16	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
44	d1y0pa2	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
45	d1kf6a2	Alignment	not modelled	99.7	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
46	d1c0pa1	Alignment	not modelled	99.7	22	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
47	d2bs2a2	Alignment	not modelled	99.7	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
48	c3ka7A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
49	c4at2A	Alignment	not modelled	99.7	16	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
50	c1y56A	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
51	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
52	c6n56A	Alignment	not modelled	99.7	18	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
						Fold: Nucleotide-binding domain

53	d1kifa1	Alignment	not modelled	99.7	18	Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
54	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
55	c3cirM	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: e. coli quinol fumarate reductase frda t234a mutation
56	c4dgkA	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crt1 from pantoea ananatis
57	c5g3sB	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase v1oa; PDBTitle: the structure of the l-tryptophan oxidase v1oa from chromobacterium2 violaceum - samarium derivative
58	c4c3yF	Alignment	not modelled	99.6	21	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
59	c3atrA	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
60	d1d5ta1	Alignment	not modelled	99.6	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
61	c5glgA	Alignment	not modelled	99.6	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
62	c6bnzA	Alignment	not modelled	99.6	13	PDB header: flavoprotein Chain: A: PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm
63	d1d4ca2	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
64	c2weuD	Alignment	not modelled	99.6	17	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
65	d2i0za1	Alignment	not modelled	99.6	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
66	c3gyxA	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
67	c5uaoA	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
68	d2gqfa1	Alignment	not modelled	99.6	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
69	c5mogB	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
70	c6ib5B	Alignment	not modelled	99.5	15	PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
71	c2fjaC	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with substrate
72	c2zxiC	Alignment	not modelled	99.5	22	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
73	c3g05B	Alignment	not modelled	99.5	26	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
74	c1zkqA	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
75	d2bcgg1	Alignment	not modelled	99.5	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
76	c3dqzA	Alignment	not modelled	99.5	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
77	c6c6rA	Alignment	not modelled	99.5	18	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad
78	c3e1tA	Alignment	not modelled	99.5	18	PDB header: flavoprotein Chain: A: PDB Molecule: halogenase; PDBTitle: structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent

					halogenases
79	d1o5wa1	Alignment	not modelled	99.5	18 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
80	c2ardA	Alignment	not modelled	99.5	12 PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase prna; PDBTitle: the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
81	d1kdga1	Alignment	not modelled	99.5	17 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
82	c3cesB	Alignment	not modelled	99.5	26 PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of e.coli mmg (gida), a highly-conserved trna2 modifying enzyme
83	c3cp2A	Alignment	not modelled	99.5	23 PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
84	c5dbjA	Alignment	not modelled	99.5	15 PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
85	c5ttkB	Alignment	not modelled	99.5	17 PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida
86	c2pyxA	Alignment	not modelled	99.5	13 PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase; PDBTitle: crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
87	c1coyA	Alignment	not modelled	99.5	17 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
88	c5bulA	Alignment	not modelled	99.5	15 PDB header: hydrolase Chain: A: PDB Molecule: flavin-dependent halogenase triple mutant; PDBTitle: structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
89	c1ltxR	Alignment	not modelled	99.5	16 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
90	d3coxa1	Alignment	not modelled	99.5	17 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
91	c3i6dA	Alignment	not modelled	99.5	14 PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
92	c1naaB	Alignment	not modelled	99.5	19 PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
93	c3cp8C	Alignment	not modelled	99.5	21 PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
94	c2f5vA	Alignment	not modelled	99.5	16 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.
95	c3i3IA	Alignment	not modelled	99.5	16 PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
96	c2e4gB	Alignment	not modelled	99.5	13 PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
97	c4y4nE	Alignment	not modelled	99.5	25 PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus
98	c4qi6A	Alignment	not modelled	99.5	20 PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcus thermophilum, mtdh
99	c3nixF	Alignment	not modelled	99.5	15 PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
100	c6friA	Alignment	not modelled	99.5	15 PDB header: flavoprotein Chain: A: PDB Molecule: tryptophan halogenase superfamily; PDBTitle: brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
101	c2igoG	Alignment	not modelled	99.5	15 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
102	c4repA	Alignment	not modelled	99.4	14 PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
103	c3jskN	Alignment	not modelled	99.4	24 PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
104	c2gawA	Alignment	not modelled	99.4	17 PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase;

104	c2gEWA	Alignment	not modelled	99.4	17	PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo) PDB header: oxidoreductase
105	c4qj4A	Alignment	not modelled	99.4	20	Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh
106	c2qa2A	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase cabe; PDBTitle: crystal structure of cabe, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
107	c2nvkX	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
108	c6a2uD	Alignment	not modelled	99.4	18	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
109	c6c87A	Alignment	not modelled	99.4	17	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
110	c2gmhA	Alignment	not modelled	99.4	17	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
111	d1vg0a1	Alignment	not modelled	99.4	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
112	c5wgyA	Alignment	not modelled	99.4	21	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex
113	d1chua2	Alignment	not modelled	99.4	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
114	c1s3bB	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase [flavin-containing] b; PDBTitle: crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
115	c1gndA	Alignment	not modelled	99.4	17	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
116	c4qi7A	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdH
117	c3cpiH	Alignment	not modelled	99.4	17	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
118	c6j0zC	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpK
119	c3cgvA	Alignment	not modelled	99.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: geranylgeranyl reductase related protein; PDBTitle: crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
120	c4cniD	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: D: PDB Molecule: l-amino acid oxidase; PDBTitle: l-aminoacetone oxidase from streptococcus oligofermentans2 belongs to a new 3-domain family of bacterial flavoproteins