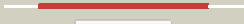



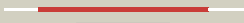



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2677c_(hemY)_2992644_2994002
Date	Wed Aug 7 12:50:33 BST 2019
Unique Job ID	2315b2f922263ddd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ivdA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
2	c3nksA_	 Alignment		100.0	25	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of human protoporphyrinogen ix oxidase
3	c3lovA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
4	c3i6dA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
5	c1s3bB_	 Alignment		100.0	16	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
6	c1sezA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase
7	c3uteB_	 Alignment		100.0	15	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
8	c4i58A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevbacterium oxydans ih-35a
9	c3rhaA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
10	c2yg4B_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
11	c4gutA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1b; PDBTitle: crystal structure of lsd2-npac

12	c3x0vA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lysine oxidase; PDBTitle: structure of l-lysine oxidase
13	c1f8sA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
14	c4dshB_	Alignment		100.0	16	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of reduced udp-galactopyranose mutase
15	c5mogB_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
16	c5ttkB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida
17	c6cr0A_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-6-hydroxynicotine oxidase; PDBTitle: 1.55 a resolution structure of (s)-6-hydroxynicotine oxidase from2 shinella hzn7
18	c2vviD_	Alignment		100.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: monoamine oxidase n; PDBTitle: the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
19	c4iv9B_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: tryptophan 2-monooxygenase; PDBTitle: structure of the flavoprotein tryptophan-2-monooxygenase
20	c5mbxA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal n(1)-acetyl-spermine/spermidine oxidase; PDBTitle: crystal structure of reduced murine n1-acetylpolymine oxidase in2 complex with n1-acetylspermine
21	c2hkoA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1
22	c2xagA_	Alignment	not modelled	100.0	19	PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
23	c2v1dA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
24	c1h83A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase; PDBTitle: structure of polyamine oxidase in complex with2 1,8-diaminooctane
25	c2jb1B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: l-amino acid oxidase; PDBTitle: the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
26	c3we0A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase/monooxygenase; PDBTitle: l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
27	c3k7tB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-hydroxy-l-nicotine oxidase; PDBTitle: crystal structure of apo-form 6-hydroxy-l-nicotine oxidase, crystal2 form p3121
28	c5g3sB_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase viaa; PDBTitle: the structure of the l-tryptophan oxidase viaa from chromobacterium2 violaceum - samarium derivative PDB header: oxidoreductase

29	c3ka7A_	Alignment	not modelled	100.0	11	Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
30	c1i8tB_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli
31	c3bnuA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase fms1; PDBTitle: crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
32	c4repA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
33	c2bi8A_	Alignment	not modelled	100.0	11	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
34	c2b9yA_	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes
35	c4mo2A_	Alignment	not modelled	100.0	11	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-n-acetylgalactopyranose mutase from2 campylobacter jejuni
36	c1v0jB_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
37	c3hdqI_	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: I: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
38	c6fjhB_	Alignment	not modelled	100.0	16	PDB header: flavoprotein Chain: B: PDB Molecule: lkce; PDBTitle: crystal structure of the seleniated lkce from streptomyces rochei
39	d1o5wa1	Alignment	not modelled	100.0	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
40	c1ltxR_	Alignment	not modelled	100.0	12	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
41	c2yr6A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pro-enzyme of l-phenylalanine oxidase; PDBTitle: crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501
42	d2v5za1	Alignment	not modelled	100.0	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
43	d2dw4a2	Alignment	not modelled	100.0	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
44	c4dgaA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crtI from pantoea ananatis
45	c3qj4A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
46	c3nrrA_	Alignment	not modelled	100.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pf1083; PDBTitle: crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
47	d1reoa1	Alignment	not modelled	100.0	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
48	d2iida1	Alignment	not modelled	100.0	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
49	c3cpiH_	Alignment	not modelled	100.0	11	PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi
50	c6c87A_	Alignment	not modelled	100.0	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
51	d2ivda1	Alignment	not modelled	100.0	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
52	c1gndA_	Alignment	not modelled	99.9	11	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
53	c1yvvB_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
54	d1b5qa1	Alignment	not modelled	99.9	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain

55	d1seza1	Alignment	not modelled	99.9	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
56	d1d5ta1	Alignment	not modelled	99.9	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
57	d2bi7a1	Alignment	not modelled	99.9	14	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
58	c2e1mA	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
59	c3p1wA	Alignment	not modelled	99.9	10	PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c
60	d1i8ta1	Alignment	not modelled	99.9	17	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
61	d2bcgg1	Alignment	not modelled	99.9	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
62	d1vg0a1	Alignment	not modelled	99.9	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
63	c4ia6B	Alignment	not modelled	99.9	14	PDB header: immune system Chain: B: PDB Molecule: myosin-crossreactive antigen; PDBTitle: hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah)
64	c4x9mA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
65	c3nlcA	Alignment	not modelled	99.7	9	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
66	c5fjnB	Alignment	not modelled	99.7	15	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
67	c2olnA	Alignment	not modelled	99.7	14	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
68	c2gmhA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
69	c4rsIA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
70	c3i3IA	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
71	c1pj6A	Alignment	not modelled	99.6	14	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
72	c3axbA	Alignment	not modelled	99.6	13	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
73	c3dmeB	Alignment	not modelled	99.6	14	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
74	c5hxwF	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
75	c6gg2A	Alignment	not modelled	99.6	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
76	c3djeA	Alignment	not modelled	99.6	13	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
77	c2gahB	Alignment	not modelled	99.6	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
78	c4xwzA	Alignment	not modelled	99.6	15	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
79	c3bhkA	Alignment	not modelled	99.6	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
80	c1v56B	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase;

80	c1y3bB	Alignment	not modelled	99.8	15	PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii PDB header: oxidoreductase
81	c5xgvB	Alignment	not modelled	99.6	17	Chain: B; PDB Molecule: pyre3; PDBTitle: the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
82	c4k2ZA	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: A; PDB Molecule: protein visc; PDBTitle: structure of the c-terminal truncated form of e.coli c5-hydroxylase2 ubii involved in ubiquinone (q8) biosynthesis
83	c2qa2A	Alignment	not modelled	99.5	18	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
84	c3ps9A	Alignment	not modelled	99.5	15	PDB header: transferase Chain: A; PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mmmc from e. coli
85	c6bznA	Alignment	not modelled	99.5	15	PDB header: flavoprotein Chain: A; PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm
86	c4p9sA	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A; PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
87	c5bulA	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A; PDB Molecule: flavin-dependent halogenase triple mutant; PDBTitle: structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
88	c1ps9A	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: A; PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
89	c3atrA	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A; PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfobolus acidocaldarius co-2 crystallized with its ligand
90	c3nixF	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: F; PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
91	c6j39A	Alignment	not modelled	99.5	16	PDB header: oxidoreductase/inhibitor Chain: A; PDB Molecule: fad-dependent glycine oxydase; PDBTitle: crystal structure of cmis2 with inhibitor
92	c3cqvA	Alignment	not modelled	99.5	16	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
93	c5dbjA	Alignment	not modelled	99.5	14	PDB header: flavoprotein Chain: A; PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
94	c6j0zC	Alignment	not modelled	99.5	19	PDB header: oxidoreductase Chain: C; PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpk
95	c3pvcA	Alignment	not modelled	99.5	14	PDB header: oxidoreductase, transferase Chain: A; PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mmmc from yersinia pestis
96	c6du7C	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: C; PDB Molecule: glutathione reductase; PDBTitle: glutathione reductase from streptococcus pneumoniae
97	c3cp2A	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A; PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
98	d2gqfa1	Alignment	not modelled	99.4	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
99	c4k2xB	Alignment	not modelled	99.4	17	PDB header: oxidoreductase, flavoprotein Chain: B; PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
100	c4bk2A	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A; PDB Molecule: probable salicylate monooxygenase; PDBTitle: crystal structure of 3-hydroxybenzoate 6-hydroxylase2 uncovers lipid-assisted flavoprotein strategy for3 regioselective aromatic hydroxylation: q301e mutant
101	d2gf3a1	Alignment	not modelled	99.4	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
102	c3nyeA	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A; PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
103	c4yshA	Alignment	not modelled	99.4	11	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus
104	c3e1tA	Alignment	not modelled	99.4	14	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
						PDB header: rna binding protein Chain: B; PDB Molecule: trna uridine 5-carboxymethylaminomethyl

105	c3g05B_	Alignment	not modelled	99.4	16	modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
106	c2rgoA_	Alignment	not modelled	99.4	11	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
107	c3cesB_	Alignment	not modelled	99.4	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
108	c2qa1A_	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis
109	c3ihgA_	Alignment	not modelled	99.4	16	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
110	c5kowA_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pentachlorophenol 4-monoxygenase; PDBTitle: structure of rifampicin monoxygenase
111	d2gmha1	Alignment	not modelled	99.4	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
112	c5ez7A_	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
113	c2uzzD_	Alignment	not modelled	99.4	10	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
114	c3cp8C_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
115	c5tukC_	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51)
116	c2e1mC_	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
117	c2rghA_	Alignment	not modelled	99.3	10	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
118	c3fmwC_	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxygenase; PDBTitle: the crystal structure of mtmoiv, a baeyer-villiger monoxygenase from2 the mithramycin biosynthetic pathway in streptomyces argillaceus.
119	c2zxiC_	Alignment	not modelled	99.3	12	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
120	c2xdoC_	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monoxygenase tetx2 from2 bacteroides thetaiotaomicron