

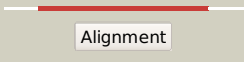

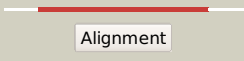

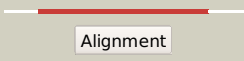

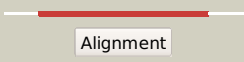

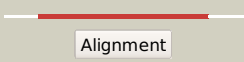

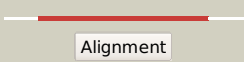

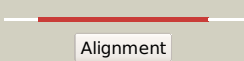

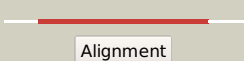

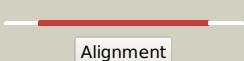

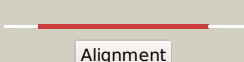
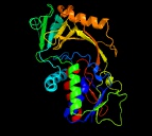

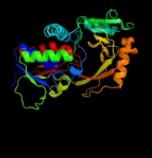

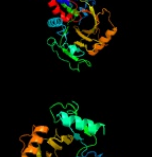

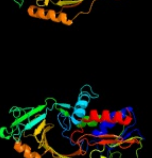


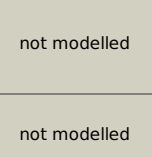


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1905c_(aao)_2151440_2152402
Date	Fri Aug 2 13:30:52 BST 2019
Unique Job ID	3671b12d4492595b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kifE_	 Alignment		100.0	32	PDB header: flavoprotein Chain: E; PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
2	c3ps9A_	 Alignment		100.0	13	PDB header: transferase Chain: A; PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmc from e. coli
3	c3dmeB_	 Alignment		100.0	21	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
4	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
5	c4p9sA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
6	c3pvcA_	 Alignment		100.0	15	PDB header: oxidoreductase, transferase Chain: A; PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmc from yersinia pestis
7	c1pj6A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
8	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
9	c4xwzA_	 Alignment		100.0	16	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
10	c2gahB_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: B; PDB Molecule: heterotetrameric sarcosine oxidase beta-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
11	c6j39A_	 Alignment		100.0	22	PDB header: oxidoreductase/inhibitor Chain: A; PDB Molecule: fad-dependent glycine oxydase; PDBTitle: crystal structure of cmis2 with inhibitor

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	c1y56B_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
14	c3djeA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine: oxygen oxidoreductase; PDBTitle: crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
15	c1c0iA_	Alignment		100.0	27	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
16	c4rsiA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
17	c5fjnB_	Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: l-amino acid deaminase; PDBTitle: structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate
18	c3nyeA_	Alignment		100.0	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
19	c5hxfW_	Alignment		100.0	17	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
20	c1ryiB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
21	c2r4iA_	Alignment	not modelled	100.0	15	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
22	c3bhkA_	Alignment	not modelled	100.0	15	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
23	c2uzzD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
24	c6gg2A_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: amino acid oxidase frmpa; PDBTitle: the structure of fsqb from aspergillus fumigatus, a flavoenzyme of the2 amine oxidase family
25	c2oInA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomyacin biosynthesis: closed form at 1.15 a resolution
26	c2rgoA_	Alignment	not modelled	100.0	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
27	d1c0pa1	Alignment	not modelled	100.0	30	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
28	c2rghA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2

					streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
29	d1kifa1	Alignment	not modelled	100.0	36 Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
30	c3da1A	Alignment	not modelled	100.0	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.
31	c5ez7A	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
32	d2gf3a1	Alignment	not modelled	99.9	19 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
33	d1ryia1	Alignment	not modelled	99.9	16 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
34	d1pj5a2	Alignment	not modelled	99.9	14 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
35	c5uaoA	Alignment	not modelled	99.7	14 PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
36	c2weuD	Alignment	not modelled	99.7	14 PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
37	c3i6dA	Alignment	not modelled	99.7	12 PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
38	c4dgaA	Alignment	not modelled	99.7	13 PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis
39	c3i3iA	Alignment	not modelled	99.7	14 PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
40	c6friA	Alignment	not modelled	99.7	17 PDB header: flavoprotein Chain: A: PDB Molecule: tryptophan halogenase superfamily; PDBTitle: brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
41	c2ardA	Alignment	not modelled	99.7	9 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
42	c6ib5B	Alignment	not modelled	99.7	11 PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
43	c2qa2A	Alignment	not modelled	99.7	16 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
44	c5x68B	Alignment	not modelled	99.6	13 PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of human kmo
45	c6j0zC	Alignment	not modelled	99.6	17 PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpk
46	c5xgvB	Alignment	not modelled	99.6	16 PDB header: oxidoreductase Chain: B: PDB Molecule: pyre3; PDBTitle: the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
47	c3atrA	Alignment	not modelled	99.6	14 PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
48	c5hy5A	Alignment	not modelled	99.6	14 PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 6-halogenase; PDBTitle: crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini
49	c6c6rA	Alignment	not modelled	99.6	15 PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad
50	c6bnzA	Alignment	not modelled	99.6	14 PDB header: flavoprotein Chain: A: PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm
51	c5bukA	Alignment	not modelled	99.6	13 PDB header: oxidoreductase Chain: A: PDB Molecule: fadh2-dependent halogenase; PDBTitle: structure of flavin-dependent chlorinase mpy16
52	c2e4gB	Alignment	not modelled	99.6	14 PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
53	c2pyxA	Alignment	not modelled	99.6	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
54	c5dbjA	Alignment	not modelled	99.6	13 PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta

55	c3e1tA	Alignment	not modelled	99.6	15	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
56	c1phhA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: p-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
57	c3nixF	Alignment	not modelled	99.6	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.
58	c3cgvA	Alignment	not modelled	99.6	14	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
59	c2qa1A	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis
60	c3fmwC	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxygenase; PDBTitle: the crystal structure of mtmoiv, a baeyer-villiger monooxygenase from2 the mithramycin biosynthetic pathway in streptomyces argillaceus.
61	c5bulA	Alignment	not modelled	99.6	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
62	c3ka7A	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
63	c4k2xB	Alignment	not modelled	99.6	17	PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
64	c5fn0C	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: C: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of pseudomonas fluorescens kynurenine-3-2 monooxygenase (kmo) in complex with gsk180
65	c2dkhA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteronei, in complex with the substrate
66	c5kowA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pentachlorophenol 4-monooxygenase; PDBTitle: structure of rifampicin monooxygenase
67	c4k22A	Alignment	not modelled	99.5	16	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
68	c4j33B	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of kynurenine 3-monooxygenase (kmo-394)
69	c2r0gB	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: rebcb; PDBTitle: chromopyrrolic acid-soaked rebcb with bound 7-carboxy-k252c
70	c4n9xA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of the octaprenyl-methyl-methoxy-benzo molecule from2 erwina carotovora subsp. atroseptica strain scri 1043 / atcc baa-672,3 northeast structural genomics consortium (nesg) target ewr161
71	c3allA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
72	c3ihgA	Alignment	not modelled	99.5	14	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
73	c4bk2A	Alignment	not modelled	99.5	17	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
74	c3rp7A	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid
75	c6aioA	Alignment	not modelled	99.5	17	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
76	c5eowA	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440
77	c3gmbB	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase

78	c2gmhA	Alignment	not modelled	99.4	13	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
79	c1ltxR	Alignment	not modelled	99.4	10	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
80	c2xdoC	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
81	c5tula	Alignment	not modelled	99.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: tetracycline destructase tet(55); PDBTitle: crystal structure of tetracycline destructase tet(55)
82	c5tukC	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51)
83	c1pn0A	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
84	c4dshB	Alignment	not modelled	99.4	16	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of reduced udp-galactopyranose mutase
85	c5wgyA	Alignment	not modelled	99.4	13	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex
86	c5tueB	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
87	c1yvvB	Alignment	not modelled	99.4	10	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
88	c3c4aA	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable tryptophan hydroxylase viod; PDBTitle: crystal structure of viod hydroxylase in complex with fad from2 chromobacterium violaceum. northeast structural genomics consortium3 target cvr158
89	c3ihmB	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
90	c2vouA	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
91	c5g3sB	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase vioda; PDBTitle: the structure of the l-tryptophan oxidase vioda from chromobacterium2 violaceum - samarium derivative
92	c2bs3A	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
93	c2acZA	Alignment	not modelled	99.3	16	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
94	d1kifa2	Alignment	not modelled	99.3	27	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
95	d2gqfa1	Alignment	not modelled	99.3	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
96	d2i0za1	Alignment	not modelled	99.3	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
97	d1neka2	Alignment	not modelled	99.3	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
98	c1yq4A	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
99	d1qo8a2	Alignment	not modelled	99.3	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
100	c4at2A	Alignment	not modelled	99.3	19	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
101	c5xmjE	Alignment	not modelled	99.3	14	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
102	d1v0aa2	Alignment	not modelled	99.3	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

102	u1yv0paz	Alignment	not modelled	99.3	12	Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain PDB header: oxidoreductase
103	c3vr8E_	Alignment	not modelled	99.3	17	Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
104	c4c3yF_	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-ketosteroid dehydrogenase; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
105	c3qj4A_	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
106	c1jrxA_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
107	d2bs2a2	Alignment	not modelled	99.3	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
108	c2rgjA_	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
109	c2x3nA_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-dependent monooxygenase; PDBTitle: crystal structure of pqsI, a probable fad-dependent monooxygenase from2 pseudomonas aeruginosa
110	d1k0ia1	Alignment	not modelled	99.2	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
111	c6bz5B_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
112	d1c0pa2	Alignment	not modelled	99.2	31	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
113	c1qo8A_	Alignment	not modelled	99.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
114	d1ryia2	Alignment	not modelled	99.2	20	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: D-aminoacid oxidase-like
115	c2yg4B_	Alignment	not modelled	99.2	34	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
116	c1f8sA_	Alignment	not modelled	99.2	37	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.
117	c2jb1B_	Alignment	not modelled	99.2	38	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
118	c1sezA_	Alignment	not modelled	99.2	40	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase
119	c3rhaA_	Alignment	not modelled	99.2	33	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aurescens
120	c3we0A_	Alignment	not modelled	99.2	27	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase/monooxygenase; PDBTitle: l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813