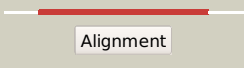

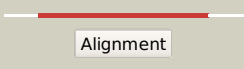

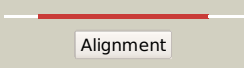

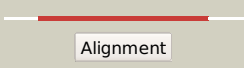
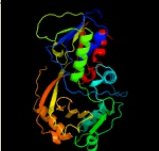
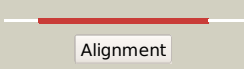
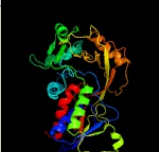
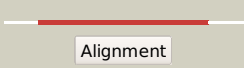

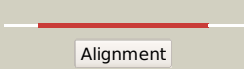

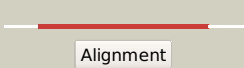
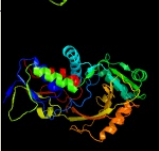
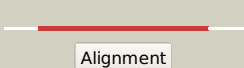

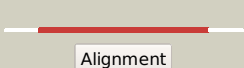
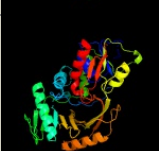
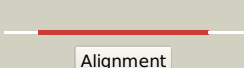
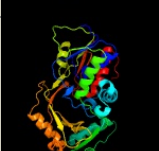


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0415_(thiO)_501151_502173
Date	Tue Jul 23 14:50:49 BST 2019
Unique Job ID	f41875b2aad751a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4p9sA_			100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgh
2	c1pj6A_			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
3	c4rs1A_			100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum
4	c4xwzA_			100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
5	c3ps9A_			100.0	19	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmC from e. coli
6	c3djeA_			100.0	17	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
7	c6j39A_			100.0	32	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: fad-dependent glycine oxydase; PDBTitle: crystal structure of cmis2 with inhibitor
8	c4x9mA_			100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
9	c3pvcA_			100.0	21	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmC from yersinia pestis
10	c2gahB_			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	c4yshA_			100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus

12	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
13	c3axbA_	Alignment		100.0	16	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
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	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
16	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
17	c5hxfF_	Alignment		100.0	16	PDB header: oxidoreductase Chain: F: PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris
18	c3bhkA_	Alignment		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
19	c1ryiB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
20	c2uzzD_	Alignment		100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
21	c2olnA_	Alignment	not modelled	100.0	19	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
22	c6gg2A_	Alignment	not modelled	100.0	16	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
23	c1kifE_	Alignment	not modelled	100.0	16	PDB header: flavoprotein Chain: E: PDB Molecule: d-amino acid oxidase; PDBTitle: d-amino acid oxidase from pig kidney
24	c2r4jA_	Alignment	not modelled	100.0	18	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
25	c2rgoA_	Alignment	not modelled	100.0	19	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
26	c1c0iA_	Alignment	not modelled	100.0	18	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
27	c2rghA_	Alignment	not modelled	100.0	18	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
						PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase;

28	c3da1A_	Alignment	not modelled	100.0	20	PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
29	d1ryia1	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
30	d2gf3a1	Alignment	not modelled	100.0	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
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	d1c0pa1	Alignment	not modelled	99.9	23	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
33	d1kifa1	Alignment	not modelled	99.9	22	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain
34	d1pj5a2	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
35	c2weuD_	Alignment	not modelled	99.8	14	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
36	c3i6dA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
37	c6fria_	Alignment	not modelled	99.8	11	PDB header: flavoprotein Chain: A: PDB Molecule: tryptophan halogenase superfamily; PDBTitle: brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
38	c6ib5B_	Alignment	not modelled	99.7	10	PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
39	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
40	c5uaoA_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
41	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
42	c2e4gB_	Alignment	not modelled	99.7	9	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
43	c2pyxA_	Alignment	not modelled	99.7	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
44	c4dggA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crt1 from pantoea ananatis
45	c5hy5A_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 6-halogenase; PDBTitle: crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini
46	c6bznA_	Alignment	not modelled	99.7	10	PDB header: flavoprotein Chain: A: PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm
47	c3atrA_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
48	c3cgvA_	Alignment	not modelled	99.6	17	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
49	c5wgyA_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex
50	c1phhA_	Alignment	not modelled	99.6	15	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
51	c5mogB_	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
52	c3nixF_	Alignment	not modelled	99.6	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.
53	c3e1tA_	Alignment	not modelled	99.6	16	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
54	c6c6rA_	Alignment	not modelled	99.6	11	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with 2 fad
55	c5bukA_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fadh2-dependent halogenase; PDBTitle: structure of flavin-dependent chlorinase mpy16
56	c3ka7A_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
57	c2gmhA_	Alignment	not modelled	99.6	15	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
58	c1txR_	Alignment	not modelled	99.6	17	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
59	c5xgvB_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: pyre3; PDBTitle: the structure of diels-alderase pyre3 in the biosynthetic pathway of 2 pyrroindomycins
60	c4k2xB_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
61	c5dbjA_	Alignment	not modelled	99.5	16	PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
62	c2xdoC_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from 2 bacteroides thetaiotaomicron
63	c5bulA_	Alignment	not modelled	99.5	12	PDB header: hydrolase Chain: A: PDB Molecule: flavin-dependent halogenase triple mutant; PDBTitle: structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
64	c4k22A_	Alignment	not modelled	99.5	15	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
65	c5g3sB_	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase viao; PDBTitle: the structure of the l-tryptophan oxidase viao from chromobacterium2 violaceum - samarium derivative
66	c4dshB_	Alignment	not modelled	99.5	11	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of reduced udp-galactopyranose mutase
67	c5x68B_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of human kmo
68	c4bk2A_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable salicylate monooxygenase; PDBTitle: crystal structure of 3-hydroxybenzoate 6-hydroxylase2 uncovers lipid-assisted flavoprotein strategy for 3 regioselective aromatic hydroxylation: q301e mutant
69	c2qa2A_	Alignment	not modelled	99.5	12	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
70	c5eowA_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from 2 pseudomonas putida kt2440
71	c6j0zC_	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpk
72	c6fjhB_	Alignment	not modelled	99.5	13	PDB header: flavoprotein Chain: B: PDB Molecule: lkce; PDBTitle: crystal structure of the seleniated lkce from streptomyces rochei
73	c3allA_	Alignment	not modelled	99.5	22	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
74	c4n9xA_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of the octaprenyl-methyl-methoxy-benzq molecule from 2 erwinia carotovora subsp. atroseptica strain scri 1043 / atcc baa-672,3 northeast structural genomics consortium (nesg) target ewr161
75	c2aczA_	Alignment	not modelled	99.5	17	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
76	d2gqfa1	Alignment	not modelled	99.5	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
77	c2qa1A_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in 2 angucycline biosynthesis

78	c2ivdA_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
79	c5ttkB_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida
80	c4j33B_	Alignment	not modelled	99.5	10	PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of kynurenine 3-monooxygenase (kmo-394)
81	c3fmwC_	Alignment	not modelled	99.5	16	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.
82	c3uteB_	Alignment	not modelled	99.5	12	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
83	c1yvvB_	Alignment	not modelled	99.5	13	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.
84	c3gmbB_	Alignment	not modelled	99.4	20	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
85	c5kowA_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pentachlorophenol 4-monooxygenase; PDBTitle: structure of rifampicin monooxygenase
86	c3k7tB_	Alignment	not modelled	99.4	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
87	c6aioA_	Alignment	not modelled	99.4	14	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
88	d2gmha1	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
89	d1neka2	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
90	c6cr0A_	Alignment	not modelled	99.4	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
91	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)
92	c5tulA_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tetracycline destructase tet(55); PDBTitle: crystal structure of tetracycline destructase tet(55)
93	c2zxiC_	Alignment	not modelled	99.4	17	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
94	c5fn0C_	Alignment	not modelled	99.4	16	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
95	c3rp7A_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid
96	c3lovA_	Alignment	not modelled	99.4	14	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
97	c3ihgA_	Alignment	not modelled	99.3	15	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
98	c3vr8E_	Alignment	not modelled	99.3	12	PDB header: oxidoreductase Chain: E: PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum
99	c2dkhA_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
100	d1kf6a2	Alignment	not modelled	99.3	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
101	c5tueB_	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
102	c1yq4A_	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and

						ubiquinone
103	d2i0za1	Alignment	not modelled	99.3	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
104	c1jrxA	Alignment	not modelled	99.3	22	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
105	d1y0pa2	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
106	c1qo8A	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase
107	c4at2A	Alignment	not modelled	99.3	22	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
108	d1qo8a2	Alignment	not modelled	99.3	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
109	c3qj4A	Alignment	not modelled	99.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
110	c3c4aA	Alignment	not modelled	99.3	15	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
111	c1pn0A	Alignment	not modelled	99.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
112	c5glgA	Alignment	not modelled	99.3	16	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
113	c2r0gB	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
114	c4cnjD	Alignment	not modelled	99.3	16	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
115	c3ihmB	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
116	c2rgjA	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
117	c2bs3A	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
118	c5xmjE	Alignment	not modelled	99.2	18	PDB header: electron transport Chain: E: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
119	c1d4cB	Alignment	not modelled	99.2	27	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
120	c4hb9A	Alignment	not modelled	99.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: similarities with probable monooxygenase; PDBTitle: crystal structure of a putative fad containing monooxygenase from2 photorhabdus luminescens subsp. laumondii tto1 (target psi-012791)