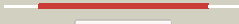



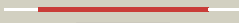



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0561c (-) _651532_652758
Date	Fri Jul 26 01:50:11 BST 2019
Unique Job ID	73b0510b27066aa1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qa1A_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis
2	c4k2xB_	 Alignment		100.0	20	PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
3	c2qa2A_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase cabc; PDBTitle: crystal structure of cabc, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
4	c5kowA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pentachlorophenol 4-monooxygenase; PDBTitle: structure of rifampicin monooxygenase
5	c6j0zC_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpik
6	c2dkhA_	 Alignment		100.0	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
7	c5xgvB_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: pyre3; PDBTitle: the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
8	c3fmwC_	 Alignment		100.0	21	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.
9	c6c6rA_	 Alignment		100.0	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad
10	c1pn0A_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
11	c5fn0C_	 Alignment		100.0	19	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

12	c3nixF_	Alignment		100.0	16	PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
13	c3ihgA_	Alignment		100.0	18	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
14	c3i3IA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
15	c2r0gB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
16	c3e1tA_	Alignment		100.0	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
17	c5wgyA_	Alignment		100.0	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex
18	c5dbjA_	Alignment		100.0	19	PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
19	c5bulA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: flavin-dependent halogenase triple mutant; PDBTitle: structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
20	c3gmbB_	Alignment		100.0	15	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
21	c1phhA_	Alignment	not modelled	100.0	16	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
22	c6bznA_	Alignment	not modelled	100.0	18	PDB header: flavoprotein Chain: A: PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm
23	c3allA_	Alignment	not modelled	100.0	15	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
24	c5bukA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fadh2-dependent halogenase; PDBTitle: structure of flavin-dependent chlorinase mpy16
25	c3atrA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
26	c4bk2A_	Alignment	not modelled	100.0	16	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
27	c5x68B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of human kmo
28	c4k22A_	Alignment	not modelled	100.0	20	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 PDB header: oxidoreductase

29	c6bz5B_	Alignment	not modelled	100.0	19	Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
30	c4cy8A_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxybiphenyl 3-monooxygenase; PDBTitle: 2-hydroxybiphenyl 3-monooxygenase (hbpa) in complex with fad
31	c5tula_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tetracycline destructase tet(55); PDBTitle: crystal structure of tetracycline destructase tet(55)
32	c2rgjA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
33	c4n9xA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of the octaprenyl-methyl-methoxy-benzo molecule from2 erwinia carotovora subsp. atroseptica strain scri 1043 / atcc baa-672,3 northeast structural genomics consortium (nesg) target ewr161
34	c6aioA_	Alignment	not modelled	100.0	15	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
35	c5eowA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440
36	c3cgvA_	Alignment	not modelled	100.0	20	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
37	c3rp7A_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid
38	c5tukC_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51)
39	c2x3nA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-dependent monooxygenase; PDBTitle: crystal structure of pqsl, a probable fad-dependent monooxygenase from2 pseudomonas aeruginosa
40	c5tueB_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
41	c5evyX_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: X: PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex
42	c2xdoC_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
43	c3c4aA_	Alignment	not modelled	100.0	13	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
44	c4j33B_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of kynurenine 3-monooxygenase (kmo-394)
45	c2vouA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
46	c2bryA_	Alignment	not modelled	100.0	17	PDB header: transport Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
47	c5uaoA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
48	c2ardA_	Alignment	not modelled	100.0	17	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
49	d1pn0a1	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
50	c2pyxA_	Alignment	not modelled	100.0	16	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
51	c2gmhA_	Alignment	not modelled	100.0	21	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
52	d1k0ia1	Alignment	not modelled	100.0	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
53	c5hy5A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 6-halogenase; PDBTitle: crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini PDB header: oxidoreductase

54	c4hb9A_	Alignment	not modelled	100.0	16	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)
55	c6ib5B_	Alignment	not modelled	100.0	15	PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
56	c2e4gB_	Alignment	not modelled	100.0	16	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
57	c2weuD_	Alignment	not modelled	100.0	18	PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
58	c6frlA_	Alignment	not modelled	100.0	21	PDB header: flavoprotein Chain: A: PDB Molecule: tryptophan halogenase superfamily; PDBTitle: brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
59	c4txkA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-methionine sulfoxide oxidase mical1; PDBTitle: construct of mical-1 containing the monooxygenase and calponin2 homology domains
60	d3c96a1	Alignment	not modelled	99.9	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
61	c3ihmB_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
62	d2gmha1	Alignment	not modelled	99.9	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
63	d2voua1	Alignment	not modelled	99.9	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
64	c3nrrA_	Alignment	not modelled	99.8	15	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
65	c1yvVB_	Alignment	not modelled	99.8	12	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.
66	c5ez7A_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
67	c3da1A_	Alignment	not modelled	99.6	12	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.
68	c3qj4A_	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
69	c1y56B_	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
70	c3dmeB_	Alignment	not modelled	99.6	17	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
71	c5mogB_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
72	c2ivdA_	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
73	c1ltxR_	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
74	c3f8rD_	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
75	c3cp2A_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli
76	c2oInA_	Alignment	not modelled	99.5	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
77	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
78	c3bhkA_	Alignment	not modelled	99.5	18	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
79	c1e3bB_	Alignment	not modelled	99.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase [flavin-containing] b;

79	c135ub	Alignment	not modelled	99.5	20	PDBTitle: crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan PDB header: oxidoreductase
80	c5ttkB	Alignment	not modelled	99.5	17	Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida PDB header: oxidoreductase
81	c4x9mA	Alignment	not modelled	99.5	13	Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound PDB header: oxidoreductase
82	c1pj6A	Alignment	not modelled	99.5	12	Chain: A: PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
83	d1neka2	Alignment	not modelled	99.5	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
84	d2gqfa1	Alignment	not modelled	99.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
85	c2gahB	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: heterotetrameric sarcosine oxidase beta-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
86	c2q7vA	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin reductase
87	c5uwvA	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005
88	c5g3sB	Alignment	not modelled	99.5	19	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
89	c6cr0A	Alignment	not modelled	99.5	19	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
90	c3nyeA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
91	c4ntdA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of hlmi
92	d1qo8a2	Alignment	not modelled	99.5	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
93	c2vvlD	Alignment	not modelled	99.5	16	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.
94	c4xwzA	Alignment	not modelled	99.5	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
95	c2r4jA	Alignment	not modelled	99.5	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
96	c5jriA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
97	c4gcmB	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
98	c1ryiB	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
99	c3ps9A	Alignment	not modelled	99.5	13	PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmC from e. coli
100	c5twcA	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferrodoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
101	c5mjkC	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of lactococcus lactis thioredoxin reductase (fo2 conformation)
102	c3i6dA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
103	c1c0iA	Alignment	not modelled	99.5	13	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
104	c5w4cA	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase;

104	cJW4A	Alignment	not modelled	99.3	18	PDBTitle: crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation) PDB header: oxidoreductase
105	c6garB	Alignment	not modelled	99.4	16	Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
106	d2bs2a2	Alignment	not modelled	99.4	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
107	d2ivda1	Alignment	not modelled	99.4	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
108	c3axbA	Alignment	not modelled	99.4	17	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
109	d1d4ca2	Alignment	not modelled	99.4	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
110	c2yg4B	Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
111	c3ka7A	Alignment	not modelled	99.4	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
112	c3pvcA	Alignment	not modelled	99.4	16	PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmc from yersinia pestis
113	c3rhaA	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
114	d1jnra2	Alignment	not modelled	99.4	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
115	c4i58A	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevibacterium oxydans ih-35a
116	c4p9sA	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgh
117	c4jnaA	Alignment	not modelled	99.4	17	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: deph; PDBTitle: crystal structure of the deph complex with dimethyl-fk228
118	c3ctyA	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
119	c3djeA	Alignment	not modelled	99.4	19	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
120	c4yshA	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus