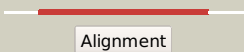

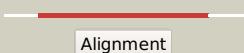

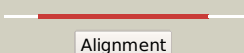

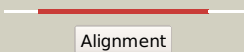





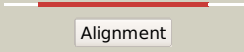

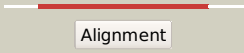



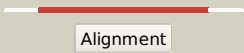

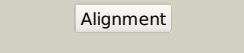



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1260_(-)_1408246_1409364
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	c420ae4ccd270533

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5tukC_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51)
2	c5tulA_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: tetracycline destructase tet(55); PDBTitle: crystal structure of tetracycline destructase tet(55)
3	c5tueB_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
4	c5xgvB_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: pyre3; PDBTitle: the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
5	c5fn0C_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: kynurenine 3-monoxygenase; PDBTitle: crystal structure of pseudomonas fluorescens kynurenine-3-2 monoxygenase (kmo) in complex with gsk180
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	c2qa2A_	 Alignment		100.0	17	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
8	c4k2xB_	 Alignment		100.0	20	PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
9	c5kowA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pentachlorophenol 4-monoxygenase; PDBTitle: structure of rifampicin monoxygenase
10	c6c6rA_	 Alignment		100.0	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monoxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monoxygenase) structure with2 fad
11	c2qa1A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis

12	c3gmbB_	Alignment		100.0	22	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
13	c4bk2A_	Alignment		100.0	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
14	c3allA_	Alignment		100.0	23	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
15	c3i3IA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
16	c6j0zC_	Alignment		100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpK
17	c3fmwC_	Alignment		100.0	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.
18	c3ihgA_	Alignment		100.0	20	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
19	c1pn0A_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
20	c3rp7A_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpoxo complexed with fad and2 uric acid
21	c5eowA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440
22	c6bz5B_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
23	c5x68B_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of human kmo
24	c1phhA_	Alignment	not modelled	100.0	13	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
25	c6aioA_	Alignment	not modelled	100.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
26	c2r0gB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
27	c4k22A_	Alignment	not modelled	100.0	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
28	c3e1tA_	Alignment	not modelled	100.0	12	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: oxidoreductase

29	c2rgjA	Alignment	not modelled	100.0	17	Chain: A; PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
30	c5evyX	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: X; PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex
31	c3c4aA	Alignment	not modelled	100.0	18	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
32	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)
33	c2x3nA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A; PDB Molecule: probable fad-dependent monooxygenase; PDBTitle: crystal structure of pqsl, a probable fad-dependent monooxygenase from2 pseudomonas aeruginosa
34	c6bznA	Alignment	not modelled	100.0	15	PDB header: flavoprotein Chain: A; PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm
35	c3nixF	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: F; PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
36	c2xdoC	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C; PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
37	c4cy8A	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-hydroxybiphenyl 3-monooxygenase; PDBTitle: 2-hydroxybiphenyl 3-monooxygenase (hbpa) in complex with fad
38	c2vouA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
39	c5bulA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: flavin-dependent halogenase triple mutant; PDBTitle: structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
40	c4n9xA	Alignment	not modelled	100.0	14	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
41	c4hb9A	Alignment	not modelled	100.0	17	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)
42	c5bukA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: fadh2-dependent halogenase; PDBTitle: structure of flavin-dependent chlorinase mpy16
43	c5wgyA	Alignment	not modelled	100.0	14	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A; PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex
44	c5dbjA	Alignment	not modelled	100.0	16	PDB header: flavoprotein Chain: A; PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
45	c3cgvA	Alignment	not modelled	100.0	13	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
46	d3c96a1	Alignment	not modelled	100.0	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
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	c3atrA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A; PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfobus acidocaldarius co-2 crystallized with its ligand
49	c5hy5A	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: tryptophan 6-halogenase; PDBTitle: crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini
50	c2weuD	Alignment	not modelled	100.0	15	PDB header: antifungal protein Chain: D; PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
51	c3ihmB	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B; PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
52	c6frlA	Alignment	not modelled	100.0	15	PDB header: flavoprotein Chain: A; PDB Molecule: tryptophan halogenase superfamily; PDBTitle: structure of brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
53	c2ardA	Alignment	not modelled	100.0	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: tryptophan halogenase prna;

53	c2atvA	Alignment	not modelled	100.0	13	PDBTitle: the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
54	c2e4gB	Alignment	not modelled	100.0	12	PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp
55	d1pn0a1	Alignment	not modelled	100.0	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
56	c6ib5B	Alignment	not modelled	100.0	12	PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
57	c2pyxA	Alignment	not modelled	100.0	14	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
58	d1k0ia1	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
59	d2voua1	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
60	c2bryA	Alignment	not modelled	100.0	18	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
61	c4txkA	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-methionine sulfoxide oxidase mical1; PDBTitle: construct of mical-1 containing the monooxygenase and calponin2 homology domains
62	c2gmhA	Alignment	not modelled	99.9	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
63	d2gmha1	Alignment	not modelled	99.9	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
64	c3nrnA	Alignment	not modelled	99.8	14	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	99.7	11	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	c3qj4A	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1)
67	c5ez7A	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
68	c6j39A	Alignment	not modelled	99.6	18	PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: fad-dependent glycine oxydase; PDBTitle: crystal structure of cmis2 with inhibitor
69	d1b5qa1	Alignment	not modelled	99.6	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
70	c5twcA	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form
71	c3ka7A	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
72	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
73	c6cr0A	Alignment	not modelled	99.5	13	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
74	c4repA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase
75	c1y56B	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
76	c3i6dA	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af
77	c5mogB	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon
78	c5ttkB	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida

79	c4d9kA	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis
80	d2ivda1	Alignment	not modelled	99.4	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
81	c3nyeA	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
82	c2oInA	Alignment	not modelled	99.4	15	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
83	c3lovA	Alignment	not modelled	99.4	17	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
84	c4x9mA	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
85	c4iv9B	Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: tryptophan 2-monooxygenase; PDBTitle: structure of the flavoprotein tryptophan-2-monooxygenase
86	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
87	c3ab1B	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
88	c3f8rD	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfobolus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
89	c2ivdA	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
90	c2yg4B	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
91	d1reoa1	Alignment	not modelled	99.4	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
92	c2r4jA	Alignment	not modelled	99.4	12	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
93	c3bhkA	Alignment	not modelled	99.3	13	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
94	c2a87A	Alignment	not modelled	99.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of m. tuberculosis thioredoxin reductase
95	c1f8sA	Alignment	not modelled	99.3	16	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.
96	c3k7tB	Alignment	not modelled	99.3	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
97	c3rhaA	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
98	c2vviD	Alignment	not modelled	99.3	14	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.
99	c1ryiB	Alignment	not modelled	99.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate
100	c1s3bB	Alignment	not modelled	99.3	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
101	c3da1A	Alignment	not modelled	99.3	7	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.
102	d2ida1	Alignment	not modelled	99.3	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
103	c1c0iA	Alignment	not modelled	99.3	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 PDB header: oxidoreductase

104	c6garB_	Alignment	not modelled	99.3	13	Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of oxidised ferredoxin/ flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
105	c3dmeB_	Alignment	not modelled	99.3	15	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
106	c1pj6A_	Alignment	not modelled	99.3	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
107	c1ltxR_	Alignment	not modelled	99.2	13	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
108	c4i58A_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevibacterium oxydans ih-35a
109	c5mbxA_	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal n(1)-acetyl-spermine/spermidine oxidase; PDBTitle: crystal structure of reduced murine n1-acetylpolyamine oxidase in2 complex with n1-acetylspermine
110	c4dshB_	Alignment	not modelled	99.2	12	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of reduced udp-galactopyranose mutase
111	c4yshA_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus
112	c5xhuA_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ycgf from bacillus subtilis
113	c4xwzA_	Alignment	not modelled	99.2	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
114	c2gahB_	Alignment	not modelled	99.2	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
115	d2bs2a2	Alignment	not modelled	99.2	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
116	c2uzzD_	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: D: PDB Molecule: n-methyl-l-tryptophan oxidase; PDBTitle: x-ray structure of n-methyl-l-tryptophan oxidase (mtx)
117	c4p9sA_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh
118	d2gqfa1	Alignment	not modelled	99.2	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
119	c3fbsB_	Alignment	not modelled	99.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
120	c5mjkC_	Alignment	not modelled	99.2	12	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of lactococcus lactis thioredoxin reductase (fo2 conformation)