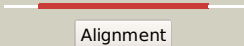

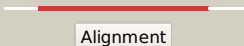

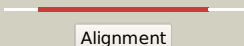







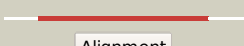











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1138c_(-)_1265477_1266493
Date	Wed Jul 31 22:05:22 BST 2019
Unique Job ID	3b5068faca839624

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qa1A_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide oxygenase pgae; <b>PDBTitle:</b> crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis
2	<a href="#">c2qa2A_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide oxygenase cabe; <b>PDBTitle:</b> crystal structure of cabe, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
3	<a href="#">c6j0zC_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative angucycline-like polyketide oxygenase; <b>PDBTitle:</b> crystal structure of alpik
4	<a href="#">c6c6rA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> squalene monooxygenase; <b>PDBTitle:</b> human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad
5	<a href="#">c4k2xB_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide oxygenase/hydroxylase; <b>PDBTitle:</b> oxys anhydrotetracycline hydroxylase from streptomyces rimosus
6	<a href="#">c5xgvB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyre3; <b>PDBTitle:</b> the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
7	<a href="#">c5kowA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pentachlorophenol 4-monooxygenase; <b>PDBTitle:</b> structure of rifampicin monooxygenase
8	<a href="#">c2dkhA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxybenzoate hydroxylase; <b>PDBTitle:</b> crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
9	<a href="#">c3fmwC_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxygenase; <b>PDBTitle:</b> the crystal structure of mtmoiv, a baeyer-villiger monooxygenase from2 the mithramycin biosynthetic pathway in streptomyces argillaceus.
10	<a href="#">c3ihgA_</a>	 Alignment		100.0	21	<b>PDB header:</b> flavoprotein, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rdme; <b>PDBTitle:</b> crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
11	<a href="#">c3i3lA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkylhalidase cmls; <b>PDBTitle:</b> crystal structure of cmls, a flavin-dependent halogenase

12	<a href="#">c1pn0A_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenol 2-monoxygenase; <b>PDBTitle:</b> phenol hydroxylase from trichosporon cutaneum
13	<a href="#">c2r0gB_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rebc; <b>PDBTitle:</b> chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
14	<a href="#">c5wgyA_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-dependent halogenase; <b>PDBTitle:</b> crystal structure of mala' c112s/c128s, malbrancheamide b complex
15	<a href="#">c3e1tA_</a>	Alignment		100.0	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> halogenase; <b>PDBTitle:</b> structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
16	<a href="#">c6bznA_</a>	Alignment		100.0	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> halogenase pltm; <b>PDBTitle:</b> crystal structure of halogenase pltm
17	<a href="#">c3nixF_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> flavoprotein/dehydrogenase; <b>PDBTitle:</b> crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
18	<a href="#">c3allA_</a>	Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
19	<a href="#">c3gmbB_</a>	Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase
20	<a href="#">c5fn0C_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> kynurenine 3-monoxygenase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens kynurenine-3-2 monoxygenase (kmo) in complex with gsk180
21	<a href="#">c1phhA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> p-hydroxybenzoate hydroxylase; <b>PDBTitle:</b> crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
22	<a href="#">c5dbjA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> fadh2-dependent halogenase plta; <b>PDBTitle:</b> crystal structure of halogenase plta
23	<a href="#">c5eowA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-hydroxynicotinate 3-monoxygenase; <b>PDBTitle:</b> crystal structure of 6-hydroxynicotinic acid 3-monoxygenase from2 pseudomonas putida kt2440
24	<a href="#">c5bukA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fadh2-dependent halogenase; <b>PDBTitle:</b> structure of flavin-dependent chlorinase mpy16
25	<a href="#">c5bulA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-dependent halogenase triple mutant; <b>PDBTitle:</b> structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w
26	<a href="#">c4bk2A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable salicylate monoxygenase; <b>PDBTitle:</b> crystal structure of 3-hydroxybenzoate 6-hydroxylase2 uncovers lipid-assisted flavoprotein strategy for3 regioselective aromatic hydroxylation: q301e mutant
27	<a href="#">c4cy8A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxybiphenyl 3-monoxygenase; <b>PDBTitle:</b> 2-hydroxybiphenyl 3-monoxygenase (hbpa) in complex with fad
28	<a href="#">c5tulA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline destructase tet(55); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(55)

29	<a href="#">c3atrA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
30	<a href="#">c4k22A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein visc; <b>PDBTitle:</b> structure of the c-terminal truncated form of e.coli c5-hydroxylase2 ubii involved in ubiquinone (q8) biosynthesis
31	<a href="#">c4n9xA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of the octaprenyl-methyl-methoxy-benzq molecule from2 erwina carotovora subsp. atroseptica strain scri 1043 / atcc baa-672,3 northeast structural genomics consortium (nesg) target ewr161
32	<a href="#">c5tueB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tetracycline destructase tet(50); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(50)
33	<a href="#">c5tukC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetracycline destructase tet(51); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(51)
34	<a href="#">c3c4aA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tryptophan hydroxylase viod; <b>PDBTitle:</b> crystal structure of viod hydroxylase in complex with fad from2 chromobacterium violaceum. northeast structural genomics consortium3 target cvr158
35	<a href="#">c5x68B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of human kmo
36	<a href="#">c6bz5B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> salicylate hydroxylase; <b>PDBTitle:</b> structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
37	<a href="#">c3rp7A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein monooxygenase; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid
38	<a href="#">c5evyX</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> salicylate hydroxylase; <b>PDBTitle:</b> salicylate hydroxylase substrate complex
39	<a href="#">c6aioA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> pnpa; <b>PDBTitle:</b> crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
40	<a href="#">c3cgvA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl reductase related protein; <b>PDBTitle:</b> crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
41	<a href="#">c2x3nA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable fad-dependent monooxygenase; <b>PDBTitle:</b> crystal structure of pqsl, a probable fad-dependent monooxygenase from2 pseudomonas aeruginosa
42	<a href="#">c4j33B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of kynurenine 3-monooxygenase (kmo-394)
43	<a href="#">c2rgiA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of flavin-containing monooxygenase phzs
44	<a href="#">c2vouA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,6-dihydropyridine hydroxylase; <b>PDBTitle:</b> structure of 2,6-dihydropyridine-3-hydroxylase from2 arthrobacter nicotinovorans
45	<a href="#">c2xdoC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
46	<a href="#">c2ardA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase prna; <b>PDBTitle:</b> the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
47	<a href="#">c5uaoA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophane-5-halogenase; <b>PDBTitle:</b> crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
48	<a href="#">d1k0ia1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
49	<a href="#">c4hb9A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> similarities with probable monooxygenase; <b>PDBTitle:</b> crystal structure of a putative fad containing monooxygenase from2 photorhabdus luminescens subsp. laumondii tto1 (target psi-012791)
50	<a href="#">c2bryA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> nedd9 interacting protein with calponin homology <b>PDBTitle:</b> crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
51	<a href="#">c6friA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase superfamily; <b>PDBTitle:</b> brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
52	<a href="#">c2weuD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> antifungal protein <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan 5-halogenase; <b>PDBTitle:</b> crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
53	<a href="#">c5hy5A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan 6-halogenase;

53	<a href="#">c1lyzA</a>	Alignment	not modelled	100.0	10	<b>PDBTitle:</b> crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini <b>PDB header:</b> biosynthetic protein
54	<a href="#">c2pyxA</a>	Alignment	not modelled	99.9	13	<b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
55	<a href="#">c3ihmB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> styrene monooxygenase a; <b>PDBTitle:</b> structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
56	<a href="#">c2e4gB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> biosynthetic protein, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> rebh with bound l-trp
57	<a href="#">d1pn0a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
58	<a href="#">c6ib5B</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan 6-halogenase; <b>PDBTitle:</b> mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
59	<a href="#">d2gmha1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
60	<a href="#">d3c96a1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
61	<a href="#">c2gmhA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone <b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
62	<a href="#">c4txkA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-methionine sulfoxide oxidase mical1; <b>PDBTitle:</b> construct of mical-1 containing the monooxygenase and calponin2 homology domains
63	<a href="#">d2voua1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
64	<a href="#">c3nrrA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf1083; <b>PDBTitle:</b> crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
65	<a href="#">c5ez7A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoenzyme pa4991; <b>PDBTitle:</b> crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa
66	<a href="#">c1yvvB</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase, flavin-containing; <b>PDBTitle:</b> x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
67	<a href="#">c6j39A</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent glycine oxydase; <b>PDBTitle:</b> crystal structure of cmis2 with inhibitor
68	<a href="#">c3qj4A</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renalase; <b>PDBTitle:</b> crystal structure of human renalase (isoform 1)
69	<a href="#">c3bhkA</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monomeric sarcosine oxidase; <b>PDBTitle:</b> crystal structure of r49k mutant of monomeric sarcosine oxidase2 crystallized in phosphate as precipitant
70	<a href="#">c1y56B</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcosine oxidase; <b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from p.horikoshii
71	<a href="#">c3ps9A</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna 5-methylaminomethyl-2-thiouridine biosynthesis <b>PDBTitle:</b> crystal structure of mnmC from e. coli
72	<a href="#">d2gqfa1</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
73	<a href="#">c4xwzA</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine:oxygen oxidoreductase; <b>PDBTitle:</b> the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
74	<a href="#">c3f8rD</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3); <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
75	<a href="#">d2bs2a2</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
76	<a href="#">c1pj6A</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethylglycine oxidase; <b>PDBTitle:</b> crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
77	<a href="#">c4y4nE</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> E: <b>PDB Molecule:</b> putative ribose 1,5-bisphosphate isomerase; <b>PDBTitle:</b> thiazole synthase thi4 from methanococcus igneus
78	<a href="#">c3da1A</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad.



						northeast3 structural genomics consortium target bhr167.
79	<a href="#">c4p9sA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethylglycine dehydrogenase; <b>PDBTitle:</b> crystal structure of the mature form of rat dmgdh
80	<a href="#">c5twcA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> oxidoreductase iruo in the oxidized form
81	<a href="#">c4x9mA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-alpha-glycerophosphate oxidase; <b>PDBTitle:</b> oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound
82	<a href="#">d1neka2</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
83	<a href="#">c2oInA_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nikd protein; <b>PDBTitle:</b> nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
84	<a href="#">c5mogB_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phytoene dehydrogenase, chloroplastic/chromoplastic; <b>PDBTitle:</b> oryza sativa phytoene desaturase inhibited by norflurazon
85	<a href="#">c2gahB_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heterotetrameric sarcosine oxidase beta-subunit; <b>PDBTitle:</b> heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
86	<a href="#">c5ttkB_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase; <b>PDBTitle:</b> crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida
87	<a href="#">c3dmeB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved exported protein; <b>PDBTitle:</b> crystal structure of conserved exported protein from bordetella2 pertussis. northeast structural genomics target ber141
88	<a href="#">c3pvcA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna 5-methylaminomethyl-2-thiouridine biosynthesis <b>PDBTitle:</b> crystal structure of apo mnmc from yersinia pestis
89	<a href="#">c1ryiB_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine oxidase; <b>PDBTitle:</b> structure of glycine oxidase with bound inhibitor glycolate
90	<a href="#">c3nyeA_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-arginine dehydrogenase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
91	<a href="#">c3ka7A_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
92	<a href="#">c3ab1B_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase
93	<a href="#">c1c0iA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-amino acid oxidase; <b>PDBTitle:</b> crystal structure of d-amino acid oxidase in complex with two2 anthranilate molecules
94	<a href="#">c2q7vA_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans thioredoxin reductase
95	<a href="#">c5uwvA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005
96	<a href="#">c3axbA_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix
97	<a href="#">c5yggB_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodospseudomonas palustris
98	<a href="#">c5jriA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
99	<a href="#">c3djeA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine: oxygen oxidoreductase; <b>PDBTitle:</b> crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
100	<a href="#">c6garB_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
101	<a href="#">c4gcmB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxin reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
102	<a href="#">c3k7tB_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-hydroxy-l-nicotine oxidase; <b>PDBTitle:</b> crystal structure of apo-form 6-hydroxy-l-nicotine oxidase, crystal2 form p3121
103	<a href="#">d2ivda1</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain

104	<a href="#">c4ntdA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of hlm1
105	<a href="#">c3ctyA_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of t. acidophilum thioredoxin reductase
106	<a href="#">c4yshA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine oxidase; <b>PDBTitle:</b> crystal structure of glycine oxidase from geobacillus kaustophilus
107	<a href="#">c6cr0A_</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-6-hydroxynicotine oxidase; <b>PDBTitle:</b> 1.55 a resolution structure of (s)-6-hydroxynicotine oxidase from2 shinella hzn7
108	<a href="#">c1ltxR_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> R: <b>PDB Molecule:</b> rab escort protein 1; <b>PDBTitle:</b> structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
109	<a href="#">c3jskN_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cypbp37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
110	<a href="#">d1qo8a2</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
111	<a href="#">c4rs1A_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl peptide oxidase; <b>PDBTitle:</b> structure of fructosyl peptide oxidase from e. terrenum
112	<a href="#">c3fbsB_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
113	<a href="#">c5w4cA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
114	<a href="#">c3cp2A_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from e. coli
115	<a href="#">c5xhuA_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ycgt from bacillus subtilis
116	<a href="#">d1rp0a1</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Thi4-like
117	<a href="#">c2zxiC_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
118	<a href="#">c4jnaA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> deph; <b>PDBTitle:</b> crystal structure of the deph complex with dimethyl-fk228
119	<a href="#">d1kf6a2</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
120	<a href="#">c3d8xB_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae ndpph dependent2 thioredoxin reductase 1