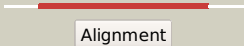

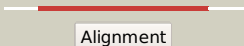
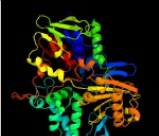
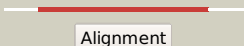







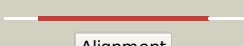











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3829c_(-)_4303576_4305186
Date	Fri Aug 9 18:20:54 BST 2019
Unique Job ID	807e53c19d7fb9dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4repA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase, flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-carotene desaturase; <b>PDBTitle:</b> crystal structure of gamma-carotenoid desaturase
2	<a href="#">c1s3bB_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase [flavin-containing] b; <b>PDBTitle:</b> crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
3	<a href="#">c5mogB_</a>	 Alignment		100.0	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
4	<a href="#">c3x0vA_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine oxidase; <b>PDBTitle:</b> structure of l-lysine oxidase
5	<a href="#">c4i58A_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexylamine oxidase; <b>PDBTitle:</b> cyclohexylamine oxidase from brevibacterium oxydans ih-35a
6	<a href="#">c2xagA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1-core1 in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
7	<a href="#">c3rhaA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putrescine oxidase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from arthrobacter aureus
8	<a href="#">c2ivdA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
9	<a href="#">c2v1dA_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase/repressor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> structural basis of lsd1-core1 selectivity in histone h32 recognition
10	<a href="#">c4iv9B_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan 2-monooxygenase; <b>PDBTitle:</b> structure of the flavoprotein tryptophan-2-monooxygenase
11	<a href="#">c2hkoA_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1

12	<a href="#">c1f8sA_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
13	<a href="#">c2yg4B_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putrescine oxidase; <b>PDBTitle:</b> structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
14	<a href="#">c4gutA_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1b; <b>PDBTitle:</b> crystal structure of lsd2-npac
15	<a href="#">c3ka7A_</a>	Alignment		100.0	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 mazeri. northeast structural genomics consortium target id3 mar208
16	<a href="#">c5ttkB_</a>	Alignment		100.0	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
17	<a href="#">c2vvlD_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> monoamine oxidase n; <b>PDBTitle:</b> the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
18	<a href="#">c3we0A_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase/monooxygenase; <b>PDBTitle:</b> l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
19	<a href="#">c3uteB_</a>	Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
20	<a href="#">c6cr0A_</a>	Alignment		100.0	15	<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
21	<a href="#">c3nksA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> structure of human protoporphyrinogen ix oxidase
22	<a href="#">c5g3sB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-tryptophan oxidase viaa; <b>PDBTitle:</b> the structure of the l-tryptophan oxidase viaa from chromobacterium2 violaceum - samarium derivative
23	<a href="#">c5mbxA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal n(1)-acetyl-spermine/spermidine oxidase; <b>PDBTitle:</b> crystal structure of reduced murine n1-acetylpolyamine oxidase in2 complex with n1-acetylspermine
24	<a href="#">c1h83A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine oxidase; <b>PDBTitle:</b> structure of polyamine oxidase in complex with2 1,8-diaminooctane
25	<a href="#">c3bnuA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine oxidase fms1; <b>PDBTitle:</b> crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
26	<a href="#">c1sezA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase, mitochondrial; <b>PDBTitle:</b> crystal structure of protoporphyrinogen ix oxidase
27	<a href="#">c3k7tB_</a>	Alignment	not modelled	100.0	18	<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
28	<a href="#">c3i6dA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> crystal structure of ppo from bacillus subtilis with af

29	<a href="#">c4dshB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of reduced udp-galactopyranose mutase
30	<a href="#">c4dgaA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytoene dehydrogenase; <b>PDBTitle:</b> crystal structure of phytoene desaturase crti from pantoea ananatis
31	<a href="#">c2jb1B_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
32	<a href="#">c3lovA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
33	<a href="#">c1ltxR_</a>	Alignment	not modelled	100.0	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
34	<a href="#">d1o5wa1</a>	Alignment	not modelled	100.0	20	<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
35	<a href="#">c2b9yA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminooxidase; <b>PDBTitle:</b> crystal structure of cla-producing fatty acid isomerase2 from p. acnes
36	<a href="#">c1v0jB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from mycobacterium tuberculosis
37	<a href="#">c1i8tB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> strcuture of udp-galactopyranose mutase from e.coli
38	<a href="#">c1naaB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam
39	<a href="#">c2bi8A_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
40	<a href="#">c4qj6A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> cellobiose dehydrogenase from myriococcum thermophilum, mtcdh
41	<a href="#">c4qj7A_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> cellobiose dehydrogenase from neurospora crassa, nccdh
42	<a href="#">c4qj4A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh
43	<a href="#">c3q9tB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> choline dehydrogenase and related flavoproteins; <b>PDBTitle:</b> crystal structure analysis of formate oxidase
44	<a href="#">c1cf3A_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> oxidoreductase(flavoprotein) <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glucose oxidase); <b>PDBTitle:</b> glucose oxidase from apergillus niger
45	<a href="#">c4yntA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose oxidase, putative; <b>PDBTitle:</b> crystal structure of aspergillus flavus fad glucose dehydrogenase
46	<a href="#">c6a2uD_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
47	<a href="#">d2v5za1</a>	Alignment	not modelled	100.0	20	<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
48	<a href="#">c1coyA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase(oxygen receptor) <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> crystal structure of cholesterol oxidase complexed with a steroid2 substrate. implications for fad dependent alcohol oxidases
49	<a href="#">c5hsaG_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alcohol oxidase 1; <b>PDBTitle:</b> alcohol oxidase aox1 from pichia pastoris
50	<a href="#">c2jbvA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> choline oxidase; <b>PDBTitle:</b> crystal structure of choline oxidase reveals insights into the2 catalytic mechanism
51	<a href="#">c4mo2A_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of udp-n-acetylgalactopyranose mutase from2 campylobacter jejuni
52	<a href="#">c6h3gC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol oxidase; <b>PDBTitle:</b> alcohol oxidase from phanerochaete chrysosporium
53	<a href="#">c5nccB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid photodecarboxylase; <b>PDBTitle:</b> structure of fatty acid photodecarboxylase in complex with fad and2 palmitic acid
54	<a href="#">c1gpeA_</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> oxidoreductase(flavoprotein) <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glucose oxidase); <b>PDBTitle:</b> glucose oxidase from penicillium amagasakiense
						<b>PDB header:</b> oxidoreductase

55	<a href="#">c3t37A_</a>	Alignment	not modelled	100.0	11	<b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> crystal structure of pyridoxine 4-oxidase from mesorhium loti
56	<a href="#">c3fimB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aryl-alcohol oxidase; <b>PDBTitle:</b> crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
57	<a href="#">c3hdqI_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> I: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
58	<a href="#">c4miqC_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyranose 2-oxidase; <b>PDBTitle:</b> pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
59	<a href="#">c3nrrA_</a>	Alignment	not modelled	100.0	16	<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
60	<a href="#">c4h7uA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyranose dehydrogenase; <b>PDBTitle:</b> crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype
61	<a href="#">c2igoG_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> pyranose oxidase; <b>PDBTitle:</b> crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose
62	<a href="#">c1ju2A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxynitrile lyase; <b>PDBTitle:</b> crystal structure of the hydroxynitrile lyase from almond
63	<a href="#">d1d5ta1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
64	<a href="#">c2gewA_</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
65	<a href="#">c2yr6A_</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pro-enzyme of l-phenylalanine oxidase; <b>PDBTitle:</b> crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501
66	<a href="#">c2f5vA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyranose 2-oxidase; <b>PDBTitle:</b> reaction geometry and thermostability mutant of pyranose 2-oxidase2 from the white-rot fungus peniophora sp.
67	<a href="#">c6fjhB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> lkce; <b>PDBTitle:</b> crystal structure of the seleniated lkce from streptomyces rochei
68	<a href="#">c1gndA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> gtpase activation <b>Chain:</b> A: <b>PDB Molecule:</b> guanine nucleotide dissociation inhibitor; <b>PDBTitle:</b> guanine nucleotide dissociation inhibitor, alpha-isoform
69	<a href="#">c4udpA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-methanol-choline oxidoreductase; <b>PDBTitle:</b> crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state
70	<a href="#">c6c87A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rab gdp dissociation inhibitor alpha; <b>PDBTitle:</b> crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri
71	<a href="#">c3cpiH_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> rab gdp-dissociation inhibitor; <b>PDBTitle:</b> crystal structure of yeast rab-gdi
72	<a href="#">d2bcgg1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
73	<a href="#">d1kdqa1</a>	Alignment	not modelled	99.9	15	<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
74	<a href="#">c4z24A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gmc-type oxidoreductase r135; <b>PDBTitle:</b> mimivirus r135 (residues 51-702)
75	<a href="#">d1vg0a1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
76	<a href="#">c3p1wA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rabgdi protein; <b>PDBTitle:</b> crystal structure of rab gdi from plasmodium falciparum, pfl2060c
77	<a href="#">d1cf3a1</a>	Alignment	not modelled	99.9	15	<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
78	<a href="#">d1reoa1</a>	Alignment	not modelled	99.9	16	<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
79	<a href="#">d2iida1</a>	Alignment	not modelled	99.9	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
80	<a href="#">d2f5va1</a>	Alignment	not modelled	99.9	16	<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
81	<a href="#">d2dw4a2</a>	Alignment	not modelled	99.9	15	<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

82	<a href="#">c2e1mA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
83	<a href="#">d1gpea1</a>	Alignment	not modelled	99.9	13	<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
84	<a href="#">d1b5qa1</a>	Alignment	not modelled	99.9	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
85	<a href="#">c3qj4A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renalase; <b>PDBTitle:</b> crystal structure of human renalase (isoform 1)
86	<a href="#">d1n4wa1</a>	Alignment	not modelled	99.8	11	<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
87	<a href="#">c1yvB</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase, flavin-containing; <b>PDBTitle:</b> x-ray structure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
88	<a href="#">c3nlcA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vp0956; <b>PDBTitle:</b> crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
89	<a href="#">d2ivda1</a>	Alignment	not modelled	99.8	16	<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
90	<a href="#">d3coxa1</a>	Alignment	not modelled	99.8	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
91	<a href="#">c4at2A</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketosteroid-delta4-5alpha-dehydrogenase; <b>PDBTitle:</b> the crystal structure of 3-ketosteroid-delta4-(5alpha)-2 dehydrogenase from rhodococcus jostii rha1 in complex3 with 4-androstene-3,17- dione
92	<a href="#">c3axbA</a>	Alignment	not modelled	99.8	14	<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
93	<a href="#">c4x9mA</a>	Alignment	not modelled	99.8	10	<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
94	<a href="#">c4c3yF</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-ketosteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-ketosteroid delta1-dehydrogenase from2 rhodococcus erythropolis sq1 in complex with 1,4-androstadiene-3,17-3 dione
95	<a href="#">c2oInA</a>	Alignment	not modelled	99.8	18	<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
96	<a href="#">c5fjnB</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid deaminase; <b>PDBTitle:</b> structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate
97	<a href="#">c4xwzA</a>	Alignment	not modelled	99.8	15	<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
98	<a href="#">d1i8ta1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
99	<a href="#">c3dmeB</a>	Alignment	not modelled	99.8	15	<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
100	<a href="#">c1pj6A</a>	Alignment	not modelled	99.8	19	<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
101	<a href="#">c4ia6B</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> myosin-crossreactive antigen; <b>PDBTitle:</b> hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah)
102	<a href="#">c3urhB</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
103	<a href="#">c5hxwF</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> l-amino acid deaminase; <b>PDBTitle:</b> l-amino acid deaminase from proteus vulgaris
104	<a href="#">c2eq8E</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
105	<a href="#">c6du7C</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae
106	<a href="#">c4rslA</a>	Alignment	not modelled	99.7	15	<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
107	<a href="#">c3cp2A_</a>	Alignment	not modelled	99.7	18 <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
108	<a href="#">c3cesB_</a>	Alignment	not modelled	99.7	19 <b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of e.coli mnmg (gida), a highly- conserved trna2 modifying enzyme
109	<a href="#">c5glgA_</a>	Alignment	not modelled	99.7	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase 2; <b>PDBTitle:</b> the novel function of osm1 under anaerobic condition in the er was2 revealed by crystal structure of osm1, a soluble fumarate reductase3 in yeast
110	<a href="#">c3djeA_</a>	Alignment	not modelled	99.7	14 <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
111	<a href="#">c3g05B_</a>	Alignment	not modelled	99.7	19 <b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmg
112	<a href="#">c2c3dB_</a>	Alignment	not modelled	99.7	11 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase; <b>PDBTitle:</b> 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
113	<a href="#">c2eq7B_</a>	Alignment	not modelled	99.7	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
114	<a href="#">d1ju2a1</a>	Alignment	not modelled	99.7	12 <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
115	<a href="#">c3bhkA_</a>	Alignment	not modelled	99.7	12 <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
116	<a href="#">c3o0hA_</a>	Alignment	not modelled	99.7	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase from bartonella henselae
117	<a href="#">c2r4jA_</a>	Alignment	not modelled	99.7	22 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aerobic glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of escherichia coli semet substituted glycerol-3-2 phosphate dehydrogenase in complex with dhap
118	<a href="#">c6gg2A_</a>	Alignment	not modelled	99.7	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid oxidase fmpa; <b>PDBTitle:</b> the structure of fsqb from aspergillus fumigatus, a flavoenzyme of the2 amine oxidase family
119	<a href="#">c1zkgA_</a>	Alignment	not modelled	99.7	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2
120	<a href="#">d2gf3a1</a>	Alignment	not modelled	99.7	15 <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