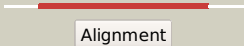

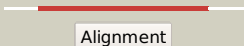

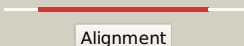







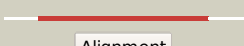








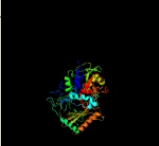


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0697 (-) _796936_798375
Date	Fri Jul 26 01:50:26 BST 2019
Unique Job ID	a209257d6063717a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5hsaG_</a>	 Alignment		100.0	26	<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
2	<a href="#">c6h3gC_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol oxidase; <b>PDBTitle:</b> alcohol oxidase from phanerochaete chrysosporium
3	<a href="#">c5nccB_</a>	 Alignment		100.0	31	<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
4	<a href="#">c2jbvA_</a>	 Alignment		100.0	28	<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
5	<a href="#">c3fimB_</a>	 Alignment		100.0	28	<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
6	<a href="#">c4yntA_</a>	 Alignment		100.0	25	<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
7	<a href="#">c3t37A_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> crystal structure of pyridoxine 4-oxidase from mesorium loti
8	<a href="#">c1cf3A_</a>	 Alignment		100.0	23	<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
9	<a href="#">c4h7uA_</a>	 Alignment		100.0	24	<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
10	<a href="#">c1gpeA_</a>	 Alignment		100.0	24	<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
11	<a href="#">c4qi7A_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> cellobiose dehydrogenase from neurospora crassa, nccdH

12	<a href="#">c4qi6A_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose dehydrogenase; <b>PDBTitle:</b> cellobiose dehydrogenase from myriococcum thermophilum, mtdh
13	<a href="#">c3q9tB_</a>	Alignment		100.0	25	<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
14	<a href="#">c4qi4A_</a>	Alignment		100.0	22	<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
15	<a href="#">c4udpA_</a>	Alignment		100.0	27	<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
16	<a href="#">c1naaB_</a>	Alignment		100.0	20	<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
17	<a href="#">c1ju2A_</a>	Alignment		100.0	23	<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
18	<a href="#">c4z24A_</a>	Alignment		100.0	20	<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)
19	<a href="#">c2gewA_</a>	Alignment		100.0	20	<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)
20	<a href="#">c1coyA_</a>	Alignment		100.0	19	<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
21	<a href="#">c6a2uD_</a>	Alignment	not modelled	100.0	19	<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
22	<a href="#">c4migC_</a>	Alignment	not modelled	100.0	16	<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
23	<a href="#">d1cf3a1</a>	Alignment	not modelled	100.0	30	<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
24	<a href="#">c2igoG_</a>	Alignment	not modelled	100.0	16	<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
25	<a href="#">c2f5vA_</a>	Alignment	not modelled	100.0	15	<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.
26	<a href="#">d1kdga1</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
27	<a href="#">d1gpea1</a>	Alignment	not modelled	100.0	28	<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
28	<a href="#">d1n4wa1</a>	Alignment	not modelled	100.0	25	<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
						<b>Fold:</b> FAD/NAD(P)-binding domain

29	<a href="#">d3coxa1</a>	Alignment	not modelled	100.0	24	<b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
30	<a href="#">d2f5va1</a>	Alignment	not modelled	100.0	22	<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
31	<a href="#">d1ju2a1</a>	Alignment	not modelled	100.0	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
32	<a href="#">c5glgA</a>	Alignment	not modelled	99.8	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
33	<a href="#">c4repA</a>	Alignment	not modelled	99.8	13	<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
34	<a href="#">c1yq4A</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> avian respiratory complex ii with 3-nitropropionate and ubiquinone
35	<a href="#">c4at2A</a>	Alignment	not modelled	99.7	21	<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
36	<a href="#">c4c3yF</a>	Alignment	not modelled	99.7	15	<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
37	<a href="#">c5xmjE</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
38	<a href="#">c3p4rM</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
39	<a href="#">c3vr8E</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> flavoprotein subunit of complex ii; <b>PDBTitle:</b> mitochondrial rhoquo:quinol-fumarate reductase from the parasitic2 nematode ascaris suum
40	<a href="#">c2ac2A</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
41	<a href="#">c1qo8A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c3 fumarate reductase; <b>PDBTitle:</b> the structure of the open conformation of a flavocytochrome c32 fumarate reductase
42	<a href="#">c1d4cB</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c fumarate reductase; <b>PDBTitle:</b> crystal structure of the uncomplexed form of the flavocytochrome c2 fumarate reductase of shewanella putrefaciens strain mr-1
43	<a href="#">c1kf6A</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase flavoprotein; <b>PDBTitle:</b> e. coli quinol-fumarate reductase with bound inhibitor hqno
44	<a href="#">c1jrxA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c; <b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
45	<a href="#">d1d5ta1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
46	<a href="#">d1y0pa2</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
47	<a href="#">c2bs3A</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinol-fumarate reductase flavoprotein subunit a; <b>PDBTitle:</b> glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
48	<a href="#">c2rghA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
49	<a href="#">c3cirM</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> e. coli quinol fumarate reductase frda t234a mutation
50	<a href="#">c5hxfF</a>	Alignment	not modelled	99.5	14	<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
51	<a href="#">c6n56A</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase, flavo protein subunit; <b>PDBTitle:</b> crystal structure of fumarate reductase, flavo protein subunit, from2 helicobacter pylori g27
52	<a href="#">d2bcgg1</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
53	<a href="#">d1nc8a2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain

53	<a href="#">c1qpoa2</a>	Alignment	not modelled	99.3	17	<b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase;
54	<a href="#">c2rgoA</a>	Alignment	not modelled	99.5	13	<b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
55	<a href="#">c4p9sA</a>	Alignment	not modelled	99.4	20	<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 dmgh
56	<a href="#">d1kf6a2</a>	Alignment	not modelled	99.4	14	<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
57	<a href="#">c2fjaC</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylsulfate reductase, subunit a; <b>PDBTitle:</b> adenosine 5'-phosphosulfate reductase in complex with substrate
58	<a href="#">c3nlcA</a>	Alignment	not modelled	99.4	13	<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
59	<a href="#">c2r4jA</a>	Alignment	not modelled	99.4	20	<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
60	<a href="#">d2gf3a1</a>	Alignment	not modelled	99.4	21	<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="#">c1pj6A</a>	Alignment	not modelled	99.4	23	<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
62	<a href="#">c4xwzA</a>	Alignment	not modelled	99.4	16	<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
63	<a href="#">d1pj5a2</a>	Alignment	not modelled	99.4	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="#">d2qqfa1</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
65	<a href="#">c1zkgA</a>	Alignment	not modelled	99.4	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
66	<a href="#">c3dqzA</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
67	<a href="#">c3ka7A</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
68	<a href="#">d2bs2a2</a>	Alignment	not modelled	99.4	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
69	<a href="#">c3axbA</a>	Alignment	not modelled	99.4	19	<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
70	<a href="#">c4x9mA</a>	Alignment	not modelled	99.4	14	<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
71	<a href="#">d1neka2</a>	Alignment	not modelled	99.4	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
72	<a href="#">c3da1A</a>	Alignment	not modelled	99.4	15	<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.
73	<a href="#">d1d4ca2</a>	Alignment	not modelled	99.3	19	<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
74	<a href="#">c6c87A</a>	Alignment	not modelled	99.3	14	<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
75	<a href="#">c2c3dB</a>	Alignment	not modelled	99.3	18	<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
76	<a href="#">c3dmeB</a>	Alignment	not modelled	99.3	21	<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
77	<a href="#">c1gndA</a>	Alignment	not modelled	99.3	11	<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

78	<a href="#">c5fjnB_</a>	Alignment	not modelled	99.3	19	<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
79	<a href="#">c2zxiC_</a>	Alignment	not modelled	99.3	23	<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
80	<a href="#">c1ltxR_</a>	Alignment	not modelled	99.3	12	<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
81	<a href="#">c2nvkX_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster
82	<a href="#">d1ryia1</a>	Alignment	not modelled	99.3	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
83	<a href="#">c2olnA_</a>	Alignment	not modelled	99.3	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
84	<a href="#">c2gahB_</a>	Alignment	not modelled	99.3	21	<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
85	<a href="#">d2i0za1</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
86	<a href="#">c3jskN_</a>	Alignment	not modelled	99.3	32	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cypbp37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
87	<a href="#">c3gyxA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylsulfate reductase from2 desulfovibrio gigas
88	<a href="#">c3cpiH_</a>	Alignment	not modelled	99.2	12	<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
89	<a href="#">c3djeA_</a>	Alignment	not modelled	99.2	23	<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
90	<a href="#">c3g05B_</a>	Alignment	not modelled	99.2	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
91	<a href="#">d1chua2</a>	Alignment	not modelled	99.2	30	<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
92	<a href="#">c1zmcG_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
93	<a href="#">c6b4oB_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad
94	<a href="#">c3cesB_</a>	Alignment	not modelled	99.1	20	<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
95	<a href="#">c6aonB_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad
96	<a href="#">c4dggA_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytoene dehydrogenase; <b>PDBTitle:</b> crystal structure of phytoene desaturase crt1 from pantoea ananatis
97	<a href="#">c6bz0C_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> 1.83 angstrom resolution crystal structure of dihydrolipoyl2 dehydrogenase from acinetobacter baumannii in complex with fad.
98	<a href="#">c1hyuA_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
99	<a href="#">c6gg2A_</a>	Alignment	not modelled	99.1	14	<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
100	<a href="#">c3urhB_</a>	Alignment	not modelled	99.1	20	<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
101	<a href="#">c1ojtA_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
102	<a href="#">c3cp8C_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl



					<b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
103	<a href="#">d1o5wa1</a>	Alignment	not modelled	99.1	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
104	<a href="#">d1rp0a1</a>	Alignment	not modelled	99.1	28 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Thi4-like
105	<a href="#">d1cf3a2</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GMC oxidoreductases
106	<a href="#">c2eq8E_</a>	Alignment	not modelled	99.1	20 <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
107	<a href="#">c6mp5B_</a>	Alignment	not modelled	99.1	17 <b>PDB header:</b> membrane protein, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfide:quinone oxidoreductase, mitochondrial; <b>PDBTitle:</b> crystal structure of native human sulfide:quinone oxidoreductase
108	<a href="#">c4rs1A_</a>	Alignment	not modelled	99.1	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
109	<a href="#">d2cula1</a>	Alignment	not modelled	99.1	28 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GidA-like
110	<a href="#">d1ju2a2</a>	Alignment	not modelled	99.1	18 <b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GMC oxidoreductases
111	<a href="#">c3cp2A_</a>	Alignment	not modelled	99.1	21 <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
112	<a href="#">c1m6iA_</a>	Alignment	not modelled	99.1	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8; <b>PDBTitle:</b> crystal structure of apoptosis inducing factor (aif)
113	<a href="#">c1chuA_</a>	Alignment	not modelled	99.1	32 <b>PDB header:</b> flavoenzyme <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-aspartate oxidase); <b>PDBTitle:</b> structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family
114	<a href="#">c2a8xA_</a>	Alignment	not modelled	99.1	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
115	<a href="#">c4y4nE_</a>	Alignment	not modelled	99.0	26 <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
116	<a href="#">c3v76A_</a>	Alignment	not modelled	99.0	20 <b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> the crystal structure of a flavoprotein from sinorhizobium meliloti
117	<a href="#">c2e5vA_</a>	Alignment	not modelled	99.0	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate oxidase; <b>PDBTitle:</b> crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfobolus tokodaii
118	<a href="#">d1gpea2</a>	Alignment	not modelled	99.0	17 <b>Fold:</b> FAD-linked reductases, C-terminal domain <b>Superfamily:</b> FAD-linked reductases, C-terminal domain <b>Family:</b> GMC oxidoreductases
119	<a href="#">c1y56B_</a>	Alignment	not modelled	99.0	15 <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
120	<a href="#">c5g3sB_</a>	Alignment	not modelled	99.0	9 <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