

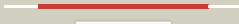

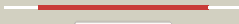

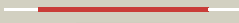

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2074 (- )_2331001_2331414
Date	Mon Aug 5 13:25:18 BST 2019
Unique Job ID	dd437bee5f6f024

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2asfa1</a>	 Alignment		100.0	99	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
2	<a href="#">d2fhqa1</a>	 Alignment		100.0	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
3	<a href="#">d2hq7a1</a>	 Alignment		100.0	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
4	<a href="#">d1rfea_</a>	 Alignment		100.0	24	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
5	<a href="#">d1w9aa_</a>	 Alignment		100.0	26	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
6	<a href="#">c3f7eB_</a>	 Alignment		100.0	24	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn- <b>PDBTitle:</b> msmeg_3380 f420 reductase
7	<a href="#">c2re7A_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution
8	<a href="#">c2iabB_</a>	 Alignment		100.0	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
9	<a href="#">c3db0B_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lin2891 protein; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
10	<a href="#">d2i02a1</a>	 Alignment		100.0	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
11	<a href="#">c3ec6A_</a>	 Alignment		100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 26; <b>PDBTitle:</b> crystal structure of the general stress protein 26 from bacillus2 anthracis str. Sterne

12	<a href="#">c4zkyB_</a>	Alignment		99.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5-phosphate oxidase; <b>PDBTitle:</b> structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
13	<a href="#">c3dmbA_</a>	Alignment		99.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative general stress protein 26 with a pnp-oxidase like <b>PDBTitle:</b> crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
14	<a href="#">c3u34D_</a>	Alignment		99.9	11	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> general stress protein; <b>PDBTitle:</b> crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri
15	<a href="#">c2htdB_</a>	Alignment		99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted flavin-nucleotide-binding protein from cog3576 <b>PDBTitle:</b> crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
16	<a href="#">c2qeaB_</a>	Alignment		99.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative general stress protein 26; <b>PDBTitle:</b> crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
17	<a href="#">c5escD_</a>	Alignment		99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hupz; <b>PDBTitle:</b> crystal structure of group a streptococcus hupz
18	<a href="#">c3tgvD_</a>	Alignment		99.9	16	<b>PDB header:</b> heme binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> heme-binding protein hutz; <b>PDBTitle:</b> crystal structure of hutz,the heme storsge protein from vibrio2 cholerae
19	<a href="#">d2htia1</a>	Alignment		99.9	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
20	<a href="#">c2htiA_</a>	Alignment		99.9	12	<b>PDB header:</b> fmn-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bh0577 protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (bh_0577)2 from bacillus halodurans at 2.50 a resolution
21	<a href="#">c2ig6B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nimc/nima family protein; <b>PDBTitle:</b> crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
22	<a href="#">d2fg9a1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
23	<a href="#">d1vl7a_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
24	<a href="#">c2q9kA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
25	<a href="#">d2hq9a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
26	<a href="#">c3u0iA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable fad-binding, putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
27	<a href="#">c3fkhB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
28	<a href="#">c3cn3A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;

28	<a href="#">c3cp3A</a>	Alignment	not modelled	99.9	41	<b>PDBTitle:</b> crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
29	<a href="#">d1flma</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
30	<a href="#">c2hhzA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
31	<a href="#">c6eciQ</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> fad-binding protein <b>Chain:</b> Q: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding <b>PDBTitle:</b> structure of the fad binding protein msmeq_5243 from mycobacterium2 smegmatis
32	<a href="#">d1t9ma</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
33	<a href="#">d2arza1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
34	<a href="#">d1ty9a</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
35	<a href="#">c4hmbW</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of phzg from burkholderia lata 383
36	<a href="#">d2fura1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
37	<a href="#">d1nrga</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
38	<a href="#">c1nrgA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate oxidase; <b>PDBTitle:</b> structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
39	<a href="#">c2ou5B</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-related, fmn-binding; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
40	<a href="#">c5bncB</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> heme binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> heme binding protein msmeq_6519; <b>PDBTitle:</b> structure of heme binding protein msmeq_6519 from mycobacterium2 smegmatis
41	<a href="#">c2a2jA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase; <b>PDBTitle:</b> crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
42	<a href="#">d1dnla</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
43	<a href="#">d2a2ja1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
44	<a href="#">c3dnhB</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein atu2129; <b>PDBTitle:</b> the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
45	<a href="#">d2vpaa1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
46	<a href="#">c3gasA</a>	Alignment	not modelled	99.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> heme oxygenase; <b>PDBTitle:</b> crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
47	<a href="#">c4ybnB</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-nucleotide-binding protein; <b>PDBTitle:</b> structure of the fad and heme binding protein msmeq_4975 from2 mycobacterium smegmatis
48	<a href="#">c6rk0A</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of the flavocytochrome anf3 from azotobacter vinelandii
49	<a href="#">d1ci0a</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
50	<a href="#">c2o15B</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> pai 2 protein; <b>PDBTitle:</b> crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
51	<a href="#">c2i51B</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized conserved protein of cog5135; <b>PDBTitle:</b> crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
52	<a href="#">d1xhna1</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> PNP-oxidase like
						<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> genomic dna, chromosome 3, p1 clone:

53	<a href="#">c4n7rD_</a>	Alignment	not modelled	99.3	16	mxl8; <b>PDBTitle:</b> crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxamine 5'-phosphate oxidase-like protein;
54	<a href="#">c3ba3A_</a>	Alignment	not modelled	98.7	13	<b>PDBTitle:</b> crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution <b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein;
55	<a href="#">c3r5yC_</a>	Alignment	not modelled	98.4	15	<b>PDBTitle:</b> structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420 <b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein;
56	<a href="#">c3r5zB_</a>	Alignment	not modelled	98.3	12	<b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420 <b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a;
57	<a href="#">c3h96B_</a>	Alignment	not modelled	98.2	10	<b>PDBTitle:</b> msmeg_3358 f420 reductase <b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> deazaflavin-dependent nitroreductase;
58	<a href="#">c3r5wO_</a>	Alignment	not modelled	98.1	14	<b>PDBTitle:</b> structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis paralogous family 11;
59	<a href="#">c4y9iA_</a>	Alignment	not modelled	98.1	13	<b>PDBTitle:</b> structure of f420-h2 dependent reductase (fdr-a) msmeg_2027 <b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
60	<a href="#">d2ptfa1</a>	Alignment	not modelled	97.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mth_863; <b>PDBTitle:</b> crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
61	<a href="#">c2ptfB_</a>	Alignment	not modelled	97.1	9	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
62	<a href="#">d2imla1</a>	Alignment	not modelled	97.0	17	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
63	<a href="#">d1ejea_</a>	Alignment	not modelled	96.1	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
64	<a href="#">c3e4vA_</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> nadh:fmn oxidoreductase like protein; <b>PDBTitle:</b> crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
65	<a href="#">c3b5mD_</a>	Alignment	not modelled	95.7	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
66	<a href="#">c4z85A_</a>	Alignment	not modelled	95.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-nitrobenzoate nitroreductase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
67	<a href="#">c3fgeA_</a>	Alignment	not modelled	95.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin reductase with split barrel domain; <b>PDBTitle:</b> crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
68	<a href="#">c3bpkB_</a>	Alignment	not modelled	95.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase component b; <b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
69	<a href="#">c2d5mA_</a>	Alignment	not modelled	92.8	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavoredoxin; <b>PDBTitle:</b> flavoredoxin of desulfovibrio vulgaris (miyazaki f)
70	<a href="#">c4l82D_</a>	Alignment	not modelled	92.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> rifea.00250.a; <b>PDBTitle:</b> structure of a putative oxidoreductase from rickettsia felis
71	<a href="#">c4xhyA_</a>	Alignment	not modelled	92.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein, fmn-binding protein; <b>PDBTitle:</b> nadh:fmn oxidoreductase from paracoccus denitrificans
72	<a href="#">c2d38A_</a>	Alignment	not modelled	91.2	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical nadh-dependent fmn oxidoreductase; <b>PDBTitle:</b> the crystal structure of flavin reductase hpac complexed with nadp+
73	<a href="#">d2nr4a1</a>	Alignment	not modelled	91.0	14	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> MTH863-like
74	<a href="#">c3pftA_</a>	Alignment	not modelled	90.9	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase; <b>PDBTitle:</b> crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
75	<a href="#">c2qckA_</a>	Alignment	not modelled	89.7	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein; <b>PDBTitle:</b> crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
76	<a href="#">c3cb0B_</a>	Alignment	not modelled	89.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxyphenylacetate 3-monooxygenase; <b>PDBTitle:</b> cobr <b>PDB header:</b> oxidoreductase

77	<a href="#">c4f07A_</a>	Alignment	not modelled	89.0	12	<b>Chain:</b> A: <b>PDB Molecule:</b> styrene monooxygenase component 2; <b>PDBTitle:</b> structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
78	<a href="#">d1rz0a_</a>	Alignment	not modelled	87.9	7	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
79	<a href="#">c3hmzA_</a>	Alignment	not modelled	87.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase domain protein, fmn-binding; <b>PDBTitle:</b> crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sba1_0626) from shewanella baltica os155 at 1.50 a resolution
80	<a href="#">c3bnkB_</a>	Alignment	not modelled	87.5	9	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans
81	<a href="#">c3rh7A_</a>	Alignment	not modelled	87.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
82	<a href="#">c3k87B_</a>	Alignment	not modelled	81.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> chlorophenol-4-monooxygenase component 1; <b>PDBTitle:</b> crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
83	<a href="#">d1wgba_</a>	Alignment	not modelled	81.2	12	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
84	<a href="#">d1lusca_</a>	Alignment	not modelled	79.9	6	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
85	<a href="#">c2r6vA_</a>	Alignment	not modelled	77.0	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0856; <b>PDBTitle:</b> crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution
86	<a href="#">c3nfwB_</a>	Alignment	not modelled	75.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin reductase-like, fmn-binding protein; <b>PDBTitle:</b> crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
87	<a href="#">c2ecrA_</a>	Alignment	not modelled	71.9	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin reductase component (hpac) of 4-hydroxyphenylacetate <b>PDBTitle:</b> crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
88	<a href="#">c2r0xA_</a>	Alignment	not modelled	71.6	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible flavin reductase; <b>PDBTitle:</b> crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
89	<a href="#">d1i0ra_</a>	Alignment	not modelled	71.4	11	<b>Fold:</b> Split barrel-like <b>Superfamily:</b> FMN-binding split barrel <b>Family:</b> NADH:FMN oxidoreductase-like
90	<a href="#">c5zc2B_</a>	Alignment	not modelled	34.9	6	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
91	<a href="#">c4hx6D_</a>	Alignment	not modelled	34.5	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
92	<a href="#">d1smao_</a>	Alignment	not modelled	30.2	10	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
93	<a href="#">d2d9ra1</a>	Alignment	not modelled	21.5	8	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AF2212/PG0164-like <b>Family:</b> PG0164-like
94	<a href="#">c4dsdA_</a>	Alignment	not modelled	12.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative periplasmic protein; <b>PDBTitle:</b> crystal structure of a putative periplasmic protein (bacova_05534)2 from bacteroides ovatus atcc 8483 at 1.75 a resolution
95	<a href="#">c5vb0E_</a>	Alignment	not modelled	11.0	14	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> fosfomycin resistance protein fosa3; <b>PDBTitle:</b> crystal structure of fosfomycin resistance protein fosa3
96	<a href="#">c4p7xA_</a>	Alignment	not modelled	10.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-proline cis-4-hydroxylase; <b>PDBTitle:</b> l-pipecolic acid-bound l-proline cis-4-hydroxylase
97	<a href="#">d2bf5a1</a>	Alignment	not modelled	9.4	3	<b>Fold:</b> Monooxygenase (hydroxylase) regulatory protein <b>Superfamily:</b> Monooxygenase (hydroxylase) regulatory protein <b>Family:</b> Monooxygenase (hydroxylase) regulatory protein
98	<a href="#">d1e5ra_</a>	Alignment	not modelled	9.4	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminatase synthase-like <b>Family:</b> Type II Proline 3-hydroxylase (proline oxidase)
99	<a href="#">c3hftA_</a>	Alignment	not modelled	9.1	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> wbms, polysaccharide deacetylase involved in o-antigen <b>PDBTitle:</b> crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution