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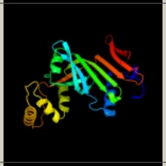
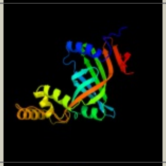
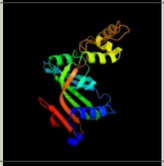
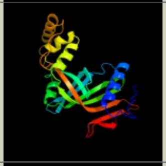
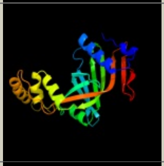
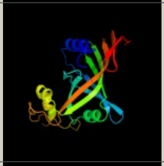
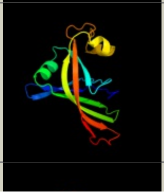
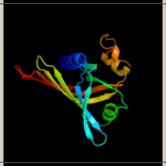
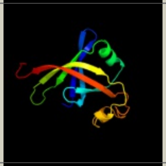
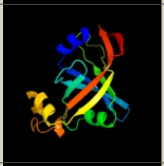
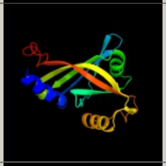
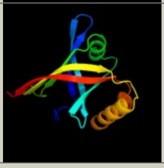
Description	P0AFI7
Date	Thu Jan 5 11:26:27 GMT 2012
Unique Job ID	d340bdb4a266f76d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a2ja1	Alignment		100.0	41	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
2	c2a2jA_	Alignment		100.0	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
3	d1nrga_	Alignment		100.0	43	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
4	c1nrgA_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate oxidase; **PDBTitle:** structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
5	d1dnla_	Alignment		100.0	98	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
6	d1ci0a_	Alignment		100.0	40	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
7	d1t9ma_	Alignment		100.0	31	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
8	d1ty9a_	Alignment		100.0	31	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
9	c2i51B_	Alignment		100.0	16	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**uncharacterized conserved protein of cog5135; **PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
10	c2ou5B_	Alignment		100.0	18	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn-binding; **PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
11	d2i02a1	Alignment		99.9	22	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like

12	c2re7A_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution
13	c2hhzA_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related; **PDBTitle:** crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
14	d2hq7a1	Alignment		99.9	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
15	c3dmbA_	Alignment		99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative general stress protein 26 with a pnp-oxidase like **PDBTitle:** crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
16	d2fhqa1	Alignment		99.9	17	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
17	c3ec6A_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 26; **PDBTitle:** crystal structure of the general stress protein 26 from bacillus2 anthracis str. sterne
18	c2ig6B_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nimc/nima family protein; **PDBTitle:** crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
19	c2iabB_	Alignment		99.9	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
20	d1vl7a_	Alignment		99.8	24	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
21	c3db0B_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lin2891 protein; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
22	c2qeaB_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative general stress protein 26; **PDBTitle:** crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
23	d2asfa1	Alignment	not modelled	99.8	17	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
24	c3f7eB_	Alignment	not modelled	99.7	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn- **PDBTitle:** msmeg_3380 f420 reductase
25	d1rfea_	Alignment	not modelled	99.7	22	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
26	c2htdB_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**predicted flavin-nucleotide-binding protein from cog3576 **PDBTitle:** crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
27	d1w9aa_	Alignment	not modelled	99.6	13	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
28	d2htia1	Alignment	not modelled	99.6	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
						PDB header:fmn-binding protein

29	c2htiA_	Alignment	not modelled	99.6	21	**Chain:** A: **PDB Molecule:**bh0577 protein; **PDBTitle:** crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution
30	c2q9kA_	Alignment	not modelled	99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
31	d2fg9a1	Alignment	not modelled	99.5	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
32	d1flma_	Alignment	not modelled	99.4	18	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
33	c3gasA_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**heme oxygenase; **PDBTitle:** crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
34	d2arza1	Alignment	not modelled	99.4	17	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
35	d2hq9a1	Alignment	not modelled	99.3	22	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
36	c3dnhB_	Alignment	not modelled	99.3	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein atu2129; **PDBTitle:** the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
37	c3fkhB_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
38	c3cp3A_	Alignment	not modelled	99.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
39	d2fura1	Alignment	not modelled	98.8	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
40	c3ba3A_	Alignment	not modelled	98.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-like protein; **PDBTitle:** crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
41	d1xhna1	Alignment	not modelled	98.6	14	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
42	d2vpaa1	Alignment	not modelled	98.4	23	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
43	c2ol5B_	Alignment	not modelled	98.3	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**pai 2 protein; **PDBTitle:** crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
44	c3h96B_	Alignment	not modelled	96.8	8	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**f420-h2 dependent reductase a; **PDBTitle:** msmeg_3358 f420 reductase
45	d2ptfa1	Alignment	not modelled	91.0	18	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
46	c2ptfB_	Alignment	not modelled	89.2	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mth_863; **PDBTitle:** crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
47	c3b5mD_	Alignment	not modelled	63.5	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
48	d2imla1	Alignment	not modelled	50.7	12	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
49	c3fgeA_	Alignment	not modelled	48.0	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative flavin reductase with split barrel domain; **PDBTitle:** crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
50	c3bjqA_	Alignment	not modelled	42.7	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phage-related protein; **PDBTitle:** crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
51	c3psqA_	Alignment	not modelled	41.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical exported protein; **PDBTitle:** crystal structure of spy0129, a streptococcus pyogenes class b sortase2 involved in pilus biogenesis
52	d1ejea_	Alignment	not modelled	40.1	22	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
53	d1usca_	Alignment	not modelled	37.8	12	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like

54	c3bnkB_	Alignment	not modelled	32.4	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoredoxin; **PDBTitle:** x-ray crystal structure of flavoredoxin from methanosarcina2 acetivorans
55	c3e4vA_	Alignment	not modelled	29.1	11	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nadh:fmn oxidoreductase like protein; **PDBTitle:** crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
56	d1rz0a_	Alignment	not modelled	28.8	11	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
57	c2d5mA_	Alignment	not modelled	24.0	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavoredoxin; **PDBTitle:** flavoredoxin of desulfovibrio vulgaris (miyazaki f)
58	d1qwza_	Alignment	not modelled	19.1	17	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
59	d1eoqa_	Alignment	not modelled	17.4	23	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
60	d1ikpa1	Alignment	not modelled	17.2	33	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Exotoxin A, N-terminal domain
61	c3bk5A_	Alignment	not modelled	14.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative outer membrane lipoprotein-sorting protein; **PDBTitle:** crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus
62	c3pftA_	Alignment	not modelled	14.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin reductase; **PDBTitle:** crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
63	c2kp7A_	Alignment	not modelled	9.7	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
64	c3rbjB_	Alignment	not modelled	8.5	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sortase family protein; **PDBTitle:** crystal structure of the lid-mutant of streptococcus agalactiae2 sortase c1
65	d1qbaa1	Alignment	not modelled	8.1	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
66	d2oqza1	Alignment	not modelled	8.0	23	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase
67	d1i0ra_	Alignment	not modelled	7.8	7	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
68	c2khxA_	Alignment	not modelled	7.2	12	**PDB header:**gene regulation,nuclear protein **Chain:** A: **PDB Molecule:**ribonuclease 3; **PDBTitle:** drosha double-stranded rna binding motif
69	c2xwgA_	Alignment	not modelled	7.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sortase; **PDBTitle:** crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
70	d1wiia_	Alignment	not modelled	7.1	12	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
71	c3rh7A_	Alignment	not modelled	6.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical oxidoreductase; **PDBTitle:** crystal structure of a hypothetical oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
72	c2zyzA_	Alignment	not modelled	5.8	14	**PDB header:**splicing **Chain:** A: **PDB Molecule:**putative uncharacterized protein pae0789; **PDBTitle:** pyrobaculum aerophilum splicing endonuclease
73	c1ikqA_	Alignment	not modelled	5.4	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**exotoxin a; **PDBTitle:** pseudomonas aeruginosa exotoxin a, wild type
74	d1qrjb1	Alignment	not modelled	5.3	24	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
75	d1ng5a_	Alignment	not modelled	5.1	18	**Fold:**Sortase **Superfamily:**Sortase **Family:**Sortase