Phyre^2

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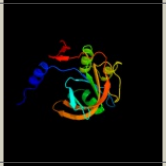
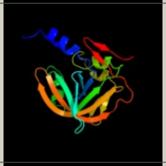
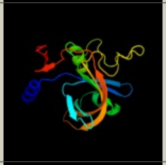
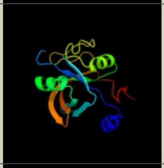
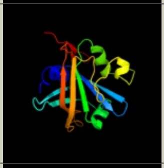
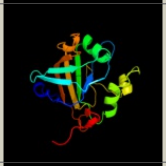
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r0xA_	Alignment		100.0	50	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible flavin reductase; **PDBTitle:** crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
2	c3k87B_	Alignment		100.0	41	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**chlorophenol-4-monooxygenase component 1; **PDBTitle:** crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
3	c3rh7A_	Alignment		100.0	31	**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
4	c3cb0B_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxyphenylacetate 3-monooxygenase; **PDBTitle:** cobr
5	c3nfwB_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase component b; **PDBTitle:** crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
6	c3pftA_	Alignment		100.0	19	**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
7	c2qckA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin reductase domain protein; **PDBTitle:** crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
8	c2d38A_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical nadh-dependent fmn oxidoreductase; **PDBTitle:** the crystal structure of flavin reductase hpac complexed with nadp+
9	c2ecrA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin reductase component (hpac) of 4-hydroxyphenylacetate **PDBTitle:** crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
10	d1wgba_	Alignment		100.0	18	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
11	d1rz0a_	Alignment		100.0	27	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like

12	d1i0ra_	Alignment		100.0	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
13	c3bnkB_	Alignment		100.0	18	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoredoxin; **PDBTitle:** x-ray crystal structure of flavoredoxin from methanosarcina2 acetivorans
14	c2r6vA_	Alignment		100.0	14	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**uncharacterized protein ph0856; **PDBTitle:** crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution
15	d1ejea_	Alignment		100.0	13	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
16	d1usca_	Alignment		100.0	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
17	c3bpkB_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase component b; **PDBTitle:** crystal structure of nitrilotriacetate monooxygenase2 component b from bacillus cereus
18	c3e4vA_	Alignment		100.0	12	**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
19	c3hmzA_	Alignment		100.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin reductase domain protein, fmn-binding; **PDBTitle:** crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sbal_0626) from shewanella baltica os155 at 1.50 a resolution
20	c2d5mA_	Alignment		100.0	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavoredoxin; **PDBTitle:** flavoredoxin of desulfovibrio vulgaris (miyazaki f)
21	c3fgeA_	Alignment	not modelled	100.0	11	**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
22	c3b5mD_	Alignment	not modelled	99.9	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
23	d2imla1	Alignment	not modelled	99.3	11	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
24	c2ptfB_	Alignment	not modelled	98.6	14	**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
25	d2nr4a1	Alignment	not modelled	98.6	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
26	d2ptfa1	Alignment	not modelled	98.5	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
27	d1flma_	Alignment	not modelled	95.3	12	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
28	c2q9kA_	Alignment	not modelled	95.0	14	**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
29	c2htdB_	Alignment	not modelled	88.3	6	**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
30	d1vl7a_	Alignment	not modelled	78.9	18	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
31	d2hq7a1	Alignment	not modelled	70.0	10	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
32	c2re7A_	Alignment	not modelled	60.5	7	**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
33	d1rfea_	Alignment	not modelled	60.2	12	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
34	d2asfa1	Alignment	not modelled	54.1	8	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
35	d2htia1	Alignment	not modelled	51.9	8	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
36	c2htiA_	Alignment	not modelled	51.9	8	**PDB header:**fmn-binding protein **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
37	c3ec6A_	Alignment	not modelled	46.4	11	**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
38	d2fhqa1	Alignment	not modelled	46.4	9	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
39	c3dmbA_	Alignment	not modelled	43.2	11	**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
40	c3db0B_	Alignment	not modelled	36.1	11	**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
41	c3f7eB_	Alignment	not modelled	34.6	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn- **PDBTitle:** msmeg_3380 f420 reductase
42	d1w9aa_	Alignment	not modelled	24.7	8	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
43	c3fkhB_	Alignment	not modelled	22.5	11	**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
44	d1xzwa1	Alignment	not modelled	19.0	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Purple acid phosphatase, N-terminal domain **Family:**Purple acid phosphatase, N-terminal domain
45	d2arza1	Alignment	not modelled	17.4	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
46	d2hq9a1	Alignment	not modelled	16.2	6	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
47	c2ou5B_	Alignment	not modelled	11.6	12	**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
48	c2ig6B_	Alignment	not modelled	9.5	13	**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
49	d2qfra1	Alignment	not modelled	9.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Purple acid phosphatase, N-terminal domain **Family:**Purple acid phosphatase, N-terminal domain
50	c2iabB_	Alignment	not modelled	8.1	14	**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
51	d2i02a1	Alignment	not modelled	7.9	13	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
52	d1mkya3	Alignment	not modelled	7.3	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Probable GTPase Der, C-terminal domain **Family:**Probable GTPase Der, C-terminal domain

53	c3cp3A_	Alignment	not modelled	7.3	13	**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
54	c1a2oB_	Alignment	not modelled	7.1	17	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
55	d1dmla2	Alignment	not modelled	7.0	24	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
56	d2fg9a1	Alignment	not modelled	6.3	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
57	c2hhzA_	Alignment	not modelled	6.0	6	**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
58	d1svba1	Alignment	not modelled	5.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
59	c1mkyA_	Alignment	not modelled	5.4	20	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**probable gtp-binding protein enga; **PDBTitle:** structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains