Phyre^2

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Description	P38489
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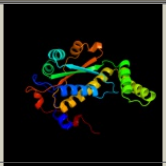
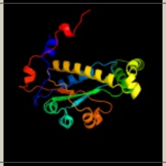
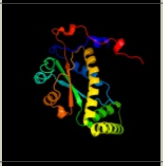
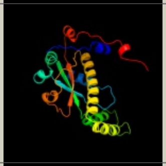
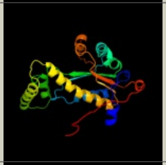
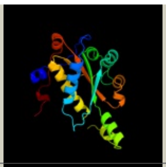
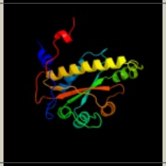
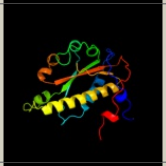
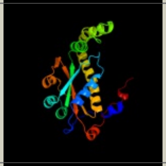
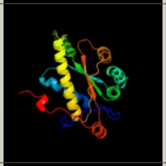
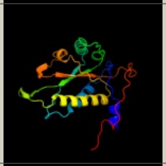
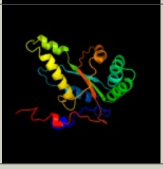
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ykia1	Alignment		100.0	100	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
2	d1kqba_	Alignment		100.0	88	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
3	d1vfra_	Alignment		100.0	31	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
4	c3of4A_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
5	c3gbhC_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p)h-flavin oxidoreductase; **PDBTitle:** crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution
6	c3ge6B_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exiguobacterium sibiricum 255-15 at 1.85 a3 resolution
7	c3bemA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nad(p)h nitroreductase ydfn; **PDBTitle:** crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
8	c3gr3B_	Alignment		100.0	16	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of a nitroreductase-like family protein (pnba,2 bh06130) from bartonella henselae str. houston-1 at 1.45 a resolution
9	c2hayD_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative nad(p)h-flavin oxidoreductase; **PDBTitle:** the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas
10	c3gagB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadh dehydrogenase, nadph nitroreductase; **PDBTitle:** crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution
11	d1noxa_	Alignment		100.0	24	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase

12	c3n2sD_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
13	d1zcha1	Alignment		100.0	24	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
14	c2wzvB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
15	d1f5va_	Alignment		100.0	23	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
16	d2b67a1	Alignment		100.0	20	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
17	c3eofB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
18	d1bkja_	Alignment		100.0	27	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
19	c3gh8A_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iodotyrosine dehalogenase 1; **PDBTitle:** crystal structure of mus musculus iodotyrosine deiodinase (iyd) bound2 to fmn and di-iodotyrosine (dit)
20	d2ifaa1	Alignment		100.0	10	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
21	c2h0uA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-flavin oxidoreductase; **PDBTitle:** crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
22	c2islB_	Alignment	not modelled	100.0	15	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
23	d1ywqa1	Alignment	not modelled	100.0	11	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
24	c3eo8A_	Alignment	not modelled	100.0	18	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**blub-like flavoprotein; **PDBTitle:** crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution
25	d2frea1	Alignment	not modelled	100.0	17	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
26	c3k6hB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
27	c3koqC_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein (cd3355) from2 clostridium difficile 630 at 1.58 a resolution
28	c2wqfA_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper induced nitroreductase d; **PDBTitle:** crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn

29	c3ge5A_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nad(p)h:fmn oxidoreductase; **PDBTitle:** crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
30	c2i7hE_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
31	c2r01A_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum tls at 1.15 a resolution
32	c3gfaB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase in complex with fmn2 (cd3205) from clostridium difficile 630 at 1.35 a resolution
33	c3g14B_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of nitroreductase family protein (yp_877874.1) from2 clostridium novyi nt at 1.75 a resolution
34	c3ek3A_	Alignment	not modelled	100.0	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of nitroreductase with bound fmn (yp_211706.1) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution
35	c3pxvD_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of a nitroreductase with bound fmn (dhaf_2018) from2 desulfitobacterium hafniense dcb-2 at 2.30 a resolution
36	c3m5kA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh dehydrogenase/nad(p)h nitroreductase; **PDBTitle:** crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (bdi_1728) from parabacteroides distasonis atcc 85033 at 1.86 a resolution
37	c3e39A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase in complex with fmn2 (dde_0787) from desulfovibrio desulfuricans subsp. at 1.70 a3 resolution
38	c3kwkA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh dehydrogenase/nad(p)h nitroreductase; **PDBTitle:** crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
39	c3e10B_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadh oxidase; **PDBTitle:** crystal structure of putative nadh oxidase (np_348178.1)2 from clostridium acetobutylicum at 1.40 a resolution
40	c3hoiA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nitroreductase bf3017; **PDBTitle:** crystal structure of fmn-dependent nitroreductase bf3017 from2 bacteroides fragilis nctc 9343 (yp_212631.1) from bacteroides3 fragilis nctc 9343 at 1.55 a resolution
41	c3hj9A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of a putative nitroreductase (reut_a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution
42	c3bm2B_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein ydja; **PDBTitle:** crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
43	c3eo7A_	Alignment	not modelled	99.9	19	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase (ava_2154) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
44	d1vkwa_	Alignment	not modelled	99.8	19	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**Putative nitroreductase TM1586
45	d2oc6a1	Alignment	not modelled	39.6	4	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
46	c3nr7A_	Alignment	not modelled	35.3	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein h-ns; **PDBTitle:** crystal structure of s. typhimurium h-ns 1-83
47	d1oeyj_	Alignment	not modelled	31.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
48	d2i8da1	Alignment	not modelled	27.7	11	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
49	d1ov9a_	Alignment	not modelled	24.9	34	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
50	c3gyxJ_	Alignment	not modelled	21.5	12	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
51	c2p1nD_	Alignment	not modelled	18.8	19	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
						Fold: Skp1 dimerisation domain-like

52	d2ovra1	Alignment	not modelled	17.7	25	**Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
53	c1nexC_	Alignment	not modelled	17.4	22	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
54	c3k4iC_	Alignment	not modelled	16.5	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
55	c1sm7A_	Alignment	not modelled	15.4	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**recombinant ib pronapin; **PDBTitle:** solution structure of the recombinant pronapin precursor,2 bnib.
56	c1pnbB_	Alignment	not modelled	14.7	23	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**napin bnib; **PDBTitle:** structure of napin bnib, nmr, 10 structures
57	c2ovqA_	Alignment	not modelled	14.3	25	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
58	c2ds2B_	Alignment	not modelled	12.0	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**sweet protein mabinlin-2 chain b; **PDBTitle:** crystal structure of mabinlin ii
59	d1vlia1	Alignment	not modelled	11.4	4	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
60	d1ni8a_	Alignment	not modelled	10.9	17	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
61	c3nznA_	Alignment	not modelled	10.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
62	d1vi4a_	Alignment	not modelled	10.3	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
63	d1fs2b1	Alignment	not modelled	9.9	22	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
64	c1jsuC_	Alignment	not modelled	9.6	9	**PDB header:**complex (transferase/cyclin/inhibitor) **Chain:** C: **PDB Molecule:**p27; **PDBTitle:** p27(kip1)/cyclin a/cdk2 complex
65	d2axpa1	Alignment	not modelled	9.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
66	c3pywA_	Alignment	not modelled	9.0	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**s-layer protein sap; **PDBTitle:** the structure of the slh domain from b. anthracis surface array2 protein at 1.8a
67	c3dnjB_	Alignment	not modelled	7.8	15	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease adapter protein clps; **PDBTitle:** the structure of the caulobacter crescentus clps protease2 adaptor protein in complex with a n-end rule peptide
68	c3fajA_	Alignment	not modelled	7.5	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of the structural protein p131 of the archaeal virus2 acidianus two-tailed virus (atv)
69	c3c8oB_	Alignment	not modelled	7.2	16	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1
70	d1gefa_	Alignment	not modelled	7.2	13	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
71	d1lr1a_	Alignment	not modelled	6.9	17	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
72	d2p5zx2	Alignment	not modelled	6.9	8	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
73	d1j3la_	Alignment	not modelled	6.7	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
74	c2qh9B_	Alignment	not modelled	6.1	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0215 protein af_1433; **PDBTitle:** the crystal structure of a protein of unknown function from2 archaeoglobus fulgidus dsm 4304
75	c2f9jP_	Alignment	not modelled	5.9	15	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
76	d2fsqa1	Alignment	not modelled	5.6	13	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**Atu0111-like
77	d1cr6a1	Alignment	not modelled	5.6	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
78	d1psya_	Alignment	not modelled	5.3	13	**Fold:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Superfamily:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin

						Family: Seed storage protein, 2S albumin
79	d1vbga1	Alignment	not modelled	5.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain