Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75894
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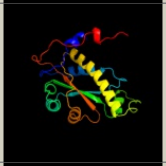
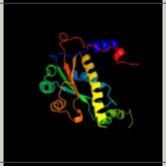
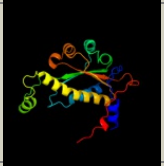
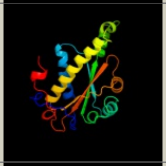
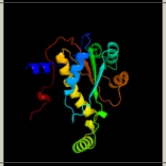
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vfra_	Alignment		100.0	16	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
2	c3of4A_	Alignment		100.0	16	**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
3	c3bemA_	Alignment		100.0	21	**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
4	c2hayD_	Alignment		100.0	19	**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
5	d1zcha1	Alignment		100.0	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
6	c3n2sD_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
7	c3eofB_	Alignment		100.0	18	**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
8	d1f5va_	Alignment		100.0	16	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
9	d1bkja_	Alignment		100.0	16	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
10	c3gagB_	Alignment		100.0	13	**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	c3gbhC_	Alignment		100.0	21	**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

12	d1ykia1	Alignment		100.0	20	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
13	c2wzvB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
14	c3gh8A_	Alignment		100.0	13	**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)
15	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
16	c3ge6B_	Alignment		100.0	19	**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
17	c2islB_	Alignment		100.0	19	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
18	d2b67a1	Alignment		100.0	20	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
19	d2frea1	Alignment		100.0	19	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
20	d1kqba_	Alignment		100.0	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
21	d1noxa_	Alignment	not modelled	100.0	25	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
22	c3eo8A_	Alignment	not modelled	100.0	14	**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
23	d2ifaa1	Alignment	not modelled	100.0	13	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
24	c2i7hE_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
25	c2h0uA_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-flavin oxidoreductase; **PDBTitle:** crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
26	c3ge5A_	Alignment	not modelled	100.0	23	**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
27	d1ywqa1	Alignment	not modelled	100.0	13	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
28	c2wqfA_	Alignment	not modelled	100.0	13	**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	c3koqC_	Alignment	not modelled	100.0	18	**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
30	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
31	c3ek3A_	Alignment	not modelled	100.0	9	**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
32	c3gfaB_	Alignment	not modelled	100.0	16	**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	c3e39A_	Alignment	not modelled	100.0	18	**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
34	c3kwkA_	Alignment	not modelled	100.0	15	**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
35	c3g14B_	Alignment	not modelled	100.0	15	**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
36	c3m5kA_	Alignment	not modelled	100.0	11	**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	c3pxvD_	Alignment	not modelled	100.0	10	**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
38	c3e10B_	Alignment	not modelled	100.0	17	**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
39	c2r01A_	Alignment	not modelled	100.0	16	**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
40	c3hoiA_	Alignment	not modelled	100.0	14	**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	16	**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	18	**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	100.0	11	**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	99.9	17	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**Putative nitroreductase TM1586
45	d1oeyj_	Alignment	not modelled	41.4	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
46	c3gyxJ_	Alignment	not modelled	33.7	7	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
47	d1fs2b1	Alignment	not modelled	26.9	21	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
48	c1nexC_	Alignment	not modelled	26.5	17	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
49	c2p1nD_	Alignment	not modelled	23.8	20	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
50	d2ovra1	Alignment	not modelled	23.8	20	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
51	c2ovqA_	Alignment	not modelled	23.3	20	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex

52	d1nexa1	Alignment	not modelled	21.2	17	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
53	d2oc6a1	Alignment	not modelled	10.7	13	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
54	d3elna1	Alignment	not modelled	10.6	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
55	d1gefa_	Alignment	not modelled	10.3	13	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
56	c2ds2B_	Alignment	not modelled	9.6	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**sweet protein mabinlin-2 chain b; **PDBTitle:** crystal structure of mabinlin ii
57	c3dnjB_	Alignment	not modelled	9.5	10	**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
58	c3nznA_	Alignment	not modelled	9.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** the crystal structure of the glutaredoxin from methanosarcina mazei2 go1
59	d2ic1a1	Alignment	not modelled	6.9	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
60	d2p5zx2	Alignment	not modelled	6.9	13	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
61	c2kl4A_	Alignment	not modelled	6.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2032 protein; **PDBTitle:** nmr structure of the protein nb7804a
62	c3ewgA_	Alignment	not modelled	6.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription antitermination protein nusg; **PDBTitle:** crystal structure of the n-terminal domain of nusg (ngn) from2 methanocaldococcus jannaschii
63	d2i8da1	Alignment	not modelled	6.1	8	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
64	d1vlia1	Alignment	not modelled	5.6	13	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
65	d2ra7a1	Alignment	not modelled	5.4	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**FAT domain of focal adhesion kinase **Family:**FAT domain of focal adhesion kinase
66	d1vbga1	Alignment	not modelled	5.3	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
67	d1vfsa1	Alignment	not modelled	5.3	27	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
68	d3ddva1	Alignment	not modelled	5.2	10	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain