Phyre2

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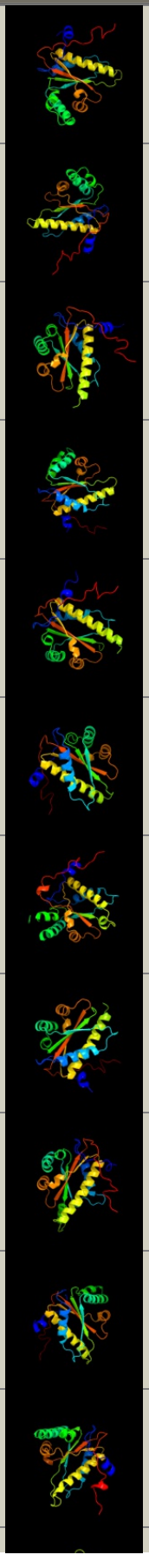
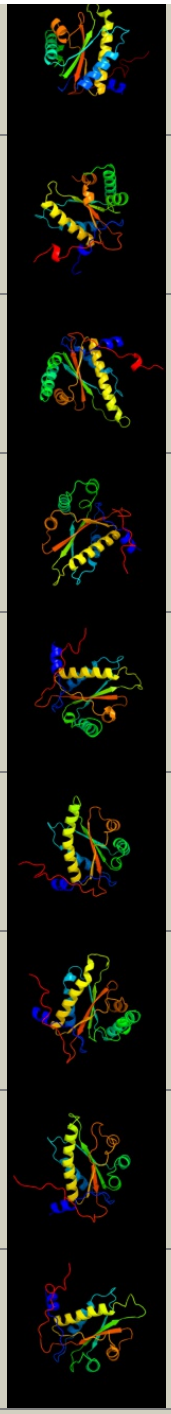
Description	P0ACY1
Date	Thu Jan 5 11:19:23 GMT 2012
Unique Job ID	625f7bcf461c8e0c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k6hB_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
2	d2ifaa1	Alignment		100.0	15	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
3	d1zcha1	Alignment		100.0	22	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
4	c2i7hE_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
5	d1f5va_	Alignment		100.0	15	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
6	c3n2sD_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
7	c3gr3B_	Alignment		100.0	17	**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
8	d1bkja_	Alignment		100.0	20	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
9	c3eofB_	Alignment		100.0	11	**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
10	d1ywqa1	Alignment		100.0	17	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
11	c3eo8A_	Alignment		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

12	c3pxvD_	Alignment		100.0	20	**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
13	c2wzvB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
14	c2wqfA_	Alignment		100.0	15	**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
15	c2islB_	Alignment		100.0	22	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
16	c3gh8A_	Alignment		100.0	18	**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)
17	d1noxa_	Alignment		100.0	25	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
18	c3ek3A_	Alignment		100.0	23	**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
19	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
20	c3kwkA_	Alignment		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 (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
21	c3bemA_	Alignment	not modelled	100.0	18	**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
22	c3ge6B_	Alignment	not modelled	100.0	21	**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
23	c3gbhC_	Alignment	not modelled	100.0	17	**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
24	c3gagB_	Alignment	not modelled	100.0	15	**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
25	c3ge5A_	Alignment	not modelled	100.0	22	**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
26	d2b67a1	Alignment	not modelled	100.0	21	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
27	c3koqC_	Alignment	not modelled	100.0	19	**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	d1vfra_	Alignment	not modelled	100.0	16	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like

						Family:NADH oxidase/flavin reductase
29	c3gfaB_	Alignment	not modelled	100.0	20	**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
30	d1ykia1	Alignment	not modelled	100.0	19	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
31	c3e10B_	Alignment	not modelled	100.0	22	**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
32	d2frea1	Alignment	not modelled	100.0	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
33	c3m5kA_	Alignment	not modelled	100.0	17	**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
34	c2h0uA_	Alignment	not modelled	100.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-flavin oxidoreductase; **PDBTitle:** crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
35	d1kqba_	Alignment	not modelled	100.0	22	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
36	c3e39A_	Alignment	not modelled	100.0	22	**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
37	c3of4A_	Alignment	not modelled	100.0	13	**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
38	c3g14B_	Alignment	not modelled	100.0	21	**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
39	c2r01A_	Alignment	not modelled	100.0	17	**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	c3bm2B_	Alignment	not modelled	100.0	91	**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
41	c3hj9A_	Alignment	not modelled	100.0	17	**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	c3hoiA_	Alignment	not modelled	100.0	15	**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
43	c3eo7A_	Alignment	not modelled	99.9	18	**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	22	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**Putative nitroreductase TM1586
45	d1oeyj_	Alignment	not modelled	36.7	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
46	d2oc6a1	Alignment	not modelled	19.6	8	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
47	c3gyxJ_	Alignment	not modelled	19.1	11	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
48	d1fs2b1	Alignment	not modelled	15.9	18	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
49	c2p1nD_	Alignment	not modelled	14.7	14	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
50	c1nexC_	Alignment	not modelled	14.4	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
51	d2ovra1	Alignment	not modelled	13.7	17	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
52	c2ovqA_	Alignment	not modelled	13.6	17	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex

53	d1cr6a1	Alignment	not modelled	12.9	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
54	d2ogga1	Alignment	not modelled	12.6	10	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
55	c2ds2B_	Alignment	not modelled	12.1	18	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**sweet protein mabinlin-2 chain b; **PDBTitle:** crystal structure of mabinlin ii
56	d1zd3a1	Alignment	not modelled	11.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
57	d1nexa1	Alignment	not modelled	11.5	17	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
58	d3ddva1	Alignment	not modelled	10.2	14	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
59	c3io0A_	Alignment	not modelled	7.8	8	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**etub protein; **PDBTitle:** crystal structure of etub from clostridium kluyveri
60	d2p19a1	Alignment	not modelled	7.6	17	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
61	c1pnbB_	Alignment	not modelled	7.3	20	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**napin bnib; **PDBTitle:** structure of napin bnib, nmr, 10 structures
62	d3cnva1	Alignment	not modelled	7.1	10	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
63	c3hfiA_	Alignment	not modelled	6.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative regulator; **PDBTitle:** the crystal structure of the putative regulator from escherichia coli2 cft073
64	d2ooia1	Alignment	not modelled	6.7	10	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
65	d2pkha1	Alignment	not modelled	6.7	14	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
66	d2ikka1	Alignment	not modelled	6.4	10	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
67	c3f8lC_	Alignment	not modelled	6.2	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hth-type transcriptional repressor phnf; **PDBTitle:** crystal structure of the effector domain of phnf from mycobacterium2 smegmatis
68	d3bwga2	Alignment	not modelled	6.1	10	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
69	c2glwA_	Alignment	not modelled	5.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
70	c1sm7A_	Alignment	not modelled	5.3	22	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**recombinant ib pronapin; **PDBTitle:** solution structure of the recombinant pronapin precursor,2 bnib.