Phyre2

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Description	RVBD2337c_(-)_2611879_2612997
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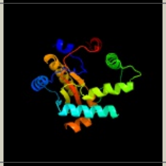
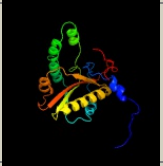
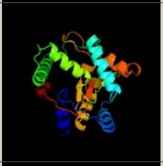
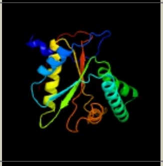
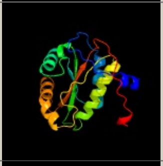
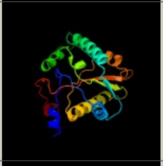
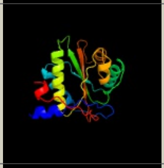
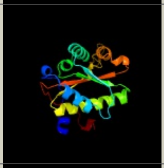
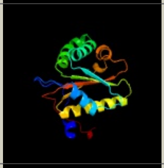
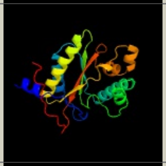
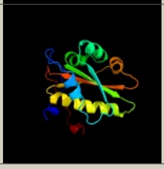
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ymvA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acg nitroreductase; **PDBTitle:** structure of reduced m smegmatis 5246, a homologue of m.2 tuberculosis acg
2	c3gr3B_	Alignment		99.7	18	**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
3	c3eo8A_	Alignment		99.7	12	**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
4	c2islB_	Alignment		99.6	21	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
5	c2wzvB_	Alignment		99.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
6	c4xomB_	Alignment		99.6	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**coenzyme f420:l-glutamate ligase; **PDBTitle:** coenzyme f420:l-glutamate ligase (fbib) from mycobacterium2 tuberculosis (c-terminal domain).
7	c3e39A_	Alignment		99.5	17	**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
8	c3kwkA_	Alignment		99.5	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
9	c3gh8A_	Alignment		99.5	10	**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)
10	c5ko8B_	Alignment		99.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of haliscomenobacter hydrossis iodotyrosine2 deiodinase (iyd) bound to fmn and mono-iodotyrosine (i-tyr)
11	d1vfra_	Alignment		99.5	13	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase

12	c3gfaB_	Alignment		99.5	12	**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
13	d1bkja_	Alignment		99.5	12	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
14	c3to0A_	Alignment		99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iodotyrosine deiodinase 1; **PDBTitle:** crystal structure of mus musculus iodotyrosine deiodinase (iyd) c217a,2 c239a bound to fmn
15	d1noxa_	Alignment		99.4	16	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
16	c3n2sD_	Alignment		99.4	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
17	c2i7hE_	Alignment		99.4	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
18	c3ek3A_	Alignment		99.4	15	**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	c5hdjA_	Alignment		99.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nfra1; **PDBTitle:** structure of b. megaterium nfra1
20	c4qlyB_	Alignment		99.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enone reductase cla-er; **PDBTitle:** crystal structure of cla-er, a novel enone reductase catalyzing a key2 step of a gut-bacterial fatty acid saturation metabolism,3 biohydrogenation
21	d1f5va_	Alignment	not modelled	99.4	17	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
22	c3m5kA_	Alignment	not modelled	99.4	14	**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
23	d1zcha1	Alignment	not modelled	99.4	19	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
24	d1ykia1	Alignment	not modelled	99.4	12	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
25	c3bm2B_	Alignment	not modelled	99.4	14	**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
26	d1kqba_	Alignment	not modelled	99.4	13	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
27	c3k6hB_	Alignment	not modelled	99.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
28	c5heiE_	Alignment	not modelled	99.3	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nfra2; **PDBTitle:** structure of b. megaterium nfra2

29	c3bemA_	Alignment	not modelled	99.3	13	**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
30	c6czpH_	Alignment	not modelled	99.3	10	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**oxygen-insensitive nad(p)h nitroreductase; **PDBTitle:** 2.2 angstrom resolution crystal structure oxygen-insensitive nad(p)h-2 dependent nitroreductase nfsb from vibrio vulnificus in complex with3 fmn
31	c3ge6B_	Alignment	not modelled	99.3	24	**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
32	c3ge5A_	Alignment	not modelled	99.3	21	**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
33	d2b67a1	Alignment	not modelled	99.3	14	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
34	c3pxvD_	Alignment	not modelled	99.3	18	**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
35	c3gagB_	Alignment	not modelled	99.3	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
36	c4eo3A_	Alignment	not modelled	99.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein/nadh dehydrogenase; **PDBTitle:** peroxiredoxin nitroreductase fusion enzyme
37	c3eofB_	Alignment	not modelled	99.3	12	**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
38	c2hayD_	Alignment	not modelled	99.3	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
39	c3of4A_	Alignment	not modelled	99.3	14	**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
40	c3qdlD_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxygen-insensitive nadph nitroreductase; **PDBTitle:** crystal structure of rdxa from helicobacter pyroli
41	c3g14B_	Alignment	not modelled	99.3	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
42	c3gbhC_	Alignment	not modelled	99.2	10	**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
43	c4dn2A_	Alignment	not modelled	99.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of putative nitroreductase from geobacter2 metallireducens gs-15
44	c3e10B_	Alignment	not modelled	99.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadh oxidase; **PDBTitle:** crystal structure of putative nadh oxidase (np_348178.1) from2 clostridium acetobutylicum at 1.40 a resolution
45	c3koqC_	Alignment	not modelled	99.2	14	**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
46	c2r01A_	Alignment	not modelled	99.2	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
47	d1ywqa1	Alignment	not modelled	99.1	12	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
48	c5j6cA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative reductase; **PDBTitle:** fmn-dependent nitroreductase (cdr20291_0767) from clostridium2 difficile r20291
49	c2h0uA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-flavin oxidoreductase; **PDBTitle:** crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
50	d2frea1	Alignment	not modelled	99.1	21	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
51	c2wqfA_	Alignment	not modelled	99.0	19	**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
52	d2ifaa1	Alignment	not modelled	99.0	14	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase

53	c4urpB_	Alignment	not modelled	99.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fatty acid repression mutant protein 2; **PDBTitle:** the crystal structure of nitroreductase from saccharomyces2 cerevisiae
54	d1vkwa_	Alignment	not modelled	98.8	28	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**Putative nitroreductase TM1586
55	c3hj9A_	Alignment	not modelled	98.8	31	**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
56	c3hoiA_	Alignment	not modelled	98.7	24	**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
57	c5j62B_	Alignment	not modelled	98.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative reductase; **PDBTitle:** fmn-dependent nitroreductase (cdr20291_0684) from clostridium2 difficile r20291
58	c3eo7A_	Alignment	not modelled	98.5	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
59	c5lq4B_	Alignment	not modelled	98.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cyagox; **PDBTitle:** the structure of thcox, the first oxidase protein from the cyanobactin2 pathways
60	c6gosC_	Alignment	not modelled	94.5	16	**PDB header:**antibiotic/inhibitor **Chain:** C: **PDB Molecule:**microcin b17-processing protein mcbc; **PDBTitle:** e. coli microcin synthetase mcbbcd complex with pro-mccb17 bound
61	c3vteA_	Alignment	not modelled	61.0	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tetrahydrocannabinolic acid synthase; **PDBTitle:** crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
62	d1f3ub_	Alignment	not modelled	33.0	15	**Fold:**triple barrel **Superfamily:**Rap30/74 interaction domains **Family:**Rap30/74 interaction domains
63	c2h1oH_	Alignment	not modelled	20.3	29	**PDB header:**gene regulation/dna complex **Chain:** H: **PDB Molecule:**trafficking protein a; **PDBTitle:** structure of fitab bound to ir36 dna fragment
64	c3fwaA_	Alignment	not modelled	19.8	5	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
65	d2bsqe1	Alignment	not modelled	19.1	29	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
66	c5sxpF_	Alignment	not modelled	12.7	23	**PDB header:**signaling protein/ligase **Chain:** F: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** structural basis for the interaction between itch prr and beta-pix
67	c4kdiC_	Alignment	not modelled	12.2	25	**PDB header:**signaling protein/hydrolase **Chain:** C: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** crystal structure of p97/vcp n in complex with otu1 ubxl
68	c3d2hA_	Alignment	not modelled	11.8	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
69	d2fcia1	Alignment	not modelled	11.1	20	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
70	d2qmsa1	Alignment	not modelled	11.0	0	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
71	c5sxpG_	Alignment	not modelled	10.9	23	**PDB header:**signaling protein/ligase **Chain:** G: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** structural basis for the interaction between itch prr and beta-pix
72	d1ecfa2	Alignment	not modelled	10.8	9	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
73	d1nrva_	Alignment	not modelled	8.7	0	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
74	c6hq9A_	Alignment	not modelled	8.6	75	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna excision repair protein ercc-6-like 2; **PDBTitle:** crystal structure of the tudor domain of human ercc6-l2
75	c2aapA_	Alignment	not modelled	7.5	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**jingzhaotoxin-vii; **PDBTitle:** solution structure of jingzhaotoxin-vii
76	c2l2rA_	Alignment	not modelled	7.3	0	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide ecamp1; **PDBTitle:** helical hairpin structure of a novel antimicrobial peptide ecamp1 from2 seeds of barnyard grass (echinochloa crus-galli)
77	c2jy0A_	Alignment	not modelled	6.8	23	**PDB header:**membrane protein, viral protein **Chain:** A: **PDB Molecule:**protease ns2-3; **PDBTitle:** solution nmr structure of hcv ns2 protein, membrane segment2 (1-27)
78	c2hzsH_	Alignment	not modelled	6.4	6	**PDB header:**transcription **Chain:** H: **PDB Molecule:**rna polymerase ii mediator complex subunit 18; **PDBTitle:** structure of the mediator head submodule med8c/18/20
						PDB header:oxidoreductase

79	c6gcsg_	Alignment	not modelled	6.3	11	**Chain:** G: **PDB Molecule:**30-kda protein (nugm); **PDBTitle:** cryo-em structure of respiratory complex i from yarrowia lipolytica
80	d2ijqa1	Alignment	not modelled	6.0	23	**Fold:**Hyaluronidase domain-like **Superfamily:**TTHA0068-like **Family:**TTHA0068-like
81	c4ml8C_	Alignment	not modelled	5.8	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytokinin oxidase 2; **PDBTitle:** structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
82	d1r5ta_	Alignment	not modelled	5.7	15	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
83	c3tsjA_	Alignment	not modelled	5.6	7	**PDB header:**allergen, oxidoreductase **Chain:** A: **PDB Molecule:**pollen allergen phl p 4; **PDBTitle:** crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
84	c2jyaA_	Alignment	not modelled	5.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
85	c5lnkc_	Alignment	not modelled	5.2	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:** **PDBTitle:** entire ovine respiratory complex i
86	d1kjqa2	Alignment	not modelled	5.2	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like