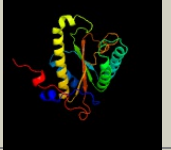
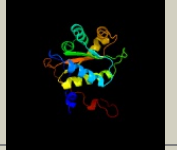
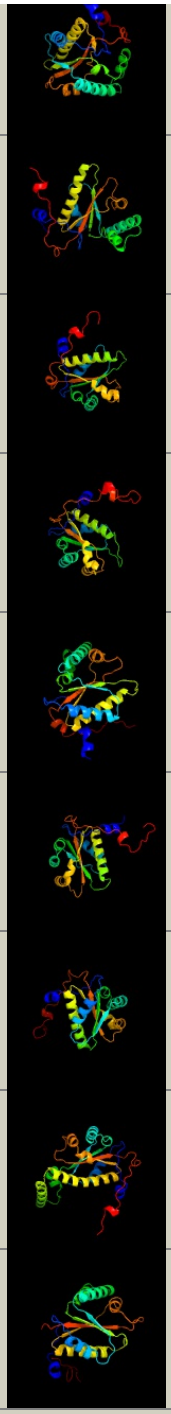
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3127_(-)_3492144_3493178
Date	Thu Aug 8 16:20:31 BST 2019
Unique Job ID	5996df69ff9bdbdf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ymvA_	Alignment		100.0	49	**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		99.9	14	**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	c2wzvB_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
4	c2islB_	Alignment		99.9	17	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
5	c3eo8A_	Alignment		99.9	11	**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
6	c3gh8A_	Alignment		99.9	16	**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)
7	c2i7hE_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
8	c3gfaB_	Alignment		99.9	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
9	d1bkja_	Alignment		99.9	19	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
10	c3to0A_	Alignment		99.9	20	**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
11	c4eo3A_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein/nadh dehydrogenase; **PDBTitle:** peroxiredoxin nitroreductase fusion enzyme

12	c5ko8B_	Alignment		99.9	17	**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)
13	c3k6hB_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
14	c5hdjA_	Alignment		99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nfra1; **PDBTitle:** structure of b. megaterium nfra1
15	d1f5va_	Alignment		99.9	15	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
16	c4xomB_	Alignment		99.9	21	**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).
17	c3e39A_	Alignment		99.9	19	**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
18	c3n2sD_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
19	d1noxa_	Alignment		99.9	20	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
20	c3bm2B_	Alignment		99.9	15	**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
21	c3eofB_	Alignment	not modelled	99.9	15	**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
22	d1zcha1	Alignment	not modelled	99.9	15	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
23	c3ek3A_	Alignment	not modelled	99.9	14	**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
24	d1vfra_	Alignment	not modelled	99.9	12	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
25	c2hayD_	Alignment	not modelled	99.8	10	**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
26	c3ge5A_	Alignment	not modelled	99.8	14	**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	c5heiE_	Alignment	not modelled	99.8	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nfra2; **PDBTitle:** structure of b. megaterium nfra2
28	c3bemA_	Alignment	not modelled	99.8	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

29	c3kwkA_	Alignment	not modelled	99.8	18	**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
30	d2ifaa1	Alignment	not modelled	99.8	11	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
31	d1ywqa1	Alignment	not modelled	99.8	14	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
32	c6czpH_	Alignment	not modelled	99.8	11	**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
33	c3pxvD_	Alignment	not modelled	99.8	16	**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
34	d2b67a1	Alignment	not modelled	99.8	17	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
35	d1ykia1	Alignment	not modelled	99.8	11	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
36	c3koqC_	Alignment	not modelled	99.8	20	**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
37	c3g14B_	Alignment	not modelled	99.8	17	**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
38	d2frea1	Alignment	not modelled	99.8	11	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
39	c3gagB_	Alignment	not modelled	99.8	12	**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
40	c3of4A_	Alignment	not modelled	99.8	12	**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
41	c4qlyB_	Alignment	not modelled	99.8	13	**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
42	c4dn2A_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of putative nitroreductase from geobacter2 metallireducens gs-15
43	c3ge6B_	Alignment	not modelled	99.8	16	**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
44	c3m5kA_	Alignment	not modelled	99.8	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
45	c3gbhC_	Alignment	not modelled	99.8	13	**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
46	d1kqba_	Alignment	not modelled	99.8	13	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
47	c3qdlD_	Alignment	not modelled	99.8	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxygen-insensitive nadph nitroreductase; **PDBTitle:** crystal structure of rdxa from helicobacter pyroli
48	c2r01A_	Alignment	not modelled	99.8	15	**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
49	c3e10B_	Alignment	not modelled	99.8	22	**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
50	c2wqfA_	Alignment	not modelled	99.8	8	**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
51	c5j6cA_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative reductase; **PDBTitle:** fmn-dependent nitroreductase (cdr20291_0767) from clostridium2 difficile r20291
						PDB header:oxidoreductase

52	c2h0uA_	Alignment	not modelled	99.7	8	**Chain:** A: **PDB Molecule:**nadph-flavin oxidoreductase; **PDBTitle:** crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
53	c5j62B_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative reductase; **PDBTitle:** fmn-dependent nitroreductase (cdr20291_0684) from clostridium2 difficile r20291
54	c3hj9A_	Alignment	not modelled	99.6	15	**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
55	c3hoiA_	Alignment	not modelled	99.6	23	**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
56	c4urpB_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fatty acid repression mutant protein 2; **PDBTitle:** the crystal structure of nitroreductase from saccharomyces2 cerevisiae
57	c3eo7A_	Alignment	not modelled	99.5	12	**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
58	d1vkwa_	Alignment	not modelled	99.5	23	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**Putative nitroreductase TM1586
59	c5lq4B_	Alignment	not modelled	99.4	25	**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	97.8	15	**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	c4lo8H_	Alignment	not modelled	27.9	11	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**ha-17; **PDBTitle:** ha70(d3)-ha17
62	c5sxpF_	Alignment	not modelled	25.2	40	**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
63	c5sxpG_	Alignment	not modelled	21.1	53	**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
64	d1f3ub_	Alignment	not modelled	16.7	23	**Fold:**triple barrel **Superfamily:**Rap30/74 interaction domains **Family:**Rap30/74 interaction domains
65	c3vteA_	Alignment	not modelled	15.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tetrahydrocannabinolic acid synthase; **PDBTitle:** crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
66	d2fcia1	Alignment	not modelled	10.3	40	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
67	c4kdiC_	Alignment	not modelled	8.7	18	**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	c6hq9A_	Alignment	not modelled	8.3	63	**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
69	c3o2iB_	Alignment	not modelled	8.2	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
70	d2qmsa1	Alignment	not modelled	7.7	30	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
71	c2l2rA_	Alignment	not modelled	7.2	57	**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)
72	c2jy0A_	Alignment	not modelled	7.1	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)
73	c2hzsH_	Alignment	not modelled	6.7	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**rna polymerase ii mediator complex subunit 18; **PDBTitle:** structure of the mediator head submodule med8c/18/20
74	c4wx8A_	Alignment	not modelled	6.6	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**ekc/keops complex subunit pcc1; **PDBTitle:** crystal structure of binary complex gon7-pcc1
75	c6a42A_	Alignment	not modelled	6.2	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**rna-directed dna polymerase homolog (r1),polyubiquitin-c; **PDBTitle:** r1en(5-223)-ubiquitin fusion
76	c5m73D_	Alignment	not modelled	6.0	18	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**signal recognition particle subunit srp72; **PDBTitle:** structure of the human srp s domain with srp72 rna-binding domain
77	c6gwjB_	Alignment	not modelled	5.9	26	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**ekc/keops complex subunit lage3; **PDBTitle:** protein complex
						PDB header:toxin

78	c2aapA_	Alignment	not modelled	5.8	42	**Chain:** A: **PDB Molecule:**jingzhaotoxin-vii; **PDBTitle:** solution structure of jingzhaotoxin-vii
79	d1nrva_	Alignment	not modelled	5.4	43	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
80	d2g3ba2	Alignment	not modelled	5.4	19	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
81	c4mh4B_	Alignment	not modelled	5.3	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**osmc-like protein; **PDBTitle:** crystal structure of osmc-like protein from burkholderia cenocepacia2 j2315
82	d1sqwa2	Alignment	not modelled	5.2	6	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Nip7p homolog, N-terminal domain
83	d1ecfa2	Alignment	not modelled	5.1	25	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases