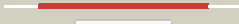



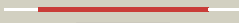



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3368c_(-)_3780515_3781159
Date	Fri Aug 9 18:20:03 BST 2019
Unique Job ID	8519d0cdb3402053

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zcha1	 Alignment		100.0	21	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
2	c2islB_	 Alignment		100.0	24	PDB header: flavoprotein Chain: B: PDB Molecule: blub; PDBTitle: blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
3	c5heiE_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: nfra2; PDBTitle: structure of b. megaterium nfra2
4	c5hdjA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nfra1; PDBTitle: structure of b. megaterium nfra1
5	c3gr3B_	 Alignment		100.0	22	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
6	c3n2sD_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh-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	c4eo3A_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein/nadh dehydrogenase; PDBTitle: peroxiredoxin nitroreductase fusion enzyme
9	d1f5va_	 Alignment		100.0	17	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
10	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
11	d1bkja_	 Alignment		100.0	20	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase

12	c4dn2A_	Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase; PDBTitle: crystal structure of putative nitroreductase from geobacter2 metallireducens gs-15
13	c4xomB_	Alignment		100.0	25	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).
14	d2ifaa1	Alignment		100.0	14	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
15	c3gbhC_	Alignment		100.0	19	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
16	c3ge6B_	Alignment		100.0	18	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	c3eo8A_	Alignment		100.0	23	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
18	c4qlyB_	Alignment		100.0	15	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
19	d1vfra_	Alignment		100.0	21	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
20	d1ykia1	Alignment		100.0	23	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
21	c6czpH_	Alignment	not modelled	100.0	21	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
22	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
23	c3bemA_	Alignment	not modelled	100.0	14	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
24	c3gh8A_	Alignment	not modelled	100.0	23	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)
25	d1ywqa1	Alignment	not modelled	100.0	19	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
26	c5ko8B_	Alignment	not modelled	100.0	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)
27	c2hayD_	Alignment	not modelled	100.0	14	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
28	d1kqba_	Alianment	not modelled	100.0	18	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like

						Family: NADH oxidase/flavin reductase
29	d2frea1	Alignment	not modelled	100.0	21	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
30	c3kwkA	Alignment	not modelled	100.0	24	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
31	c3of4A	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (fnbn, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
32	c3m5kA	Alignment	not modelled	100.0	23	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
33	d1noxa	Alignment	not modelled	100.0	23	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
34	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
35	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
36	c3e10B	Alignment	not modelled	100.0	14	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
37	c3ge5A	Alignment	not modelled	100.0	24	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
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	c3pxvD	Alignment	not modelled	100.0	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
40	d2b67a1	Alignment	not modelled	100.0	18	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
41	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
42	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
43	c2i7hE	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: E: PDB Molecule: nitroreductase-like family protein; PDBTitle: crystal structure of the nitroreductase-like family protein from2 bacillus cereus
44	c3to0A	Alignment	not modelled	100.0	30	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
45	c5j6cA	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase; PDBTitle: fmn-dependent nitroreductase (cdr20291_0767) from clostridium2 difficile r20291
46	c3koqC	Alignment	not modelled	100.0	21	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
47	c2h0uA	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-flavin oxidoreductase; PDBTitle: crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
48	c3ek3A	Alignment	not modelled	100.0	21	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
49	c2r01A	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum t1s at 1.15 a resolution
50	c3qdID	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: oxygen-insensitive nadph nitroreductase; PDBTitle: crystal structure of rdxa from helicobacter pylori
51	c5j62B	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative reductase; PDBTitle: fmn-dependent nitroreductase (cdr20291_0684) from clostridium2 difficile r20291

52	c4urpB	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid repression mutant protein 2; PDBTitle: the crystal structure of nitroreductase from <i>saccharomyces2 cerevisiae</i>
53	c3hoiA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nitroreductase bf3017; PDBTitle: crystal structure of fmn-dependent nitroreductase bf3017 from <i>bacteroides fragilis</i> nctc 9343 (yp_212631.1) from <i>bacteroides fragilis</i> nctc 9343 at 1.55 a resolution
54	c3hj9A	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative nitroreductase (reut_a1228) from <i>ralstonia eutropha jmp134</i> at 2.00 a resolution
55	c3bm2B	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: protein ydja; PDBTitle: crystal structure of a minimal nitroreductase ydja from <i>escherichia2 coli k12</i> with and without fmn cofactor
56	c5lq4B	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cyagox; PDBTitle: the structure of thcox, the first oxidase protein from the cyanobactin2 pathways
57	c3eo7A	Alignment	not modelled	99.9	14	PDB header: flavoprotein Chain: A: PDB Molecule: putative nitroreductase; PDBTitle: crystal structure of a putative nitroreductase (ava_2154) from <i>anabaena variabilis</i> atcc 29413 at 1.80 a resolution
58	d1vkwa	Alignment	not modelled	99.9	21	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
59	c2ymvA	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: acg nitroreductase; PDBTitle: structure of reduced <i>m smegmatis</i> 5246, a homologue of <i>m.2 tuberculosis</i> acg
60	c6gosC	Alignment	not modelled	99.7	12	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	d1oeyj	Alignment	not modelled	37.8	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
62	c3zeyl	Alignment	not modelled	36.2	17	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the <i>trypanosoma2 brucei</i> ribosome
63	c4v1am	Alignment	not modelled	27.9	19	PDB header: ribosome Chain: M: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
64	d2oc6a1	Alignment	not modelled	27.5	16	Fold: Secretion chaperone-like Superfamily: YdhG-like Family: YdhG-like
65	d2ic1a1	Alignment	not modelled	25.9	10	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Cysteine dioxygenase type I
66	c5abxB	Alignment	not modelled	22.2	35	PDB header: translation Chain: B: PDB Molecule: 4e-binding protein mex1li; PDBTitle: complex of <i>c. elegans</i> eif4e-3 with the 4e-binding protein2 mex1li and cap analog
67	c3j38P	Alignment	not modelled	20.2	17	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s15, isoform a; PDBTitle: structure of the <i>d. melanogaster</i> 40s ribosomal proteins
68	d2i8da1	Alignment	not modelled	20.0	12	Fold: Secretion chaperone-like Superfamily: YdhG-like Family: YdhG-like
69	c2p1nD	Alignment	not modelled	19.8	11	PDB header: signaling protein Chain: D: PDB Molecule: skp1-like protein 1a; PDBTitle: mechanism of auxin perception by the tir1 ubiquitin ligase
70	d1fs2b1	Alignment	not modelled	19.5	11	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
71	c5xxuP	Alignment	not modelled	18.4	14	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of <i>toxoplasma gondii</i> ribosome
72	d2ovra1	Alignment	not modelled	18.3	11	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
73	c2ds2B	Alignment	not modelled	18.1	18	PDB header: plant protein Chain: B: PDB Molecule: sweet protein mabinlin-2 chain b; PDBTitle: crystal structure of mabinlin ii
74	c2kl4A	Alignment	not modelled	18.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2032 protein; PDBTitle: nmr structure of the protein nb7804a
75	c2ovqA	Alignment	not modelled	17.8	11	PDB header: transcription/cell cycle Chain: A: PDB Molecule: s-phase kinase-associated protein 1a; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex
76	c3gyxj	Alignment	not modelled	17.8	19	PDB header: oxidoreductase Chain: J: PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylsulfate reductase from <i>desulfovibrio gigas</i>
77	c1nexC	Alignment	not modelled	17.0	11	PDB header: ligase, cell cycle Chain: C: PDB Molecule: centromere dna-binding protein complex cbf3 PDBTitle: crystal structure of scskp1-sccdc4-cpd peptide complex Fold: lambda repressor-like DNA-binding domains

78	d2auwa1	Alignment	not modelled	16.2	29	Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
79	c5domA_	Alignment	not modelled	14.7	18	PDB header: plant protein Chain: A: PDB Molecule: 2s albumin; PDBTitle: crystal structure, maturation and flocculating properties of a 2s2 albumin from moringa oleifera seeds
80	c5t0fB_	Alignment	not modelled	13.1	17	PDB header: transcription Chain: B: PDB Molecule: protein tify 9; PDBTitle: crystal structure of the myc3 n-terminal domain [44-242] in complex2 with jaz10 cmid domain [16-58] from arabidopsis
81	c3o30I_	Alignment	not modelled	12.3	17	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15; PDBTitle: yeast 80s ribosome. this entry consists of the 40s subunit of the2 second 80s in the asymmetric unit.
82	c5u87A_	Alignment	not modelled	12.2	18	PDB header: plant protein Chain: A: PDB Molecule: preproalbumin paws1; PDBTitle: nmr structure of the precursor protein paws1 comprising sfti-1 and a2 seed storage albumin
83	d3elna1	Alignment	not modelled	11.1	10	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Cysteine dioxygenase type I
84	c2fhoA_	Alignment	not modelled	11.1	14	PDB header: rna binding protein Chain: A: PDB Molecule: spliceosomal protein sf3b155; PDBTitle: nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
85	d1nexa1	Alignment	not modelled	10.8	14	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
86	c4n0hF_	Alignment	not modelled	10.3	22	PDB header: ligase Chain: F: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit f, PDBTitle: crystal structure of s. cerevisiae mitochondrial gatfab
87	c3nr7A_	Alignment	not modelled	10.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein h-ns; PDBTitle: crystal structure of s. typhimurium h-ns 1-83
88	d1gefa_	Alignment	not modelled	9.8	16	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
89	d2olra2	Alignment	not modelled	9.0	25	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
90	c1pnbB_	Alignment	not modelled	8.6	14	PDB header: seed storage protein Chain: B: PDB Molecule: napin bnib; PDBTitle: structure of napin bnib, nmr, 10 structures
91	c2lvfA_	Alignment	not modelled	8.6	19	PDB header: allergen Chain: A: PDB Molecule: 2s albumin; PDBTitle: solution structure of the brazil nut 2s albumin ber e 1
92	c4iumA_	Alignment	not modelled	8.2	37	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: papain-like protease 2; PDBTitle: equine arteritis virus papain-like protease 2 (plp2) covalently bound2 to ubiquitin
93	c1sm7A_	Alignment	not modelled	8.1	15	PDB header: plant protein Chain: A: PDB Molecule: recombinant ib pronapin; PDBTitle: solution structure of the recombinant pronapin precursor, bnib.
94	c5xyiP_	Alignment	not modelled	8.0	10	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
95	c3fajA_	Alignment	not modelled	7.8	14	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)
96	c4gxtA_	Alignment	not modelled	6.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
97	c2x49A_	Alignment	not modelled	6.6	9	PDB header: protein transport Chain: A: PDB Molecule: invasion protein inva; PDBTitle: crystal structure of the c-terminal domain of inva
98	c6chgE_	Alignment	not modelled	6.1	22	PDB header: transferase Chain: E: PDB Molecule: klla0e03521p; PDBTitle: crystal structure of the yeast compass catalytic module
99	c2f5uA_	Alignment	not modelled	6.1	12	PDB header: viral protein Chain: A: PDB Molecule: virion protein ul25; PDBTitle: structural characterization of the ul25 dna packaging2 protein from herpes simplex virus type 1