



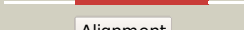











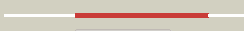









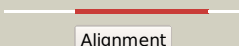

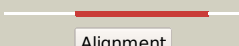

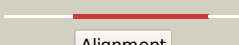

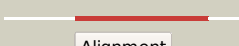







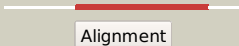
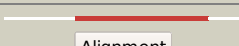
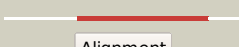


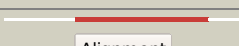

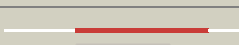


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3131 (-) _3496548_3497546
Date	Thu Aug 8 16:20:31 BST 2019
Unique Job ID	6a3a90167158bad2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ymvA_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acg nitroreductase; <b>PDBTitle:</b> structure of reduced m smegmatis 5246, a homologue of m.2 tuberculosis acg
2	<a href="#">c3gr3B_</a>	 Alignment		100.0	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase-like family protein (pnba,2 bh06130) from bartonella henselae str. houston-1 at 1.45 a resolution
3	<a href="#">c2wzvB_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nfnb protein; <b>PDBTitle:</b> crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
4	<a href="#">c3gh8A_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iodotyrosine dehalogenase 1; <b>PDBTitle:</b> crystal structure of mus musculus iodotyrosine deiodinase (iyd) bound2 to fmn and di-iodotyrosine (dit)
5	<a href="#">c2islB_</a>	 Alignment		100.0	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> blub; <b>PDBTitle:</b> blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
6	<a href="#">c4eo3A_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterioferritin comigratory protein/nadh dehydrogenase; <b>PDBTitle:</b> peroxiredoxin nitroreductase fusion enzyme
7	<a href="#">c5ko8B_</a>	 Alignment		99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of haliscomenobacter hydrossis iodotyrosine2 deiodinase (iyd) bound to fmn and mono-iodotyrosine (i-tyr)
8	<a href="#">c3eo8A_</a>	 Alignment		99.9	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> blub-like flavoprotein; <b>PDBTitle:</b> crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution
9	<a href="#">d1vfra_</a>	 Alignment		99.9	11	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
10	<a href="#">d1zcha1</a>	 Alignment		99.9	14	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
11	<a href="#">d1noxa_</a>	 Alignment		99.9	21	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase

12	<a href="#">c5hdjA_</a>	 Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nfra1; <b>PDBTitle:</b> structure of b. megaterium nfra1
13	<a href="#">c3k6hB_</a>	 Alignment		99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
14	<a href="#">c5heiE_</a>	 Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nfra2; <b>PDBTitle:</b> structure of b. megaterium nfra2
15	<a href="#">d1bkja_</a>	 Alignment		99.9	22	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
16	<a href="#">c3bemA_</a>	 Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h nitroreductase ydfn; <b>PDBTitle:</b> crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
17	<a href="#">c2hayD_</a>	 Alignment		99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas
18	<a href="#">c6czpH_</a>	 Alignment		99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> oxygen-insensitive nad(p)h nitroreductase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure oxygen-insensitive nad(p)h-2 dependent nitroreductase nfsb from vibrio vulnificus in complex with3 fmn
19	<a href="#">c3n2sD_</a>	 Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadph-dependent nitro/flavin reductase; <b>PDBTitle:</b> structure of nfra1 nitroreductase from b. subtilis
20	<a href="#">c3ek3A_</a>	 Alignment		99.9	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of nitroreductase with bound fmn (yp_211706.1) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution
21	<a href="#">d1ykia1</a>	 Alignment	not modelled	99.9	12	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
22	<a href="#">c2i7hE_</a>	 Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> nitroreductase-like family protein; <b>PDBTitle:</b> crystal structure of the nitroreductase-like family protein from2 bacillus cereus
23	<a href="#">c3eofB_</a>	 Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
24	<a href="#">c3gfaB_</a>	 Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (cd3205) from clostridium difficile 630 at 1.35 a resolution
25	<a href="#">c3ge6B_</a>	 Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exiguobacterium sibiricum 255-15 at 1.85 a3 resolution
26	<a href="#">d1f5va_</a>	 Alignment	not modelled	99.9	24	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
27	<a href="#">c4xomB_</a>	 Alignment	not modelled	99.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme f420:l-glutamate ligase; <b>PDBTitle:</b> coenzyme f420:l-glutamate ligase (fbib) from mycobacterium2 tuberculosis (c-terminal domain).
28	<a href="#">c3ge5A_</a>	 Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h:fmn oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn

						oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
29	<a href="#">c3gbhC_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p)h-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution
30	<a href="#">c3e39A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase in complex with fmn2 (dde_0787) from desulfovibrio desulfuricans subsp. at 1.70 a3 resolution
31	<a href="#">c3to0A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iodotyrosine deiodinase 1; <b>PDBTitle:</b> crystal structure of mus musculus iodotyrosine deiodinase (iyd) c217a,2 c239a bound to fmn
32	<a href="#">c4qlyB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enone reductase cla-er; <b>PDBTitle:</b> crystal structure of cla-er, a novel enone reductase catalyzing a key2 step of a gut-bacterial fatty acid saturation metabolism,3 biohydrogenation
33	<a href="#">c3gagB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh dehydrogenase, nadph nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution
34	<a href="#">c3of4A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (fnfb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
35	<a href="#">d2b67a1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
36	<a href="#">c3pxvD_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of a nitroreductase with bound fmn (dhaf_2018) from2 desulfitobacterium hafniense dcb-2 at 2.30 a resolution
37	<a href="#">d1kqba_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
38	<a href="#">c3kwaA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
39	<a href="#">d1ywqa1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
40	<a href="#">c3koqC_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of a nitroreductase family protein (cd3355) from2 clostridium difficile 630 at 1.58 a resolution
41	<a href="#">d2ifaa1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
42	<a href="#">c2h0uA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-flavin oxidoreductase; <b>PDBTitle:</b> crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
43	<a href="#">c2r01A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum t1s at 1.15 a resolution
44	<a href="#">c3m5kA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nadh dehydrogenase/nad(p)h nitroreductase; <b>PDBTitle:</b> crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (bdi_1728) from parabacteroides distasonis atcc 85033 at 1.86 a resolution
45	<a href="#">c4dn2A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitroreductase; <b>PDBTitle:</b> crystal structure of putative nitroreductase from geobacter2 metallireducens gs-15
46	<a href="#">d2frea1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> NADH oxidase/flavin reductase
47	<a href="#">c3qdlD_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxygen-insensitive nadph nitroreductase; <b>PDBTitle:</b> crystal structure of rdxa from helicobacter pylori
48	<a href="#">c3e10B_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh oxidase; <b>PDBTitle:</b> crystal structure of putative nadh oxidase (np_348178.1) from2 clostridium acetobutylicum at 1.40 a resolution
49	<a href="#">c3g14B_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitroreductase family protein; <b>PDBTitle:</b> crystal structure of nitroreductase family protein (yp_877874.1) from2 clostridium novyi nt at 1.75 a resolution
50	<a href="#">c2wafA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> copper induced nitroreductase d; <b>PDBTitle:</b> crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn
51	<a href="#">c5j6cA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative reductase; <b>PDBTitle:</b> fmn-dependent nitroreductase (cdr20291_0767) from clostridium2 difficile r20291

52	<a href="#">c3bm2B_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein ydja; <b>PDBTitle:</b> crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
53	<a href="#">c5j62B_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative reductase; <b>PDBTitle:</b> fmn-dependent nitroreductase (cdr20291_0684) from clostridium2 difficile r20291
54	<a href="#">c3hj9A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase (reut_a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution
55	<a href="#">c3hoiA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nitroreductase bf3017; <b>PDBTitle:</b> 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	<a href="#">c4urpB_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid repression mutant protein 2; <b>PDBTitle:</b> the crystal structure of nitroreductase from saccharomyces2 cerevisiae
57	<a href="#">d1vkwa_</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> FMN-dependent nitroreductase-like <b>Superfamily:</b> FMN-dependent nitroreductase-like <b>Family:</b> Putative nitroreductase TM1586
58	<a href="#">c3eo7A_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> putative nitroreductase; <b>PDBTitle:</b> crystal structure of a putative nitroreductase (ava_2154) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
59	<a href="#">c5lq4B_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cyagox; <b>PDBTitle:</b> the structure of thcox, the first oxidase protein from the cyanobactin2 pathways
60	<a href="#">c6gosC_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> antibiotic/inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> microcin b17-processing protein mcbc; <b>PDBTitle:</b> e. coli microcin synthetase mcbbcd complex with promccb17 bound
61	<a href="#">c3vteA_</a>	Alignment	not modelled	55.4	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydrocannabinolic acid synthase; <b>PDBTitle:</b> crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa
62	<a href="#">d1f3ub_</a>	Alignment	not modelled	24.8	38	<b>Fold:</b> triple barrel <b>Superfamily:</b> Rap30/74 interaction domains <b>Family:</b> Rap30/74 interaction domains
63	<a href="#">c4kdiC_</a>	Alignment	not modelled	21.2	38	<b>PDB header:</b> signaling protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin thioesterase otu1; <b>PDBTitle:</b> crystal structure of p97/vcp n in complex with otu1 ubxl
64	<a href="#">c3fwaA_</a>	Alignment	not modelled	18.5	9	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> reticuline oxidase; <b>PDBTitle:</b> structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
65	<a href="#">c5sxpF_</a>	Alignment	not modelled	18.3	50	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> F: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
66	<a href="#">d2pnwa1</a>	Alignment	not modelled	15.8	13	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> Barwin-like endoglucanases <b>Family:</b> MLTA-like
67	<a href="#">c5sxpG_</a>	Alignment	not modelled	11.8	50	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
68	<a href="#">d2g5da1</a>	Alignment	not modelled	10.0	15	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> Barwin-like endoglucanases <b>Family:</b> MLTA-like
69	<a href="#">c3d2hA_</a>	Alignment	not modelled	10.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> berberine bridge-forming enzyme; <b>PDBTitle:</b> structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
70	<a href="#">d2qmsa1</a>	Alignment	not modelled	8.8	50	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
71	<a href="#">d2fcia1</a>	Alignment	not modelled	8.5	40	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
72	<a href="#">c3r74B_</a>	Alignment	not modelled	8.5	21	<b>PDB header:</b> lyase, biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate/para-aminobenzoate synthases component i; <b>PDBTitle:</b> crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
73	<a href="#">c1lqlE_</a>	Alignment	not modelled	8.4	7	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> osmotical inducible protein c like family; <b>PDBTitle:</b> crystal structure of osmc like protein from mycoplasma2 pneumoniae
74	<a href="#">d1lqla_</a>	Alignment	not modelled	8.4	7	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> Ohr/OsmC resistance proteins
75	<a href="#">d1kjqaa2</a>	Alignment	not modelled	8.1	7	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
76	<a href="#">c6hq9A_</a>	Alignment	not modelled	8.1	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna excision repair protein ercc-6-like 2; <b>PDBTitle:</b> crystal structure of the tudor domain of human ercc6-12
77	<a href="#">c3fajA_</a>	Alignment	not modelled	7.9	35	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of the structural protein p131 of the archaeal virus2 acidianus two-tailed virus (atv)

78	<a href="#">d1ecfa2</a>	Alignment	not modelled	7.5	14	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Class II glutamine amidotransferases
79	<a href="#">d1lf6a2</a>	Alignment	not modelled	6.9	17	<b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Bacterial glucoamylase N-terminal domain-like
80	<a href="#">c2aapA</a>	Alignment	not modelled	6.2	50	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> jingzhaotoxin-vii; <b>PDBTitle:</b> solution structure of jingzhaotoxin-vii
81	<a href="#">d1kona</a>	Alignment	not modelled	6.2	14	<b>Fold:</b> YebC-like <b>Superfamily:</b> YebC-like <b>Family:</b> YebC-like
82	<a href="#">c3tsjA</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> allergen, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pollen allergen phl p 4; <b>PDBTitle:</b> crystal structure of phl p 4, a grass pollen allergen with glucose2 dehydrogenase activity
83	<a href="#">d2r4qa1</a>	Alignment	not modelled	5.8	25	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
84	<a href="#">c4ml8C</a>	Alignment	not modelled	5.8	5	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> cytokinin oxidase 2; <b>PDBTitle:</b> structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2)
85	<a href="#">d1ki0a1</a>	Alignment	not modelled	5.6	27	<b>Fold:</b> Kringle-like <b>Superfamily:</b> Kringle-like <b>Family:</b> Kringle modules
86	<a href="#">c2l2rA</a>	Alignment	not modelled	5.4	57	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide ecamp1; <b>PDBTitle:</b> helical hairpin structure of a novel antimicrobial peptide ecamp1 from2 seeds of barnyard grass (echinochloa crus-galli)
87	<a href="#">c5abxB</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> 4e-binding protein mexkli; <b>PDBTitle:</b> complex of c. elegans eif4e-3 with the 4e-binding protein2 mexkli and cap analog
88	<a href="#">c2xu8B</a>	Alignment	not modelled	5.3	33	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> pa1645; <b>PDBTitle:</b> structure of pa1645
89	<a href="#">d2bkwa1</a>	Alignment	not modelled	5.2	10	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like