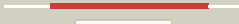






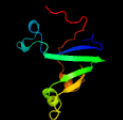



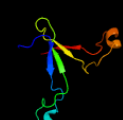

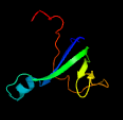








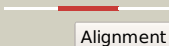

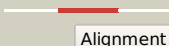





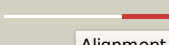

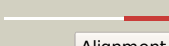

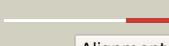
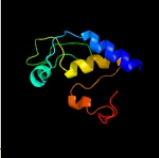

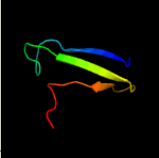

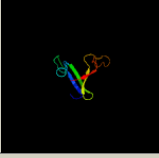
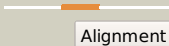
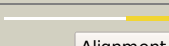

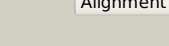

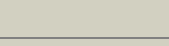
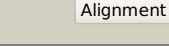
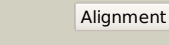


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1118c_(- )_1241976_1242836
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	0f2d86880905e991

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kw0D_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine peptidase; <b>PDBTitle:</b> crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
2	<a href="#">d2if6a1</a>	 Alignment		99.9	25	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> YiiX-like
3	<a href="#">c2p1gA_</a>	 Alignment		97.0	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative xylanase; <b>PDBTitle:</b> crystal structure of a putative xylanase from bacteroides fragilis
4	<a href="#">d2evra2</a>	 Alignment		96.3	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> NlpC/P60
5	<a href="#">c2fg0B_</a>	 Alignment		95.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cog0791: cell wall-associated hydrolases (invasion- <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
6	<a href="#">c6biqA_</a>	 Alignment		95.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> clan ca, family c40, nlpC/p60 superfamily cysteine <b>PDBTitle:</b> structure of nlpC2 from trichomonas vaginalis
7	<a href="#">c3nfpB_</a>	 Alignment		94.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
8	<a href="#">c2k1gA_</a>	 Alignment		94.3	39	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein spr; <b>PDBTitle:</b> solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
9	<a href="#">c4h4jA_</a>	 Alignment		93.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a n-acetylmuramoyl-l-alanine amidase2 (bacuni_02947) from bacteroides uniformis atcc 8492 at 1.15 a3 resolution
10	<a href="#">c6b8cA_</a>	 Alignment		93.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60; <b>PDBTitle:</b> crystal structure of nlpC/p60 domain of peptidoglycan hydrolase saga
11	<a href="#">c3h41A_</a>	 Alignment		93.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60 family protein; <b>PDBTitle:</b> crystal structure of a nlpC/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution

12	<a href="#">c3pbiA</a>	 Alignment		92.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein; <b>PDBTitle:</b> structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
13	<a href="#">c2xivA</a>	 Alignment		92.1	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical invasion protein; <b>PDBTitle:</b> structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
14	<a href="#">c2im9A</a>	 Alignment		91.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
15	<a href="#">d2im9a1</a>	 Alignment		91.7	11	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Lpg0564-like
16	<a href="#">c4hpeA</a>	 Alignment		91.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell wall hydrolase tn916-like,ctn1-orf17; <b>PDBTitle:</b> crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution
17	<a href="#">c4fdyA</a>	 Alignment		90.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> similar to lipoprotein, nlp/p60 family; <b>PDBTitle:</b> crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
18	<a href="#">c3gt2A</a>	 Alignment		90.3	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
19	<a href="#">d2io8a2</a>	 Alignment		87.5	12	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> CHAP domain
20	<a href="#">c4xcmB</a>	 Alignment		86.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell wall-binding endopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the putative nlpc/p60 d,l endopeptidase from t.2 thermophilus
21	<a href="#">c4olkB</a>	 Alignment	not modelled	85.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> the chap domain of lysgh15
22	<a href="#">c3i86A</a>	 Alignment	not modelled	76.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
23	<a href="#">c2lrjA</a>	 Alignment	not modelled	68.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> staphyloxanthin biosynthesis protein, putative; <b>PDBTitle:</b> nmr solution structure of staphyloxanthin biosynthesis protein
24	<a href="#">c3mvnA</a>	 Alignment	not modelled	60.5	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- <b>PDBTitle:</b> crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
25	<a href="#">d2jfga2</a>	 Alignment	not modelled	57.6	15	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
26	<a href="#">c2vpmB</a>	 Alignment	not modelled	54.8	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> trypanothione synthetase; <b>PDBTitle:</b> trypanothione synthetase
27	<a href="#">c2am1A</a>	 Alignment	not modelled	48.2	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- <b>PDBTitle:</b> sp protein ligand 1
28	<a href="#">c2lktA</a>	 Alignment	not modelled	44.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor responder protein 3;

28	<a href="#">c2kruA</a>	Alignment	not modelled	44.4	18	<b>PDBTitle:</b> solution structure of n-terminal domain of human tig3 in 2 m urea <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine
29	<a href="#">c4bubA</a>	Alignment	not modelled	42.1	30	<b>PDBTitle:</b> crystal structure of mure ligase from thermotoga maritima2 in complex with adp
30	<a href="#">c2f00A</a>	Alignment	not modelled	42.0	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
31	<a href="#">c2wtzC</a>	Alignment	not modelled	41.7	30	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate- <b>PDBTitle:</b> mure ligase of mycobacterium tuberculosis
32	<a href="#">c1e8cB</a>	Alignment	not modelled	41.3	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamate-2,6-diaminopimelate <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
33	<a href="#">c3uagA</a>	Alignment	not modelled	41.3	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
34	<a href="#">c3lk7A</a>	Alignment	not modelled	41.1	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murd) ligase from streptococcus agalactiae to 1.5a
35	<a href="#">c5ibzD</a>	Alignment	not modelled	38.5	32	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a novel cyclase (pfam04199).
36	<a href="#">c2k3aA</a>	Alignment	not modelled	37.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chap domain protein; <b>PDBTitle:</b> nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
37	<a href="#">d1ofla</a>	Alignment	not modelled	33.6	21	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Chondroitinase B
38	<a href="#">c4eyzB</a>	Alignment	not modelled	33.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cellulosome-related protein module from ruminococcus <b>PDBTitle:</b> crystal structure of an uncommon cellulosome-related protein module2 from ruminococcus flavefaciens that resembles papain-like cysteine3 peptidases
39	<a href="#">c5udmA</a>	Alignment	not modelled	32.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phage-associated cell wall hydrolase; <b>PDBTitle:</b> phage-associated cell wall hydrolase plypy from streptococcus2 pyogenes, space group p6522
40	<a href="#">c4c13A</a>	Alignment	not modelled	31.5	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; <b>PDBTitle:</b> x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys
41	<a href="#">c2xjaD</a>	Alignment	not modelled	31.3	30	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure from m.tuberculosis with dipeptide and adp
42	<a href="#">c4ba6A</a>	Alignment	not modelled	30.4	36	<b>PDB header:</b> carbohydrate-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase cel5a; <b>PDBTitle:</b> high resolution structure of the c-terminal family 65 carbohydrate2 binding module (cbm65b) of endoglucanase cel5a from eubacterium3 cellulosolvens
43	<a href="#">c4bucA</a>	Alignment	not modelled	29.6	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine--d-glutamate ligase; <b>PDBTitle:</b> crystal structure of murd ligase from thermotoga maritima in apo form
44	<a href="#">c3m1uB</a>	Alignment	not modelled	29.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid endopeptidase; <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
45	<a href="#">d2v4ja2</a>	Alignment	not modelled	27.1	47	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
46	<a href="#">d1p3da2</a>	Alignment	not modelled	27.1	24	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
47	<a href="#">d1e8ca2</a>	Alignment	not modelled	25.8	25	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
48	<a href="#">c3hn7A</a>	Alignment	not modelled	23.6	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
49	<a href="#">c1dbgA</a>	Alignment	not modelled	23.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> chondroitinase b; <b>PDBTitle:</b> crystal structure of chondroitinase b
50	<a href="#">c2ioaA</a>	Alignment	not modelled	22.8	14	<b>PDB header:</b> ligase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional glutathionylspermidine <b>PDBTitle:</b> e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
						<b>Fold:</b> Restriction endonuclease-like

51	<a href="#">d1y88a2</a>	Alignment	not modelled	21.9	31	<b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> MRR-like
52	<a href="#">c4lt5A</a>	Alignment	not modelled	20.1	33	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> naegleria tet-like dioxygenase; <b>PDBTitle:</b> structure of a naegleria tet-like dioxygenase in complex with 5-2 methylcytosine dna
53	<a href="#">c2eb0B</a>	Alignment	not modelled	18.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> manganese-dependent inorganic pyrophosphatase; <b>PDBTitle:</b> crystal structure of methanococcus jannaschii putative family ii2 inorganic pyrophosphatase
54	<a href="#">c1gqqA</a>	Alignment	not modelled	18.4	24	<b>PDB header:</b> cell wall biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-l-alanine ligase; <b>PDBTitle:</b> murc - crystal structure of the apo-enzyme from haemophilus influenzae
55	<a href="#">c2kytA</a>	Alignment	not modelled	18.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> group xvi phospholipase a2; <b>PDBTitle:</b> solution structure of the h-rev107 n-terminal domain
56	<a href="#">c4pyzA</a>	Alignment	not modelled	17.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 7; <b>PDBTitle:</b> crystal structure of the first two ubl domains of deubiquitylase usp7
57	<a href="#">c6odmK</a>	Alignment	not modelled	16.0	22	<b>PDB header:</b> viral protein <b>Chain:</b> K: <b>PDB Molecule:</b> capsid vertex component 2; <b>PDBTitle:</b> herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
58	<a href="#">c3vsvD</a>	Alignment	not modelled	14.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> xylosidase; <b>PDBTitle:</b> the complex structure of xylc with xylose
59	<a href="#">d1k20a</a>	Alignment	not modelled	14.3	14	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
60	<a href="#">c5t1qB</a>	Alignment	not modelled	13.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase domain-containing <b>PDBTitle:</b> 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus.
61	<a href="#">d2ahua2</a>	Alignment	not modelled	13.6	24	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> CoA transferase alpha subunit-like
62	<a href="#">c1w78A</a>	Alignment	not modelled	12.9	17	<b>PDB header:</b> synthase <b>Chain:</b> A: <b>PDB Molecule:</b> folc bifunctional protein; <b>PDBTitle:</b> e.coli folc in complex with dhpp and adp
63	<a href="#">d1wpna</a>	Alignment	not modelled	12.9	21	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
64	<a href="#">c2fphX</a>	Alignment	not modelled	12.9	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> ylmh; <b>PDBTitle:</b> cell division protein ylmh from streptococcus pneumoniae
65	<a href="#">d1s04a</a>	Alignment	not modelled	12.6	25	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> ProFAR isomerase associated domain
66	<a href="#">d1d02a</a>	Alignment	not modelled	12.6	26	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease MunI
67	<a href="#">c4rpaA</a>	Alignment	not modelled	12.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable manganese-dependent inorganic pyrophosphatase; <b>PDBTitle:</b> crystal structure of inorganic pyrophosphatase from staphylococcus2 aureus in complex with mn2+
68	<a href="#">c3a9lB</a>	Alignment	not modelled	12.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> poly-gamma-glutamate hydrolase; <b>PDBTitle:</b> structure of bacteriophage poly-gamma-glutamate hydrolase
69	<a href="#">d1uw4a</a>	Alignment	not modelled	11.4	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Smg-4/UPF3
70	<a href="#">d1i74a</a>	Alignment	not modelled	11.2	29	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
71	<a href="#">d1ltqa1</a>	Alignment	not modelled	11.2	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> phosphatase domain of polynucleotide kinase
72	<a href="#">c6bs5B</a>	Alignment	not modelled	10.7	25	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> anion transporter; <b>PDBTitle:</b> crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
73	<a href="#">c3j6vQ</a>	Alignment	not modelled	10.4	25	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> 28s ribosomal protein s17, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
74	<a href="#">c4yooA</a>	Alignment	not modelled	10.4	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> retinoblastoma-like protein 1,retinoblastoma-like protein <b>PDBTitle:</b> p107 pocket domain in complex with lin52 p29a peptide
75	<a href="#">d1o57a1</a>	Alignment	not modelled	10.3	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> N-terminal domain of Bacillus PurR
76	<a href="#">c5dniB</a>	Alignment	not modelled	10.3	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative l(+)-tartrate dehydratase subunit beta; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii fumarate hydratase2 beta subunit <b>PDB header:</b> electron transport

77	<a href="#">c6hwhX_</a>	Alignment	not modelled	10.2	21	<b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
78	<a href="#">d2a1xa1</a>	Alignment	not modelled	10.0	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminate synthase-like <b>Family:</b> PhyH-like
79	<a href="#">d1zj8a1</a>	Alignment	not modelled	8.6	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
80	<a href="#">c4j0nA_</a>	Alignment	not modelled	8.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isatin hydrolase b; <b>PDBTitle:</b> crystal structure of a manganese dependent isatin hydrolase
81	<a href="#">c5ykaA_</a>	Alignment	not modelled	8.2	27	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kdo0; <b>PDBTitle:</b> crystal structure of the kdo hydroxylase kdo0, a non-heme fe(ii)2 alphaketoglutarate dependent dioxygenase in complex with cobalt(ii)
82	<a href="#">c4m1bA_</a>	Alignment	not modelled	8.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> polysaccharide deacetylase; <b>PDBTitle:</b> structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
83	<a href="#">d2g40a1</a>	Alignment	not modelled	8.0	23	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> YkgG-like
84	<a href="#">c2g40A_</a>	Alignment	not modelled	8.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
85	<a href="#">d2hawa1</a>	Alignment	not modelled	8.0	21	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Manganese-dependent inorganic pyrophosphatase (family II)
86	<a href="#">c1j6uA_</a>	Alignment	not modelled	7.8	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
87	<a href="#">d1e0ta1</a>	Alignment	not modelled	7.7	11	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
88	<a href="#">d1g03a_</a>	Alignment	not modelled	7.6	33	<b>Fold:</b> Retrovirus capsid protein, N-terminal core domain <b>Superfamily:</b> Retrovirus capsid protein, N-terminal core domain <b>Family:</b> Retrovirus capsid protein, N-terminal core domain
89	<a href="#">d2g50a1</a>	Alignment	not modelled	7.6	11	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
90	<a href="#">d2uubp1</a>	Alignment	not modelled	7.6	12	<b>Fold:</b> Ribosomal protein S16 <b>Superfamily:</b> Ribosomal protein S16 <b>Family:</b> Ribosomal protein S16
91	<a href="#">d1d8ja_</a>	Alignment	not modelled	7.4	47	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> The central core domain of TFII E beta
92	<a href="#">d1wu2a2</a>	Alignment	not modelled	7.3	16	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
93	<a href="#">c3c7xA_</a>	Alignment	not modelled	7.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-14; <b>PDBTitle:</b> hemopexin-like domain of matrix metalloproteinase 14
94	<a href="#">c5nmpF_</a>	Alignment	not modelled	7.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> isatin hydrolase; <b>PDBTitle:</b> isatin hydrolase a (iha) from ralstonia solanacearum
95	<a href="#">d1a3xa1</a>	Alignment	not modelled	7.1	5	<b>Fold:</b> PK beta-barrel domain-like <b>Superfamily:</b> PK beta-barrel domain-like <b>Family:</b> Pyruvate kinase beta-barrel domain
96	<a href="#">c5lz6B_</a>	Alignment	not modelled	7.1	29	<b>PDB header:</b> antiviral protein <b>Chain:</b> B: <b>PDB Molecule:</b> 3a; <b>PDBTitle:</b> crystal structure of human acbd3 gold domain in complex with 3a2 protein of aichivirus b
97	<a href="#">c4akrC_</a>	Alignment	not modelled	7.1	26	<b>PDB header:</b> actin-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> f-actin-capping protein subunit alpha; <b>PDBTitle:</b> crystal structure of the cytoplasmic actin capping protein2 cap32_34 from dictyostelium discoideum
98	<a href="#">c5onkA_</a>	Alignment	not modelled	7.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yndl; <b>PDBTitle:</b> native yndl
99	<a href="#">d1zgha2</a>	Alignment	not modelled	6.9	21	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase