

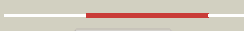




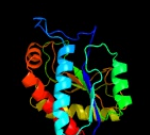

























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3915 (- )_4403369_4404589
Date	Sat Aug 10 22:05:10 BST 2019
Unique Job ID	b1df0b5eba6a6b9a

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4binA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase amic; <b>PDBTitle:</b> crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
2	<a href="#">c5j72B_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative n-acetylmuramoyl-l-alanine amidase,autolysin cwp6; <b>PDBTitle:</b> cwp6 from clostridium difficile
3	<a href="#">d1jwqa_</a>	 Alignment		100.0	23	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
4	<a href="#">c3ne8A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
5	<a href="#">c4rn7A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> the crystal structure of n-acetylmuramoyl-l-alanine amidase from2 clostridium difficile 630
6	<a href="#">c5emiA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cell wall hydrolase/autolysin; <b>PDBTitle:</b> n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
7	<a href="#">c4m6iA_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> peptidoglycan amidase rv3717; <b>PDBTitle:</b> structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
8	<a href="#">c1xovA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ply protein; <b>PDBTitle:</b> the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
9	<a href="#">c3czxA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
10	<a href="#">d1xova2</a>	 Alignment		100.0	17	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
11	<a href="#">c3qayC_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> catalytic domain of cd27l endolysin targeting clostridia difficile

12	<a href="#">c1lbuA</a>	Alignment		99.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> muramoyl-pentapeptide carboxypeptidase; <b>PDBTitle:</b> hydrolase metallo (zn) dd-peptidase
13	<a href="#">c3bkhA</a>	Alignment		99.7	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lytic transglycosylase; <b>PDBTitle:</b> crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
14	<a href="#">c5tv7A</a>	Alignment		99.7	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidoglycan-binding/hydrolysing protein; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of peptidoglycan-binding2 protein from clostridioides difficile in complex with glutamine3 hydroxamate.
15	<a href="#">c5bmqA</a>	Alignment		99.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> erfk/ybis/ycfcs/ynhg family protein; <b>PDBTitle:</b> crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
16	<a href="#">c4lpqA</a>	Alignment		99.7	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> erfk/ybis/ycfcs/ynhg family protein; <b>PDBTitle:</b> crystal structure of a periplasmic domain of the epsab fusion protein2 of the vibrio vulnificus type ii secretion system
17	<a href="#">d1lbuA1</a>	Alignment		99.6	35	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> Peptidoglycan binding domain, PGBD
18	<a href="#">c5nm7A</a>	Alignment		99.6	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan-binding domain 1; <b>PDBTitle:</b> crystal structure of burkholderia ap3 phage endolysin
19	<a href="#">c4g54A</a>	Alignment		99.6	21	<b>PDB header:</b> peptidoglycan-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> general secretion pathway protein; <b>PDBTitle:</b> crystal structure of a periplasmic domain of the epsab fusion protein2 of the vibrio vulnificus type ii secretion system
20	<a href="#">c4xxtA</a>	Alignment		99.5	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fusion of predicted zn-dependent amidase/peptidase (cell <b>PDBTitle:</b> crystal structure of fused zn-dependent2 amidase/peptidase/peptidoglycan-binding domain-containing protein3 from clostridium acetobutylicum atcc 824
21	<a href="#">c5anzA</a>	Alignment	not modelled	99.5	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble lytic transglycosylase b3; <b>PDBTitle:</b> crystal structure of sltb3 from pseudomonas aeruginosa.
22	<a href="#">c4bolA</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ampdh2; <b>PDBTitle:</b> crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
23	<a href="#">c2bh7A</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase; <b>PDBTitle:</b> crystal structure of a semet derivative of amid at 2.22 angstroms
24	<a href="#">c4bxdB</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> B: <b>PDB Molecule:</b> ampdh3; <b>PDBTitle:</b> crystal structure of ampdh3 from pseudomonas aeruginosa in2 complex with tetrasaccharide pentapeptide
25	<a href="#">c6ntwA</a>	Alignment	not modelled	99.2	36	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> probable l,d-transpeptidase yccb; <b>PDBTitle:</b> crystal structure of e. coli yccb
26	<a href="#">c4c2dC</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> carboxy-terminal processing protease ctpb; <b>PDBTitle:</b> crystal structure of the protease ctpb in an active state
27	<a href="#">c2mzeA</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrilysin; <b>PDBTitle:</b> nmr solution structure of the pro form of human matrilysin (prommp-7)
28	<a href="#">d1eak1</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
						<b>Fold:</b> PGBD-like

29	<a href="#">d2bgxa1</a>	Alignment	not modelled	97.8	23	<b>Superfamily:</b> PGBD-like <b>Family:</b> Peptidoglycan binding domain, PGBD
30	<a href="#">c1slmA</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> stromelysin-1; <b>PDBTitle:</b> crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
31	<a href="#">d1slmA1</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
32	<a href="#">d1l6ja1</a>	Alignment	not modelled	97.6	22	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
33	<a href="#">d1su3a1</a>	Alignment	not modelled	97.6	23	<b>Fold:</b> PGBD-like <b>Superfamily:</b> PGBD-like <b>Family:</b> MMP N-terminal domain
34	<a href="#">c1eakA</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 72 kda type iv collagenase; <b>PDBTitle:</b> catalytic domain of prommp-2 e404q mutant
35	<a href="#">c5th6D</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> matrix metalloproteinase-9,matrix metalloproteinase-9; <b>PDBTitle:</b> structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)
36	<a href="#">c1l6jA</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> matrix metalloproteinase-9; <b>PDBTitle:</b> crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
37	<a href="#">c1su3A</a>	Alignment	not modelled	97.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interstitial collagenase; <b>PDBTitle:</b> x-ray structure of human prommp-1: new insights into2 collagenase action
38	<a href="#">d2ikba1</a>	Alignment	not modelled	96.3	27	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> NMB1012-like
39	<a href="#">d2nr7a1</a>	Alignment	not modelled	96.1	32	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> NMB1012-like
40	<a href="#">c1gxdA</a>	Alignment	not modelled	95.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 72 kda type iv collagenase; <b>PDBTitle:</b> prommp-2/timp-2 complex
41	<a href="#">d2gfa1</a>	Alignment	not modelled	87.2	11	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> AF0625-like <b>Family:</b> AF0625-like
42	<a href="#">c2gfaC</a>	Alignment	not modelled	86.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> upf0204 protein ph0006; <b>PDBTitle:</b> structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
43	<a href="#">c1u83A</a>	Alignment	not modelled	83.6	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphosulfolactate synthase; <b>PDBTitle:</b> psl synthase from bacillus subtilis
44	<a href="#">d1u83a</a>	Alignment	not modelled	83.6	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
45	<a href="#">d1yqea1</a>	Alignment	not modelled	80.6	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> AF0625-like <b>Family:</b> AF0625-like
46	<a href="#">c3na6A</a>	Alignment	not modelled	79.4	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinylglutamate desuccinylase/aspartoacylase; <b>PDBTitle:</b> crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
47	<a href="#">c3nh8A</a>	Alignment	not modelled	78.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartoacylase-2; <b>PDBTitle:</b> crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
48	<a href="#">c5kojD</a>	Alignment	not modelled	77.5	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitrogenase femo beta subunit protein nifk; <b>PDBTitle:</b> nitrogenase mofep protein in the ids oxidized state
49	<a href="#">c3cdxB</a>	Alignment	not modelled	69.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> succinylglutamatedesuccinylase/aspartoacylase; <b>PDBTitle:</b> crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides
50	<a href="#">d1nyra1</a>	Alignment	not modelled	69.4	18	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
51	<a href="#">d1nj1a1</a>	Alignment	not modelled	67.3	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
52	<a href="#">d2q4ca1</a>	Alignment	not modelled	64.8	16	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
53	<a href="#">d1m1nb</a>	Alignment	not modelled	64.7	22	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
54	<a href="#">c3t4xA</a>	Alignment	not modelled	58.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor

55	<a href="#">c4hjha</a>	Alignment	not modelled	58.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphomannomutase; <b>PDBTitle:</b> iodide sad phased crystal structure of a phosphoglucomutase from <i>Brucella melitensis</i> complexed with glucose-6-phosphate
56	<a href="#">c1g5ha</a>	Alignment	not modelled	57.3	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial dna polymerase accessory subunit; <b>PDBTitle:</b> crystal structure of the accessory subunit of murine mitochondrial $\gamma$ polymerase
57	<a href="#">c4axvA</a>	Alignment	not modelled	54.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mpaa; <b>PDBTitle:</b> biochemical and structural characterization of the mpaa2 amidase as part of a conserved scavenging pathway for $\gamma$ peptidoglycan derived peptides in <i>Gamma</i> -proteobacteria
58	<a href="#">c3o38D</a>	Alignment	not modelled	53.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a short chain dehydrogenase from <i>Mycobacterium</i> $\gamma$ smegmatis
59	<a href="#">d1miob</a>	Alignment	not modelled	53.6	21	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
60	<a href="#">c3netB</a>	Alignment	not modelled	53.0	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> crystal structure of histidyl-trna synthetase from <i>Nostoc</i> sp. pcc 7120
61	<a href="#">d1wu7a1</a>	Alignment	not modelled	52.1	13	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
62	<a href="#">c5hxdB</a>	Alignment	not modelled	48.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein mpaa; <b>PDBTitle:</b> crystal structure of murein-tripeptide amidase mpaa from <i>Escherichia coli</i> o157
63	<a href="#">c1nj2A</a>	Alignment	not modelled	47.7	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> proline-trna synthetase; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from <i>Methanothermobacter</i> $\gamma$ thermautotrophicus
64	<a href="#">d1yw6a1</a>	Alignment	not modelled	47.6	8	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> AstE/AspA-like
65	<a href="#">c3r6yG</a>	Alignment	not modelled	46.9	29	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> aspartase; <b>PDBTitle:</b> crystal structure of chymotrypsin-treated aspartase from <i>Bacillus</i> sp.2 ym55-1
66	<a href="#">d1g5ha1</a>	Alignment	not modelled	46.4	6	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
67	<a href="#">d1qe0a1</a>	Alignment	not modelled	45.2	16	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
68	<a href="#">c2xdqA</a>	Alignment	not modelled	44.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-n-chl-b) $\gamma$ 2 complex
69	<a href="#">c3ikmC</a>	Alignment	not modelled	43.9	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase subunit gamma-2; <b>PDBTitle:</b> crystal structure of human mitochondrial dna polymerase holoenzyme
70	<a href="#">c3a9IB</a>	Alignment	not modelled	41.4	17	<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
71	<a href="#">c6mn8A</a>	Alignment	not modelled	41.1	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of prolyl-trna synthetase from <i>Onchocerca volvulus</i> 2 with bound halofuginone and nucleotide
72	<a href="#">d1vdka</a>	Alignment	not modelled	40.8	21	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
73	<a href="#">c5zy9D</a>	Alignment	not modelled	40.8	7	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> threonyl-trna synthase; <b>PDBTitle:</b> structural basis for a trna synthetase
74	<a href="#">d1qh8b</a>	Alignment	not modelled	38.4	23	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
75	<a href="#">d2i3ca1</a>	Alignment	not modelled	37.6	11	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Zn-dependent exopeptidases <b>Family:</b> AstE/AspA-like
76	<a href="#">d1nj8a1</a>	Alignment	not modelled	37.5	19	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
77	<a href="#">c4hwtA</a>	Alignment	not modelled	37.4	6	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> threonine--trna ligase, cytoplasmic; <b>PDBTitle:</b> crystal structure of human threonyl-trna synthetase bound to a novel2 inhibitor
78	<a href="#">c3i3wB</a>	Alignment	not modelled	35.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglucosamine mutase; <b>PDBTitle:</b> structure of a phosphoglucosamine mutase from <i>Francisella tularensis</i>
79	<a href="#">c3no9C</a>	Alignment	not modelled	34.3	17	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of apo fumarate hydratase from <i>Mycobacterium</i> $\gamma$ tuberculosis
80	<a href="#">c3ndiB</a>	Alignment	not modelled	33.9	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis

80	<a href="#">c3pudB</a>	Alignment	not modelled	33.9	21	protein nifn; <b>PDBTitle:</b> precursor bound nifen
81	<a href="#">c1wwpA</a>	Alignment	not modelled	33.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein ttha0636; <b>PDBTitle:</b> crystal structure of ttk003001694 from thermus thermophilus2 hb8
82	<a href="#">c2i4IC</a>	Alignment	not modelled	33.7	17	<b>PDB header:</b> ligase <b>Chain:</b> C; <b>PDB Molecule:</b> proline-trna ligase; <b>PDBTitle:</b> rhodopseudomonas palustris prolyl-trna synthetase
83	<a href="#">c2ynmC</a>	Alignment	not modelled	32.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
84	<a href="#">d1qwga</a>	Alignment	not modelled	30.5	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
85	<a href="#">c1y80A</a>	Alignment	not modelled	29.5	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
86	<a href="#">d1j3ua</a>	Alignment	not modelled	29.3	28	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
87	<a href="#">c6n1mA</a>	Alignment	not modelled	29.2	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of fumarate hydratase class ii from legionella2 pneumophila philadelphia 1
88	<a href="#">c2j3mA</a>	Alignment	not modelled	29.1	22	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> prolyl-trna synthetase; <b>PDBTitle:</b> prolyl-trna synthetase from enterococcus faecalis complexed2 with atp, manganese and prolinol
89	<a href="#">c1fyfB</a>	Alignment	not modelled	27.1	9	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> threonyl-trna synthetase; <b>PDBTitle:</b> crystal structure of a truncated form of threonyl-trna2 synthetase complexed with a seryl adenylate analog
90	<a href="#">c4kr3A</a>	Alignment	not modelled	26.9	16	<b>PDB header:</b> ligase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> glycyl-trna synthetase mutant e71g in complex with trna-gly
91	<a href="#">c3hriF</a>	Alignment	not modelled	26.4	13	<b>PDB header:</b> ligase <b>Chain:</b> F; <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> histidyl-trna synthetase (apo) from trypanosoma brucei
92	<a href="#">c5jydA</a>	Alignment	not modelled	25.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
93	<a href="#">c5z5eB</a>	Alignment	not modelled	25.9	15	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> neq417; <b>PDBTitle:</b> crystal structure of the glycyl-trna synthetase (glyrs) in2 nanoarchaeum equitans
94	<a href="#">d1jswc</a>	Alignment	not modelled	25.8	26	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
95	<a href="#">c1ggmB</a>	Alignment	not modelled	25.8	20	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> glycyl-trna synthetase from thermus thermophilus complexed with2 glycyl-adenylate
96	<a href="#">d1iy8a</a>	Alignment	not modelled	25.8	35	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
97	<a href="#">d1jswa</a>	Alignment	not modelled	25.4	26	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
98	<a href="#">c1c4gB</a>	Alignment	not modelled	24.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> protein (alpha-d-glucose 1-phosphate phosphoglucomutase); <b>PDBTitle:</b> phosphoglucomutase vanadate based transition state analog complex
99	<a href="#">c3gtdB</a>	Alignment	not modelled	24.3	22	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
100	<a href="#">c6gyzB</a>	Alignment	not modelled	24.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoglucosamine mutase; <b>PDBTitle:</b> crystal structure of glmm from staphylococcus aureus
101	<a href="#">c4hgvC</a>	Alignment	not modelled	23.8	22	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> fumarate hydratase class ii; <b>PDBTitle:</b> crystal structure of a fumarate hydratase
102	<a href="#">c5e6mA</a>	Alignment	not modelled	23.8	18	<b>PDB header:</b> ligase/rna <b>Chain:</b> A; <b>PDB Molecule:</b> glycine--trna ligase; <b>PDBTitle:</b> crystal structure of human wild type glyrs bound with trnagly
103	<a href="#">c3uw2A</a>	Alignment	not modelled	23.5	21	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoglucomutase/phosphomannomutase family protein; <b>PDBTitle:</b> x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth j1489)from burkholderia thailandensis
104	<a href="#">d1aora1</a>	Alignment	not modelled	23.3	30	<b>Fold:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Superfamily:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains <b>Family:</b> Aldehyde ferredoxin oxidoreductase, C-terminal domains



105	<a href="#">d2qwx1</a>	Alignment	not modelled	23.1	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
106	<a href="#">d1v8za1</a>	Alignment	not modelled	23.1	24	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
107	<a href="#">c1atiA</a>	Alignment	not modelled	22.9	20	<b>PDB header:</b> protein biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-trna synthetase; <b>PDBTitle:</b> crystal structure of glycyl-trna synthetase from thermus thermophilus
108	<a href="#">c3e04C</a>	Alignment	not modelled	22.5	26	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fumarate hydratase; <b>PDBTitle:</b> crystal structure of human fumarate hydratase
109	<a href="#">c1yfmA</a>	Alignment	not modelled	22.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarase; <b>PDBTitle:</b> recombinant yeast fumarase
110	<a href="#">d1yfma</a>	Alignment	not modelled	22.5	17	<b>Fold:</b> L-aspartase-like <b>Superfamily:</b> L-aspartase-like <b>Family:</b> L-aspartase/fumarase
111	<a href="#">c1wu7A</a>	Alignment	not modelled	22.3	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidyl-trna synthetase; <b>PDBTitle:</b> crystal structure of histidyl-trna synthetase from2 thermoplasma acidophilum
112	<a href="#">c5onkA</a>	Alignment	not modelled	22.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yndl; <b>PDBTitle:</b> native yndl
113	<a href="#">c4a37A</a>	Alignment	not modelled	22.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metallo-carboxypeptidase; <b>PDBTitle:</b> metallo-carboxypeptidase from pseudomonas aeruginosa
114	<a href="#">d1qf6a1</a>	Alignment	not modelled	22.1	11	<b>Fold:</b> Anticodon-binding domain-like <b>Superfamily:</b> Class II aaRS ABD-related <b>Family:</b> Anticodon-binding domain of Class II aaRS
115	<a href="#">d1gtda</a>	Alignment	not modelled	21.6	30	<b>Fold:</b> PurS-like <b>Superfamily:</b> PurS-like <b>Family:</b> PurS subunit of FGAM synthetase
116	<a href="#">c2zw2B</a>	Alignment	not modelled	21.5	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein sts178; <b>PDBTitle:</b> crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
117	<a href="#">c2yx5A</a>	Alignment	not modelled	21.4	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0062 protein mj1593; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
118	<a href="#">c4e51B</a>	Alignment	not modelled	21.1	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> histidine--trna ligase; <b>PDBTitle:</b> crystal structure of a histidyl-trna synthetase hisrs from2 burkholderia thailandensis bound to histidine
119	<a href="#">d1kfia2</a>	Alignment	not modelled	21.0	17	<b>Fold:</b> Phosphoglucomutase, first 3 domains <b>Superfamily:</b> Phosphoglucomutase, first 3 domains <b>Family:</b> Phosphoglucomutase, first 3 domains
120	<a href="#">c6nhiA</a>	Alignment	not modelled	20.9	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine--trna ligase; <b>PDBTitle:</b> crystal structure of histidine--trna ligase from elizabethkingia sp.2 ccug 26117