

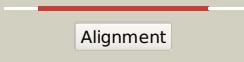

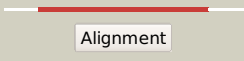

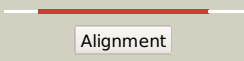
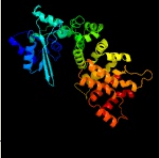
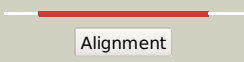

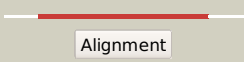

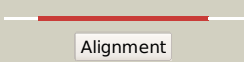

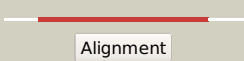

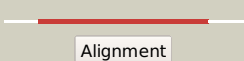

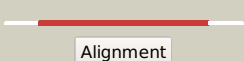

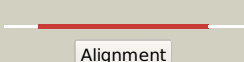

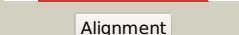







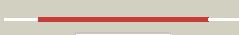









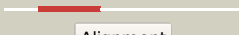



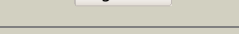
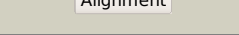
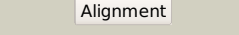
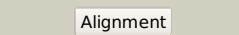
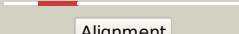


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3907c_pcnA_4391809_4393251
Date	Sat Aug 10 22:05:09 BST 2019
Unique Job ID	fbf157f3c1db7674

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3wfrH_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
2	<a href="#">c3wfpA_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme (apo form 2)
3	<a href="#">c1miyB_</a>	 Alignment		100.0	32	<b>PDB header:</b> translation, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna cca-adding enzyme; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
4	<a href="#">c3wfrG_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> G: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
5	<a href="#">c3h37B_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna nucleotidyl transferase-related protein; <b>PDBTitle:</b> the structure of cca-adding enzyme apo form i
6	<a href="#">c3wfsD_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 3
7	<a href="#">c6q52A_</a>	 Alignment		100.0	30	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cca-adding enzyme; <b>PDBTitle:</b> structure of a psychrophilic cca-adding enzyme in complex with cmpcpp2 at room temperature in chipx microfluidic device
8	<a href="#">c4x4wB_</a>	 Alignment		100.0	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cca trna nucleotidyltransferase 1, mitochondrial; <b>PDBTitle:</b> crystal structure of the full-length human mitochondrial cca-adding2 enzyme
9	<a href="#">c3wfgH_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase/rna <b>Chain:</b> H: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
10	<a href="#">c3wfpB_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme (apo form 2)
11	<a href="#">c3wfgE_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1

12	<a href="#">c3wfrF_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> F: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
13	<a href="#">c3wfgG_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> G: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 1
14	<a href="#">c3wfrE_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> E: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 2
15	<a href="#">c3wfsC_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme complex 3
16	<a href="#">c3wfoB_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> trna processing enzyme (apo form 1)
17	<a href="#">c1vfgB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> poly a polymerase; <b>PDBTitle:</b> crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
18	<a href="#">c3aqnA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) polymerase; <b>PDBTitle:</b> complex structure of bacterial protein (apo form ii)
19	<a href="#">c1ou5A_</a>	 Alignment		100.0	25	<b>PDB header:</b> translation, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna cca-adding enzyme; <b>PDBTitle:</b> crystal structure of human cca-adding enzyme
20	<a href="#">d1miwa1</a>	 Alignment		100.0	25	<b>Fold:</b> Poly A polymerase C-terminal region-like <b>Superfamily:</b> Poly A polymerase C-terminal region-like <b>Family:</b> Poly A polymerase C-terminal region-like
21	<a href="#">d1vfga2</a>	 Alignment	not modelled	100.0	34	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
22	<a href="#">d1miwa2</a>	 Alignment	not modelled	100.0	42	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
23	<a href="#">d1ou5a2</a>	 Alignment	not modelled	100.0	30	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly A polymerase head domain-like
24	<a href="#">d1vfga1</a>	 Alignment	not modelled	99.9	16	<b>Fold:</b> Poly A polymerase C-terminal region-like <b>Superfamily:</b> Poly A polymerase C-terminal region-like <b>Family:</b> Poly A polymerase C-terminal region-like
25	<a href="#">d1ou5a1</a>	 Alignment	not modelled	99.9	21	<b>Fold:</b> Poly A polymerase C-terminal region-like <b>Superfamily:</b> Poly A polymerase C-terminal region-like <b>Family:</b> Poly A polymerase C-terminal region-like
26	<a href="#">c4wqkA_</a>	 Alignment	not modelled	98.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2"-aminoglycoside nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of aminoglycoside nucleotidyltransferase ant(2")-2 ia, apo form
27	<a href="#">d2pq7a1</a>	 Alignment	not modelled	97.4	18	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
28	<a href="#">c4e8iA_</a>	 Alignment	not modelled	97.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lincosamide resistance protein; <b>PDBTitle:</b> crystal structure of lincosamide antibiotic adenyltransferase lina,2 apo
29	<a href="#">d2qgsa1</a>	 Alignment	not modelled	97.0	19	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like

					Family:HD domain
30	<a href="#">c5ihyB</a>	Alignment	not modelled	96.9	19 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of bacillus subtilis semet-yppgq
31	<a href="#">c4n71A</a>	Alignment	not modelled	96.7	25 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted hd phosphohydrolase phnz; <b>PDBTitle:</b> x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
32	<a href="#">c2la3A</a>	Alignment	not modelled	96.7	15 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
33	<a href="#">c6npaD</a>	Alignment	not modelled	96.7	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> tmpb, (r)-1-hydroxy-2-trimethylaminoethylphosphonate <b>PDBTitle:</b> x-ray crystal structure of tmpb, (r)-1-hydroxy-2-2-trimethylaminoethylphosphonate oxygenase, with (r)-1-hydroxy-2-3-trimethylaminoethylphosphonate
34	<a href="#">c3m5fA</a>	Alignment	not modelled	96.2	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal dependent phosphohydrolase; <b>PDBTitle:</b> structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
35	<a href="#">d3djbA1</a>	Alignment	not modelled	96.1	24 <b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
36	<a href="#">d1r89a2</a>	Alignment	not modelled	95.7	18 <b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Archaeal tRNA CCA-adding enzyme catalytic domain
37	<a href="#">c6dk9I</a>	Alignment	not modelled	95.1	26 <b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> dna damage-inducible protein; <b>PDBTitle:</b> yeast ddi2 cyanamide hydratase
38	<a href="#">d3b57a1</a>	Alignment	not modelled	94.9	18 <b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
39	<a href="#">d3dtoa1</a>	Alignment	not modelled	94.6	24 <b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
40	<a href="#">c2q14A</a>	Alignment	not modelled	93.9	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohydrolase; <b>PDBTitle:</b> crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
41	<a href="#">c1sz1A</a>	Alignment	not modelled	93.2	18 <b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna nucleotidyltransferase; <b>PDBTitle:</b> mechanism of cca-adding enzymes specificity revealed by crystal2 structures of ternary complexes
42	<a href="#">c5uvdA</a>	Alignment	not modelled	92.7	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidyltransferase-like protein; <b>PDBTitle:</b> crystal structure of an antigenic nucleotidyltransferase-like protein2 from paracoccidioides brasiliensis
43	<a href="#">d1u6za1</a>	Alignment	not modelled	92.6	19 <b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> Ppx associated domain
44	<a href="#">d2heka1</a>	Alignment	not modelled	92.2	23 <b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
45	<a href="#">c4bzbB</a>	Alignment	not modelled	92.0	21 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> deoxynucleoside triphosphate triphosphohydrolase samhd1; <b>PDBTitle:</b> crystal structure of the tetrameric dgtp-bound samhd12 mutant catalytic core
46	<a href="#">c2ogiA</a>	Alignment	not modelled	91.6	31 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sag1661; <b>PDBTitle:</b> crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
47	<a href="#">c4s1cA</a>	Alignment	not modelled	91.0	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo1466 protein; <b>PDBTitle:</b> crystal structure of l. monocytogenes phosphodiesterase ppph hd domain
48	<a href="#">c2floA</a>	Alignment	not modelled	90.8	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
49	<a href="#">c3skdA</a>	Alignment	not modelled	89.7	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tthb187; <b>PDBTitle:</b> crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
50	<a href="#">c3ccgA</a>	Alignment	not modelled	89.3	26 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hd superfamily hydrolase; <b>PDBTitle:</b> crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
51	<a href="#">c4r8zB</a>	Alignment	not modelled	89.0	26 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic di-gmp phosphodiesterase; <b>PDBTitle:</b> crystal structure of pa4781 hd-gyp domain from pseudomonas aeruginosa2 at 2.2a resolution showing a bi-metallic ni ion center
52	<a href="#">c2o08B</a>	Alignment	not modelled	87.3	27 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bh1327 protein; <b>PDBTitle:</b> crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
53	<a href="#">c6ifnA</a>	Alignment	not modelled	87.0	33 <b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type iii-a crispr-associated protein csm1; <b>PDBTitle:</b> crystal structure of type iii-a crispr csm complex
					<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> deoxynucleoside triphosphate

54	<a href="#">c5ao4D_</a>	Alignment	not modelled	86.9	25	triphosphohydrolase samhd1; <b>PDBTitle:</b> crystal structure of in vitro phosphorylated human samhd1 (amino acid2 residues 115-626) bound to gtp
55	<a href="#">c6brhA_</a>	Alignment	not modelled	85.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxynucleoside triphosphate triphosphohydrolase samhd1; <b>PDBTitle:</b> the sam domain of mouse samhd1 is critical for its activation and2 regulation
56	<a href="#">d2gz4a1</a>	Alignment	not modelled	85.4	12	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
57	<a href="#">d2pqja1</a>	Alignment	not modelled	84.0	21	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
58	<a href="#">c2o6iA_</a>	Alignment	not modelled	83.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hd domain protein; <b>PDBTitle:</b> structure of an enterococcus faecalis hd domain phosphohydrolase
59	<a href="#">d2o6ia1</a>	Alignment	not modelled	83.4	22	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> HD domain
60	<a href="#">c2dqB_</a>	Alignment	not modelled	83.3	15	<b>PDB header:</b> hydrolase, dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> deoxyguanosinetriphosphate triphosphohydrolase, putative; <b>PDBTitle:</b> crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
61	<a href="#">c3hc1A_</a>	Alignment	not modelled	82.2	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hdod domain protein; <b>PDBTitle:</b> crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution
62	<a href="#">c4gxtA_</a>	Alignment	not modelled	81.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> a conserved functionally unknown protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
63	<a href="#">c3u1nC_</a>	Alignment	not modelled	81.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> sam domain and hd domain-containing protein 1; <b>PDBTitle:</b> structure of the catalytic core of human samhd1
64	<a href="#">c6iqwA_</a>	Alignment	not modelled	81.3	28	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> csm1; <b>PDBTitle:</b> cryo-em structure of csm effector complex
65	<a href="#">d1wota_</a>	Alignment	not modelled	80.4	23	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
66	<a href="#">c4uw2A_</a>	Alignment	not modelled	79.8	29	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> csm1; <b>PDBTitle:</b> crystal structure of csm1 in t.onnurineus
67	<a href="#">c3gw7A_</a>	Alignment	not modelled	79.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yedj; <b>PDBTitle:</b> crystal structure of a metal-dependent phosphohydrolase with conserved2 hd domain (yedj) from escherichia coli in complex with nickel ions.3 northeast structural genomics consortium target er63
68	<a href="#">d2fcla1</a>	Alignment	not modelled	79.2	30	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> TM1012-like
69	<a href="#">c3m1tA_</a>	Alignment	not modelled	78.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphohydrolase; <b>PDBTitle:</b> crystal structure of putative phosphohydrolase (yp_929327.1) from2 shewanella amazonensis sb2b at 1.62 a resolution
70	<a href="#">c5wufA_</a>	Alignment	not modelled	70.8	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> structural basis for conductance through tric cation channels
71	<a href="#">c4qqxA_</a>	Alignment	not modelled	69.9	22	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated helicase, cas3 family; <b>PDBTitle:</b> crystal structure of t. fusca cas3-atp
72	<a href="#">d1vqra_</a>	Alignment	not modelled	69.6	10	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> modified HD domain
73	<a href="#">c4as2D_</a>	Alignment	not modelled	69.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
74	<a href="#">c4q2dA_</a>	Alignment	not modelled	68.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated helicase cas3; <b>PDBTitle:</b> crystal structure of crispr-associated protein in complex with 2'-2' deoxyadenosine 5'-triphosphate
75	<a href="#">c5h35C_</a>	Alignment	not modelled	67.6	46	<b>PDB header:</b> immune system/membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> membrane protein tric; <b>PDBTitle:</b> crystal structures of the tric trimeric intracellular cation channel2 orthologue from sulfolobus solfataricus
76	<a href="#">c5wudA_</a>	Alignment	not modelled	66.9	38	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structural basis for conductance through tric cation channels
77	<a href="#">c6e0kA_</a>	Alignment	not modelled	65.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgas/dncv-like nucleotidyltransferase in e. coli homolog; <b>PDBTitle:</b> structure of rhodothermus marinus cdne c-ump-amp synthase
78	<a href="#">c5h36E_</a>	Alignment	not modelled	63.0	54	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein tric; <b>PDBTitle:</b> crystal structures of the tric trimeric intracellular cation

						channel2 orthologue from rhodobacter sphaeroides
79	<a href="#">c2wmkB_</a>	Alignment	not modelled	62.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fucolectin-related protein; <b>PDBTitle:</b> crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae sp3-bs713 (sp3gh98) in complex with the a-lewisy pentasaccharide4 blood group antigen.
80	<a href="#">c3jivA_</a>	Alignment	not modelled	60.9	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mmoq response regulator; <b>PDBTitle:</b> crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
81	<a href="#">c4ep7A_</a>	Alignment	not modelled	60.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) rna polymerase protein cid1; <b>PDBTitle:</b> functional implications from the cid1 poly(u) polymerase crystal2 structure
82	<a href="#">c3i7aA_</a>	Alignment	not modelled	60.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphohydrolase; <b>PDBTitle:</b> crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
83	<a href="#">c2pgsA_</a>	Alignment	not modelled	58.7	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyguanosinetriphosphate triphosphohydrolase; <b>PDBTitle:</b> crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
84	<a href="#">d1jmsa4</a>	Alignment	not modelled	55.9	23	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> DNA polymerase beta-like
85	<a href="#">c2w9mB_</a>	Alignment	not modelled	53.7	19	<b>PDB header:</b> dna replication <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase x; <b>PDBTitle:</b> structure of family x dna polymerase from deinococcus2 radiodurans
86	<a href="#">c5z7cA_</a>	Alignment	not modelled	53.1	28	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 3'3'-cgamp-specific phosphodiesterase 3; <b>PDBTitle:</b> crystal structure of cyclic gmp-amp specific phosphodiesterases in2 v.cholerae (v-cgap3)
87	<a href="#">c4e80B_</a>	Alignment	not modelled	50.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(a) rna polymerase protein cid1; <b>PDBTitle:</b> structural basis for the activity of a cytoplasmic rna terminal u-2 transferase
88	<a href="#">c3auoB_</a>	Alignment	not modelled	48.6	21	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase beta family (x family); <b>PDBTitle:</b> dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
89	<a href="#">c3hi0B_</a>	Alignment	not modelled	48.2	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative exopolyphosphatase; <b>PDBTitle:</b> crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
90	<a href="#">c2rffA_</a>	Alignment	not modelled	46.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of a putative nucleotidyltransferase (np_343093.1)2 from sulfobolus solfataricus at 1.40 a resolution
91	<a href="#">c2wmhA_</a>	Alignment	not modelled	46.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fucolectin-related protein; <b>PDBTitle:</b> crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae tigr4 in3 complex with the h-disaccharide blood group antigen.
92	<a href="#">d1vlqa1</a>	Alignment	not modelled	45.7	22	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
93	<a href="#">c3jz0B_</a>	Alignment	not modelled	44.8	14	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> lincomamide nucleotidyltransferase; <b>PDBTitle:</b> linb complexed with clindamycin and ampcpp
94	<a href="#">d1knya2</a>	Alignment	not modelled	44.7	7	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
95	<a href="#">d1kewa_</a>	Alignment	not modelled	43.2	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
96	<a href="#">c3kq5A_</a>	Alignment	not modelled	40.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical cytosolic protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from coxiella burnetii
97	<a href="#">c5b7iA_</a>	Alignment	not modelled	40.1	27	<b>PDB header:</b> hydrolase/unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> crispr-associated nuclease/helicase cas3 subtype i-f/ypest; <b>PDBTitle:</b> cas3-acrf3 complex
98	<a href="#">d2q66a2</a>	Alignment	not modelled	37.8	13	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly(A) polymerase, PAP, N-terminal domain
99	<a href="#">c1q78A_</a>	Alignment	not modelled	37.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) polymerase alpha; <b>PDBTitle:</b> crystal structure of poly(a) polymerase in complex with 3'-2 datp and magnesium chloride
100	<a href="#">d1no5a_</a>	Alignment	not modelled	37.4	12	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
101	<a href="#">d1u0ma1</a>	Alignment	not modelled	35.4	22	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
102	<a href="#">c5wb4H_</a>	Alignment	not modelled	34.0	22	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> n-acetylglucosaminyldiphosphoundecaprenol n-acetyl-beta-d-

						<b>PDBTitle:</b> crystal structure of the tara wall teichoic acid glycosyltransferase
103	<a href="#">d1q79a2</a>	Alignment	not modelled	33.4	11	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Poly(A) polymerase, PAP, N-terminal domain
104	<a href="#">c2pcnA</a>	Alignment	not modelled	31.4	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine:2-demethylmenaquinone <b>PDBTitle:</b> crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
105	<a href="#">d1q5xa</a>	Alignment	not modelled	30.5	23	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
106	<a href="#">c4ok0B</a>	Alignment	not modelled	29.3	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative; <b>PDBTitle:</b> crystal structure of putative nucleotidyltransferase from h. pylori
107	<a href="#">d1vi4a</a>	Alignment	not modelled	29.1	27	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
108	<a href="#">c6e0aA</a>	Alignment	not modelled	28.3	10	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> cgas/dncv-like nucleotidyltransferase in e. coli homolog; <b>PDBTitle:</b> structure of elizabethkingia meningoseptica cdne cyclic dinucleotide2 synthase with pppa[3'-5']pa
109	<a href="#">d1j3la</a>	Alignment	not modelled	27.5	32	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> RraA-like <b>Family:</b> RraA-like
110	<a href="#">c1u0mA</a>	Alignment	not modelled	27.5	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyketide synthase; <b>PDBTitle:</b> crystal structure of 1,3,6,8-tetrahydroxynaphthalene synthase (thns)2 from streptomyces coelicolor a3(2): a bacterial type iii polyketide3 synthase (pks) provides insights into enzymatic control of reactive4 polyketide intermediates
111	<a href="#">d2b7oa1</a>	Alignment	not modelled	27.2	46	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class-II DAHP synthetase
112	<a href="#">c4xq7A</a>	Alignment	not modelled	27.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2'-5'-oligoadenylate synthase-like protein; <b>PDBTitle:</b> the crystal structure of the oas-like domain (old) of human oas1
113	<a href="#">c3c8oB</a>	Alignment	not modelled	26.8	36	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of ribonuclease activity a; <b>PDBTitle:</b> the crystal structure of rraa from pao1
114	<a href="#">c5hudA</a>	Alignment	not modelled	26.6	54	<b>PDB header:</b> transferase/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) <b>PDBTitle:</b> non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
115	<a href="#">d2ibna1</a>	Alignment	not modelled	26.4	18	<b>Fold:</b> HD-domain/PDEase-like <b>Superfamily:</b> HD-domain/PDEase-like <b>Family:</b> MioX-like
116	<a href="#">c3nybA</a>	Alignment	not modelled	26.2	10	<b>PDB header:</b> transferase/rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> poly(a) rna polymerase protein 2; <b>PDBTitle:</b> structure and function of the polymerase core of tramp, a rna2 surveillance complex
117	<a href="#">c5x15C</a>	Alignment	not modelled	25.8	36	<b>PDB header:</b> transferase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> putative transferase; <b>PDBTitle:</b> crystal structure of streptomyces coelicolor rraas2, an unusual member2 of the rnase es inhibitor rraa protein family
118	<a href="#">c3k4iC</a>	Alignment	not modelled	25.7	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
119	<a href="#">c3bg2A</a>	Alignment	not modelled	25.7	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dgtp triphosphohydrolase; <b>PDBTitle:</b> crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
120	<a href="#">c1nxjA</a>	Alignment	not modelled	25.6	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable s-adenosylmethionine:2- <b>PDBTitle:</b> structure of rv3853 from mycobacterium tuberculosis