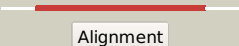



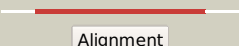





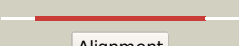














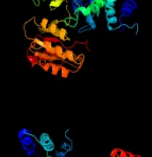
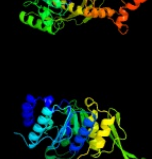
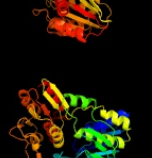


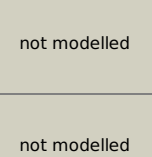


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2158c_murE_2419009_2420616
Date	Mon Aug 5 13:25:28 BST 2019
Unique Job ID	11b154967b1856b1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xjaD_</a>	 Alignment		100.0	99	<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
2	<a href="#">c4c13A_</a>	 Alignment		100.0	29	<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
3	<a href="#">c1e8cB_</a>	 Alignment		100.0	37	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-alanyl-d-glutamate--2,6-diaminopimelate <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
4	<a href="#">c2wtzC_</a>	 Alignment		100.0	98	<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
5	<a href="#">c4bubA_</a>	 Alignment		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine <b>PDBTitle:</b> crystal structure of mure ligase from thermotoga maritima2 in complex with adp
6	<a href="#">c4qdiA_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine ligase; <b>PDBTitle:</b> crystal structure ii of murf from acinetobacter baumannii
7	<a href="#">c2am1A_</a>	 Alignment		100.0	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
8	<a href="#">c3zl8A_</a>	 Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine <b>PDBTitle:</b> crystal structure of murf ligase from thermotoga maritima2 in complex with adp
9	<a href="#">c4cvkA_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine <b>PDBTitle:</b> pamurf in complex with udp-murnac-tripeptide (mdap)
10	<a href="#">c1gg4A_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanine-d-glutamyl-2,6-diaminopimelate- <b>PDBTitle:</b> crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution
11	<a href="#">c3lk7A_</a>	 Alignment		100.0	23	<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

12	<a href="#">c2vosA</a>	Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folylpolyglutamate synthase protein folc; <b>PDBTitle:</b> mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
13	<a href="#">c2f00A</a>	Alignment		100.0	18	<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
14	<a href="#">c3hn7A</a>	Alignment		100.0	21	<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
15	<a href="#">c1o5zA</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folylpolyglutamate synthase/dihydrofolate synthase; <b>PDBTitle:</b> crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
16	<a href="#">c2qc6A</a>	Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folylpolyglutamate synthase; <b>PDBTitle:</b> s73a mutant of l. casei fpgs
17	<a href="#">c1w78A</a>	Alignment		100.0	23	<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
18	<a href="#">c3uagA</a>	Alignment		100.0	25	<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
19	<a href="#">c1gqgA</a>	Alignment		100.0	17	<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
20	<a href="#">c1j6uA</a>	Alignment		100.0	21	<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
21	<a href="#">c4bucA</a>	Alignment	not modelled	100.0	19	<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
22	<a href="#">c3n2aA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional folylpolyglutamate synthase/dihydrofolate <b>PDBTitle:</b> crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
23	<a href="#">c6gs2B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> sa1708 protein; <b>PDBTitle:</b> crystal structure of the gatd/murt enzyme complex from staphylococcus2 aureus
24	<a href="#">c6fqbd</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> mur ligase family protein; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
25	<a href="#">d1e8ca3</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
26	<a href="#">c5vwwA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> structure of murc from pseudomonas aeruginosa
27	<a href="#">d2qc6a2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> Folylpolyglutamate synthetase
28	<a href="#">d1p3da3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF

29	<a href="#">c3eagA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- <b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
30	<a href="#">c6cauA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
31	<a href="#">d2jfga3</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
32	<a href="#">d1o5za2</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> Folylpolyglutamate synthetase
33	<a href="#">d1e8ca2</a>	Alignment	not modelled	100.0	45	<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
34	<a href="#">d1j6ua3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
35	<a href="#">d1gg4a4</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
36	<a href="#">d1gg4a3</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> MurE/MurF N-terminal domain <b>Family:</b> MurE/MurF N-terminal domain
37	<a href="#">d1e8ca1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> MurE/MurF N-terminal domain <b>Family:</b> MurE/MurF N-terminal domain
38	<a href="#">d1p3da2</a>	Alignment	not modelled	99.8	17	<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
39	<a href="#">c3mvnA</a>	Alignment	not modelled	99.8	27	<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
40	<a href="#">d1j6ua2</a>	Alignment	not modelled	99.8	26	<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
41	<a href="#">d2jfga2</a>	Alignment	not modelled	99.8	20	<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
42	<a href="#">d1gg4a1</a>	Alignment	not modelled	99.7	26	<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
43	<a href="#">d1o5za1</a>	Alignment	not modelled	99.7	27	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain
44	<a href="#">d2gc6a1</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> Folylpolyglutamate synthetase, C-terminal domain
45	<a href="#">c3pmoA</a>	Alignment	not modelled	98.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; <b>PDBTitle:</b> the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
46	<a href="#">c3eh0C</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine n- <b>PDBTitle:</b> crystal structure of lpxd from escherichia coli
47	<a href="#">c2iu9C</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-3-o-[3-hydroxymyristoyl] glucosamine <b>PDBTitle:</b> chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
48	<a href="#">c4e75A</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-3-o-acylglucosamine n-acyltransferase; <b>PDBTitle:</b> structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form)
49	<a href="#">d1a7ja</a>	Alignment	not modelled	96.5	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
50	<a href="#">c3fmfA</a>	Alignment	not modelled	96.3	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
51	<a href="#">c2j37W</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
52	<a href="#">c3b9qA</a>	Alignment	not modelled	96.1	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpfts5 from arabidopsis thaliana
53	<a href="#">c2og2A</a>	Alignment	not modelled	96.0	26	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2

						thaliana
54	<a href="#">c2cnwF_</a>	Alignment	not modelled	95.9	27	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases fff and ftsy
55	<a href="#">c5l3sF_</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
56	<a href="#">c6cy1B_</a>	Alignment	not modelled	95.8	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
57	<a href="#">c3tqcB_</a>	Alignment	not modelled	95.6	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii
58	<a href="#">c3dm5A_</a>	Alignment	not modelled	95.6	22	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
59	<a href="#">c3of5A_</a>	Alignment	not modelled	95.5	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
60	<a href="#">c2qy9A_</a>	Alignment	not modelled	95.5	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
61	<a href="#">c1qzwC_</a>	Alignment	not modelled	95.2	20	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
62	<a href="#">c5l3qB_</a>	Alignment	not modelled	95.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor subunit alpha; <b>PDBTitle:</b> structure of the gtpase heterodimer of human srp54 and sralpha
63	<a href="#">c2f1rA_</a>	Alignment	not modelled	95.1	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis <b>PDBTitle:</b> crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
64	<a href="#">c1vmaA_</a>	Alignment	not modelled	95.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
65	<a href="#">d1byia_</a>	Alignment	not modelled	95.0	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
66	<a href="#">d1xjca_</a>	Alignment	not modelled	94.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
67	<a href="#">c4dzzB_</a>	Alignment	not modelled	94.7	30	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partitioning protein parf; <b>PDBTitle:</b> structure of parf-adp, crystal form 1
68	<a href="#">c4nkrB_</a>	Alignment	not modelled	94.5	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis protein b; <b>PDBTitle:</b> the crystal structure of bacillus subtilis mobb
69	<a href="#">c3cioA_</a>	Alignment	not modelled	94.4	20	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase etk; <b>PDBTitle:</b> the kinase domain of escherichia coli tyrosine kinase etk
70	<a href="#">c2bekB_</a>	Alignment	not modelled	94.3	29	<b>PDB header:</b> chromosome segregation <b>Chain:</b> B: <b>PDB Molecule:</b> segregation protein; <b>PDBTitle:</b> structure of the bacterial chromosome segregation protein soj
71	<a href="#">c2yhsA_</a>	Alignment	not modelled	94.2	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
72	<a href="#">d1vmaa2</a>	Alignment	not modelled	94.2	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
73	<a href="#">c2qmoA_</a>	Alignment	not modelled	94.2	34	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
74	<a href="#">c2iy3A_</a>	Alignment	not modelled	94.1	21	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
75	<a href="#">d2qy9a2</a>	Alignment	not modelled	93.9	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
76	<a href="#">d2afhe1</a>	Alignment	not modelled	93.9	31	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
77	<a href="#">c2ozeA_</a>	Alignment	not modelled	93.9	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf delta'; <b>PDBTitle:</b> the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
78	<a href="#">c1hyqA_</a>	Alignment	not modelled	93.7	27	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division inhibitor (mind-1); <b>PDBTitle:</b> mind bacterial cell division regulator from a. fulgidus
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

79	<a href="#">d1hyqa_</a>	Alignment	not modelled	93.7	27	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
80	<a href="#">c3la6P_</a>	Alignment	not modelled	93.7	18	<b>PDB header:</b> transferase <b>Chain:</b> P: <b>PDB Molecule:</b> tyrosine-protein kinase wzc; <b>PDBTitle:</b> octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
81	<a href="#">c2vedA_</a>	Alignment	not modelled	93.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein capa1, protein tyrosine kinase; <b>PDBTitle:</b> crystal structure of the chimerical mutant capabk55m2 protein
82	<a href="#">d2g0ta1</a>	Alignment	not modelled	93.6	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
83	<a href="#">c4ru8C_</a>	Alignment	not modelled	93.6	50	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnoB8 para with amppnp
84	<a href="#">c5jljA_</a>	Alignment	not modelled	93.6	37	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> structure of flen-ampnp complex
85	<a href="#">d1sq5a_</a>	Alignment	not modelled	93.5	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
86	<a href="#">d1rz3a_</a>	Alignment	not modelled	93.4	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
87	<a href="#">c3c8uA_</a>	Alignment	not modelled	93.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
88	<a href="#">c2v3cC_</a>	Alignment	not modelled	93.1	34	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
89	<a href="#">d1iona_</a>	Alignment	not modelled	93.1	34	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
90	<a href="#">d1okkd2</a>	Alignment	not modelled	93.1	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
91	<a href="#">c2xj9B_</a>	Alignment	not modelled	93.1	26	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> mipz; <b>PDBTitle:</b> dimer structure of the bacterial cell division regulator mipz
92	<a href="#">c4pfsA_</a>	Alignment	not modelled	93.0	37	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cobyrinic acid a,c-diamide synthase; <b>PDBTitle:</b> crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
93	<a href="#">c4v02B_</a>	Alignment	not modelled	92.9	44	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> minc:mind cell division protein complex, aquifex aeolicus
94	<a href="#">c6g2gA_</a>	Alignment	not modelled	92.9	28	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic fe-s cluster assembly factor cfd1; <b>PDBTitle:</b> fe-s assembly cfd1
95	<a href="#">c2ph1A_</a>	Alignment	not modelled	92.8	28	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
96	<a href="#">d1ihua2</a>	Alignment	not modelled	92.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
97	<a href="#">c4rz3B_</a>	Alignment	not modelled	92.6	24	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> crystal structure of the mind-like atpase flhg
98	<a href="#">c3dmdA_</a>	Alignment	not modelled	92.6	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
99	<a href="#">c1zu4A_</a>	Alignment	not modelled	92.5	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyl; <b>PDBTitle:</b> crystal structure of ftsyl from mycoplasma mycoides-space2 group p21212
100	<a href="#">d1np6a_</a>	Alignment	not modelled	91.9	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
101	<a href="#">c4xc8B_</a>	Alignment	not modelled	91.9	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> isobutyryl-coa mutase fused; <b>PDBTitle:</b> isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
102	<a href="#">c2q9cA_</a>	Alignment	not modelled	91.4	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsyl; <b>PDBTitle:</b> structure of ftsyl:gmpnp with mgcl complex
103	<a href="#">c3vx3A_</a>	Alignment	not modelled	91.4	25	<b>PDB header:</b> adp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase involved in chromosome partitioning, para/mind <b>PDBTitle:</b> crystal structure of [nife] hydrogenase maturation protein hyb from2 thermococcus kodakarensis kod1
104	<a href="#">c3pndA_</a>	Alignment	not modelled	91.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase



104	<a href="#">c9enrA</a>	Alignment	not modelled	91.4	30	<b>PDBTitle:</b> crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
105	<a href="#">d1g3qa</a>	Alignment	not modelled	91.2	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
106	<a href="#">c4ak9A</a>	Alignment	not modelled	91.0	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpftsyl; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
107	<a href="#">d1qzxa3</a>	Alignment	not modelled	90.6	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
108	<a href="#">d1odfa</a>	Alignment	not modelled	90.3	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
109	<a href="#">c5zmfA</a>	Alignment	not modelled	90.2	15	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase arsa1; <b>PDBTitle:</b> amppnp complex of c. reinhardtii arsa1
110	<a href="#">c2gesA</a>	Alignment	not modelled	90.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
111	<a href="#">c3k9gA</a>	Alignment	not modelled	90.0	27	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pf-32 protein; <b>PDBTitle:</b> crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
112	<a href="#">c5l3rC</a>	Alignment	not modelled	89.9	28	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
113	<a href="#">c5gafi</a>	Alignment	not modelled	89.5	21	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l10; <b>PDBTitle:</b> rnc in complex with srp
114	<a href="#">c3q9lB</a>	Alignment	not modelled	89.4	14	<b>PDB header:</b> cell cycle, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> septum site-determining protein mind; <b>PDBTitle:</b> the structure of the dimeric e.coli mind-atp complex
115	<a href="#">c3fkqA</a>	Alignment	not modelled	88.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc-like two-domain protein; <b>PDBTitle:</b> crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
116	<a href="#">d2ioja1</a>	Alignment	not modelled	88.9	11	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> HprK N-terminal domain-like <b>Family:</b> DRTGG domain
117	<a href="#">c6iucC</a>	Alignment	not modelled	88.7	34	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> spooj regulator (soj); <b>PDBTitle:</b> structure of helicobacter pylori soj-atp complex bound to dna
118	<a href="#">c3ez6B</a>	Alignment	not modelled	88.5	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition protein a; <b>PDBTitle:</b> structure of para-adp complex:tetragonal form
119	<a href="#">d1nkSa</a>	Alignment	not modelled	88.4	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
120	<a href="#">c2obnA</a>	Alignment	not modelled	88.1	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1611 family protein (ava_3511) from anaena2 variabilis atcc 29413 at 2.30 a resolution