







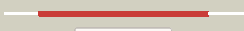















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2157c_(murF)_2417480_2419012
Date	Mon Aug 5 13:25:28 BST 2019
Unique Job ID	bc259ed1125fa8d8

Detailed template information

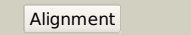
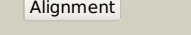
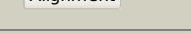
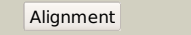
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4qdiA_</a>	Alignment 		100.0	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine ligase; <b>PDBTitle:</b> crystal structure ii of murf from acinetobacter baumannii
2	<a href="#">c2am1A_</a>	Alignment 		100.0	28	<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
3	<a href="#">c4c13A_</a>	Alignment 		100.0	20	<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
4	<a href="#">c4cvkA_</a>	Alignment 		100.0	34	<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)
5	<a href="#">c1gg4A_</a>	Alignment 		100.0	32	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoylanyl-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
6	<a href="#">c3z18A_</a>	Alignment 		100.0	30	<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
7	<a href="#">c2xjaD_</a>	Alignment 		100.0	29	<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
8	<a href="#">c2wtzC_</a>	Alignment 		100.0	28	<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
9	<a href="#">c1e8cB_</a>	Alignment 		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylanyl-d-glutamate-2,6-diaminopimelate <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
10	<a href="#">c4bubA_</a>	Alignment 		100.0	19	<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
11	<a href="#">c3lk7A_</a>	Alignment 		100.0	27	<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="#">c2f00A_</a>	Alignment		100.0	20	<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
13	<a href="#">c3uagA_</a>	Alignment		100.0	23	<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
14	<a href="#">c3hn7A_</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> crystal structure of a murein peptide ligase mpl (psyc_0032) from psychrobacter arcticus 273-4 at 1.65 a resolution
15	<a href="#">c2vosA_</a>	Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase protein folc; <b>PDBTitle:</b> mycobacterium tuberculosis folypolyglutamate synthase2 complexed with adp
16	<a href="#">c4bucA_</a>	Alignment		100.0	16	<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
17	<a href="#">c1gqqA_</a>	Alignment		100.0	19	<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
18	<a href="#">c1j6uA_</a>	Alignment		100.0	18	<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
19	<a href="#">c2gc6A_</a>	Alignment		100.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase; <b>PDBTitle:</b> s73a mutant of l. casei fpgs
20	<a href="#">c1w78A_</a>	Alignment		100.0	18	<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
21	<a href="#">c1o5zA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase/dihydrofolate synthase; <b>PDBTitle:</b> crystal structure of folypolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
22	<a href="#">c6gs2B_</a>	Alignment	not modelled	100.0	20	<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
23	<a href="#">c3n2aA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional folypolyglutamate synthase/dihydrofolate <b>PDBTitle:</b> crystal structure of bifunctional folypolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
24	<a href="#">c6fqbd_</a>	Alignment	not modelled	100.0	17	<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="#">c5vvwA_</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
26	<a href="#">d1p3da3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
27	<a href="#">d1e8ca3</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
28	<a href="#">c3eagA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso-

28	<a href="#">c3eayA</a>	Alignment	not modelled	100.0	20	<b>PDBTitle:</b> the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
29	<a href="#">d1gg4a4</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
30	<a href="#">c6cauA</a>	Alignment	not modelled	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> udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with amppnp
31	<a href="#">d2jfga3</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
32	<a href="#">d2gc6a2</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
33	<a href="#">d1j6ua3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
34	<a href="#">d1o5za2</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
35	<a href="#">d1gg4a1</a>	Alignment	not modelled	99.9	30	<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
36	<a href="#">d1gg4a3</a>	Alignment	not modelled	99.9	34	<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="#">d2jfga2</a>	Alignment	not modelled	99.9	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
38	<a href="#">d1e8ca2</a>	Alignment	not modelled	99.8	22	<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="#">d1e8ca1</a>	Alignment	not modelled	99.8	23	<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
40	<a href="#">d1p3da2</a>	Alignment	not modelled	99.8	14	<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="#">c3mvaA</a>	Alignment	not modelled	99.7	22	<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
42	<a href="#">d1j6ua2</a>	Alignment	not modelled	99.5	19	<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	99.5	16	<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	99.5	19	<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="#">c3eh0C</a>	Alignment	not modelled	97.0	16	<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
46	<a href="#">c3pmoA</a>	Alignment	not modelled	96.6	19	<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
47	<a href="#">d1a7ja</a>	Alignment	not modelled	96.5	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
48	<a href="#">c4e75A</a>	Alignment	not modelled	96.4	18	<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="#">c3fmaA</a>	Alignment	not modelled	95.9	31	<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
50	<a href="#">c2vedA</a>	Alignment	not modelled	95.8	14	<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
51	<a href="#">c3cioA</a>	Alignment	not modelled	95.7	31	<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
52	<a href="#">c3la6P</a>	Alignment	not modelled	95.5	25	<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
53	<a href="#">c3of5A</a>	Alignment	not modelled	95.4	17	<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 <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
54	<a href="#">c2j37W_</a>	Alignment	not modelled	95.1	15	<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
55	<a href="#">c5l3qB_</a>	Alignment	not modelled	95.0	17	<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
56	<a href="#">c3b9qA_</a>	Alignment	not modelled	94.9	16	<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
57	<a href="#">d1byia_</a>	Alignment	not modelled	94.8	22	<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
58	<a href="#">c4nkrB_</a>	Alignment	not modelled	94.5	11	<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
59	<a href="#">c5l3sF_</a>	Alignment	not modelled	94.4	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
60	<a href="#">d1np6a_</a>	Alignment	not modelled	94.4	17	<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
61	<a href="#">c3tqcB_</a>	Alignment	not modelled	94.3	26	<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
62	<a href="#">c4dzzB_</a>	Alignment	not modelled	94.2	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
63	<a href="#">d2qy9a2</a>	Alignment	not modelled	94.1	19	<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
64	<a href="#">c3c8uA_</a>	Alignment	not modelled	94.1	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
65	<a href="#">c2qmoA_</a>	Alignment	not modelled	94.1	22	<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
66	<a href="#">c2ph1A_</a>	Alignment	not modelled	94.1	24	<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
67	<a href="#">c2cnwF_</a>	Alignment	not modelled	94.1	16	<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
68	<a href="#">d1vmaa2</a>	Alignment	not modelled	94.0	21	<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)
69	<a href="#">c2f1rA_</a>	Alignment	not modelled	94.0	39	<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
70	<a href="#">c6cy1B_</a>	Alignment	not modelled	93.9	24	<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
71	<a href="#">d2afhe1</a>	Alignment	not modelled	93.7	31	<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
72	<a href="#">c2bekB_</a>	Alignment	not modelled	93.6	35	<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
73	<a href="#">c2og2A_</a>	Alignment	not modelled	93.6	26	<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
74	<a href="#">d2vo1a1</a>	Alignment	not modelled	93.5	23	<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
75	<a href="#">d1hyqa_</a>	Alignment	not modelled	93.5	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
76	<a href="#">c1hyqA_</a>	Alignment	not modelled	93.5	27	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsy; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
77	<a href="#">c1zu4A_</a>	Alignment	not modelled	93.4	16	<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
78	<a href="#">c2iy3A_</a>	Alignment	not modelled	93.4	15	

79	<a href="#">c2ozeA</a>	Alignment	not modelled	93.3	20	<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
80	<a href="#">c2qy9A</a>	Alignment	not modelled	93.1	14	<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
81	<a href="#">c4ru8C</a>	Alignment	not modelled	93.1	34	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnob8 para with amppnp
82	<a href="#">d1rz3a</a>	Alignment	not modelled	93.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
83	<a href="#">c3endA</a>	Alignment	not modelled	92.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase <b>PDBTitle:</b> crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
84	<a href="#">d1g3qa</a>	Alignment	not modelled	92.7	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
85	<a href="#">c2v3cC</a>	Alignment	not modelled	92.6	14	<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
86	<a href="#">c4rz3B</a>	Alignment	not modelled	92.6	26	<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
87	<a href="#">c51ljA</a>	Alignment	not modelled	92.5	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> structure of flen-amppnp complex
88	<a href="#">d1cp2a</a>	Alignment	not modelled	92.5	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
89	<a href="#">d1qzxa3</a>	Alignment	not modelled	92.4	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
90	<a href="#">c4v02B</a>	Alignment	not modelled	92.3	38	<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
91	<a href="#">d1okkd2</a>	Alignment	not modelled	92.2	24	<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
92	<a href="#">d1iona</a>	Alignment	not modelled	92.2	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
93	<a href="#">c6g2gA</a>	Alignment	not modelled	92.1	31	<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
94	<a href="#">c4pfsA</a>	Alignment	not modelled	92.0	27	<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
95	<a href="#">d1sq5a</a>	Alignment	not modelled	92.0	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
96	<a href="#">c2xj9B</a>	Alignment	not modelled	91.9	24	<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
97	<a href="#">c2yhsA</a>	Alignment	not modelled	91.9	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
98	<a href="#">c1qzwC</a>	Alignment	not modelled	91.3	16	<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
99	<a href="#">c2iu9C</a>	Alignment	not modelled	91.3	13	<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)
100	<a href="#">c5b3fB</a>	Alignment	not modelled	91.2	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribulokinase/uridine kinase; <b>PDBTitle:</b> crystal structure of phosphoribulokinase from methanospirillum2 hungatei
101	<a href="#">c2gesA</a>	Alignment	not modelled	91.1	35	<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)
102	<a href="#">c1vmaA</a>	Alignment	not modelled	91.1	18	<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
103	<a href="#">c5l3rC</a>	Alignment	not modelled	90.8	23	<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
104	<a href="#">d2g0ta1</a>	Alignment	not modelled	90.7	18	<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

105	<a href="#">c3dm5A_</a>	 Alignment	not modelled	90.6	16	<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.
106	<a href="#">c3vx3A_</a>	 Alignment	not modelled	90.6	34	<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 hypb from2 thermococcus kodakarensis kod1
107	<a href="#">c4ak9A_</a>	 Alignment	not modelled	90.5	15	<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
108	<a href="#">c3dmdA_</a>	 Alignment	not modelled	90.4	31	<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
109	<a href="#">c3q9lB_</a>	 Alignment	not modelled	90.3	34	<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
110	<a href="#">c2q9cA_</a>	 Alignment	not modelled	90.3	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmppnp with mgcl complex
111	<a href="#">c3k9gA_</a>	 Alignment	not modelled	89.7	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="#">c5he8J_</a>	 Alignment	not modelled	89.2	24	<b>PDB header:</b> protein binding <b>Chain:</b> J: <b>PDB Molecule:</b> helicase loader; <b>PDBTitle:</b> bacterial initiation protein
113	<a href="#">d1ihua2</a>	 Alignment	not modelled	89.2	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
114	<a href="#">c2j7pA_</a>	 Alignment	not modelled	89.1	14	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
115	<a href="#">c2px0D_</a>	 Alignment	not modelled	88.2	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmppnp/mg(2+)
116	<a href="#">d1nksa_</a>	 Alignment	not modelled	88.2	23	<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
117	<a href="#">d1ls1a2</a>	 Alignment	not modelled	88.2	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
118	<a href="#">c6b8vA_</a>	 Alignment	not modelled	87.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylsulfate kinase; <b>PDBTitle:</b> crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
119	<a href="#">c6iucC_</a>	 Alignment	not modelled	87.7	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
120	<a href="#">c3ibgF_</a>	 Alignment	not modelled	87.7	29	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp