



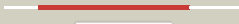




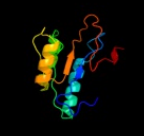

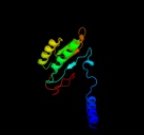











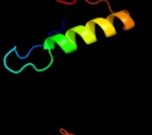


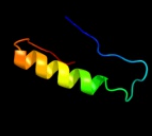
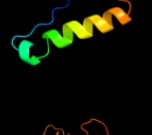

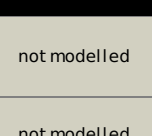
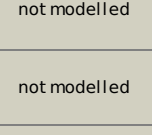


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2iy3A_</a>	 Alignment		98.0	16	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein ffh; <b>PDBTitle:</b> structure of the e. coli signal recognition particle2 bound to a translating ribosome
2	<a href="#">c2v3cC_</a>	 Alignment		97.9	20	<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
3	<a href="#">c1qzwC_</a>	 Alignment		97.9	23	<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
4	<a href="#">c2cnwF_</a>	 Alignment		97.4	26	<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 ffh and ftsy
5	<a href="#">c2yhsA_</a>	 Alignment		97.3	25	<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
6	<a href="#">c3b9qA_</a>	 Alignment		97.2	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 cpftsyt from arabidopsis thaliana
7	<a href="#">c2og2A_</a>	 Alignment		97.2	23	<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
8	<a href="#">d1nija1</a>	 Alignment		97.1	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
9	<a href="#">c3dm5A_</a>	 Alignment		97.1	28	<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 assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
10	<a href="#">c2qy9A_</a>	 Alignment		97.0	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
11	<a href="#">c2j37W_</a>	 Alignment		96.9	21	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs

12	<a href="#">c2j7pA_</a>	Alignment		96.9	16	<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
13	<a href="#">c2ozeA_</a>	Alignment		96.9	18	<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
14	<a href="#">c1vmaA_</a>	Alignment		96.9	25	<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
15	<a href="#">c3dmdA_</a>	Alignment		96.7	19	<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
16	<a href="#">c2px0D_</a>	Alignment		96.6	14	<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+)
17	<a href="#">dliona_</a>	Alignment		96.4	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
18	<a href="#">c2bekB_</a>	Alignment		96.4	36	<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 protein2 soj
19	<a href="#">c2j289_</a>	Alignment		96.3	19	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
20	<a href="#">dlg3qa_</a>	Alignment		96.3	35	<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
21	<a href="#">dlhyqa_</a>	Alignment	not modelled	96.3	35	<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
22	<a href="#">c1hyqA_</a>	Alignment	not modelled	96.3	35	<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
23	<a href="#">c2xj9B_</a>	Alignment	not modelled	96.1	47	<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
24	<a href="#">c3q9lB_</a>	Alignment	not modelled	96.1	31	<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
25	<a href="#">c3endA_</a>	Alignment	not modelled	96.0	28	<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
26	<a href="#">c3ug7D_</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of get3 from methanocaldococcus jannaschii
27	<a href="#">c3ez6B_</a>	Alignment	not modelled	96.0	24	<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
28	<a href="#">d2afhe1</a>	Alignment	not modelled	95.9	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate

28	<a href="#">c2ame1</a>	Alignment	not modelled	95.9	29	hydrolases <b>Family:</b> Nitrogenase iron protein-like
29	<a href="#">c3zq6D</a>	Alignment	not modelled	95.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative arsenical pump-driving atpase; <b>PDBTitle:</b> adp-alf4 complex of m. therm. trc40
30	<a href="#">c2eyqA</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transcription-repair coupling factor; <b>PDBTitle:</b> crystal structure of escherichia coli transcription-repair2 coupling factor
31	<a href="#">c3fkqA</a>	Alignment	not modelled	95.6	13	<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
32	<a href="#">d1xjca</a>	Alignment	not modelled	95.5	33	<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
33	<a href="#">c3nxsA</a>	Alignment	not modelled	95.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lao/ao transport system atpase; <b>PDBTitle:</b> crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
34	<a href="#">c3pg5A</a>	Alignment	not modelled	95.4	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
35	<a href="#">c3ibgF</a>	Alignment	not modelled	95.4	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
36	<a href="#">c2wwwB</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> methylmalonic aciduria type a protein, <b>PDBTitle:</b> crystal structure of methylmalonic acidemia type a protein
37	<a href="#">d1byia</a>	Alignment	not modelled	95.3	25	<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
38	<a href="#">d1ihua2</a>	Alignment	not modelled	95.2	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
39	<a href="#">c2ph1A</a>	Alignment	not modelled	95.2	35	<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
40	<a href="#">c3cwqB</a>	Alignment	not modelled	95.2	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> para family chromosome partitioning protein; <b>PDBTitle:</b> crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
41	<a href="#">c3ea0B</a>	Alignment	not modelled	95.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase, para family; <b>PDBTitle:</b> crystal structure of para family atpase from chlorobium tepidum t1s
42	<a href="#">d1ihua1</a>	Alignment	not modelled	95.1	41	<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
43	<a href="#">c2wooc</a>	Alignment	not modelled	95.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> nucleotide-free form of s. pombe get3
44	<a href="#">c1ii0A</a>	Alignment	not modelled	95.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of the escherichia coli arsenite-translocating2 atpase
45	<a href="#">c3k9gA</a>	Alignment	not modelled	95.0	21	<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
46	<a href="#">c3of5A</a>	Alignment	not modelled	94.9	25	<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
47	<a href="#">d1cp2a</a>	Alignment	not modelled	94.8	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
48	<a href="#">c3kjgB</a>	Alignment	not modelled	94.7	28	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory <b>PDBTitle:</b> adp-bound state of cooc1
49	<a href="#">c2vedA</a>	Alignment	not modelled	94.6	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
50	<a href="#">c1zu4A</a>	Alignment	not modelled	94.4	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyt; <b>PDBTitle:</b> crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
51	<a href="#">c1nijA</a>	Alignment	not modelled	94.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
52	<a href="#">c3md0A</a>	Alignment	not modelled	94.2	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine/ornithine transport system atpase; <b>PDBTitle:</b> crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like

						gtpase superfamily protein) <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="#">c3la6P_</a>	Alignment	not modelled	94.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> deha2d07832p; <b>PDBTitle:</b> get3 with adp from d. hansenii in closed form
54	<a href="#">c3io3A_</a>	Alignment	not modelled	93.9	26	<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
55	<a href="#">c3fmfA_</a>	Alignment	not modelled	93.9	36	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
56	<a href="#">c3ezfA_</a>	Alignment	not modelled	93.8	22	<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
57	<a href="#">c2qmoA_</a>	Alignment	not modelled	93.7	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
58	<a href="#">d2qm8a1</a>	Alignment	not modelled	93.5	17	<b>PDB header:</b> atp binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> all4481 protein; <b>PDBTitle:</b> crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
59	<a href="#">c3igfB_</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
60	<a href="#">d1np6a_</a>	Alignment	not modelled	92.7	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
61	<a href="#">d1qzxa3</a>	Alignment	not modelled	92.6	31	<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
62	<a href="#">c1w78A_</a>	Alignment	not modelled	92.5	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
63	<a href="#">c3cioA_</a>	Alignment	not modelled	92.5	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
64	<a href="#">d1gm5a3</a>	Alignment	not modelled	92.4	18	<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)
65	<a href="#">c2f1rA_</a>	Alignment	not modelled	92.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> adp-alf4 complex of s. cerevisiae get3
66	<a href="#">c2wojD_</a>	Alignment	not modelled	91.8	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
67	<a href="#">d1a7ja_</a>	Alignment	not modelled	91.6	15	<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="#">d1j8yf2</a>	Alignment	not modelled	91.5	28	<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
69	<a href="#">c2vosA_</a>	Alignment	not modelled	91.3	29	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> Folypolyglutamate synthetase
70	<a href="#">d1o5za2</a>	Alignment	not modelled	91.2	26	<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
71	<a href="#">c3tqcB_</a>	Alignment	not modelled	90.6	23	<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
72	<a href="#">c1o5zA_</a>	Alignment	not modelled	90.6	29	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
73	<a href="#">c1j8yF_</a>	Alignment	not modelled	90.3	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
74	<a href="#">d1sq5a_</a>	Alignment	not modelled	89.8	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> folypolyglutamate synthase; <b>PDBTitle:</b> s73a mutant of l. casei fpgs
75	<a href="#">c2gc6A_</a>	Alignment	not modelled	89.7	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> Folypolyglutamate synthetase
76	<a href="#">d2gc6a2</a>	Alignment	not modelled	89.7	26	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-P <b>PDBTitle:</b> crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
77	<a href="#">c1k6mA_</a>	Alignment	not modelled	89.5	23	<b>PDB header:</b> ligase

78	<a href="#">c3n2aA</a>	Alignment	not modelled	89.3	38	<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
79	<a href="#">d2eyqa3</a>	Alignment	not modelled	89.2	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
80	<a href="#">c2wtzC</a>	Alignment	not modelled	88.0	19	<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
81	<a href="#">c1bifA</a>	Alignment	not modelled	87.9	27	<b>PDB header:</b> bifunctional enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; <b>PDBTitle:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
82	<a href="#">c3c8uA</a>	Alignment	not modelled	87.8	23	<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
83	<a href="#">d1rz3a</a>	Alignment	not modelled	87.4	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
84	<a href="#">d2jfga3</a>	Alignment	not modelled	86.7	34	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
85	<a href="#">c3eagA</a>	Alignment	not modelled	86.4	27	<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
86	<a href="#">d1gg4a4</a>	Alignment	not modelled	86.3	34	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
87	<a href="#">d1j6ua3</a>	Alignment	not modelled	86.3	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
88	<a href="#">d1khta</a>	Alignment	not modelled	86.1	32	<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
89	<a href="#">c1j6uA</a>	Alignment	not modelled	86.1	17	<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 ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
90	<a href="#">d1ki9a</a>	Alignment	not modelled	85.9	32	<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
91	<a href="#">c1xnbB</a>	Alignment	not modelled	85.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> aps complex of human paps synthetase 1
92	<a href="#">d1e8ca3</a>	Alignment	not modelled	84.8	32	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
93	<a href="#">c1e8cB</a>	Alignment	not modelled	84.7	26	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoylalanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
94	<a href="#">c1gl9B</a>	Alignment	not modelled	84.5	18	<b>PDB header:</b> topoisomerase <b>Chain:</b> B: <b>PDB Molecule:</b> reverse gyrase; <b>PDBTitle:</b> archaeoglobus fulgidus reverse gyrase complexed with adpnp
95	<a href="#">c3e1sA</a>	Alignment	not modelled	84.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exodeoxyribonuclease v, subunit recd; <b>PDBTitle:</b> structure of an n-terminal truncation of deinococcus radiodurans recd2
96	<a href="#">c3hn7A</a>	Alignment	not modelled	84.5	32	<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
97	<a href="#">d1nksa</a>	Alignment	not modelled	83.8	27	<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
98	<a href="#">c2i1vB</a>	Alignment	not modelled	83.7	30	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6- <b>PDBTitle:</b> crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
99	<a href="#">c3b85A</a>	Alignment	not modelled	82.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate starvation-inducible protein; <b>PDBTitle:</b> crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
100	<a href="#">d1l8qa2</a>	Alignment	not modelled	82.3	35	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
101	<a href="#">c3lv8A</a>	Alignment	not modelled	82.2	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate kinase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tnk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp



102	<a href="#">c2w58B_</a>	Alignment	not modelled	82.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI
103	<a href="#">c2hcbC_</a>	Alignment	not modelled	82.0	35	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus
104	<a href="#">c3uagA_</a>	Alignment	not modelled	81.5	36	<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
105	<a href="#">c1a1vA_</a>	Alignment	not modelled	81.5	14	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (ns3 protein); <b>PDBTitle:</b> hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
106	<a href="#">c2kjqA_</a>	Alignment	not modelled	81.5	23	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnaa-related protein; <b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
107	<a href="#">c2qgzA_</a>	Alignment	not modelled	81.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative primosome component; <b>PDBTitle:</b> crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
108	<a href="#">d1k6ma1</a>	Alignment	not modelled	81.2	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
109	<a href="#">c1gqqA_</a>	Alignment	not modelled	80.9	26	<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 haemophilus2 influenzae
110	<a href="#">d1odfa_</a>	Alignment	not modelled	80.8	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
111	<a href="#">d2qy9a2</a>	Alignment	not modelled	80.3	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
112	<a href="#">c3lfuA_</a>	Alignment	not modelled	79.9	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase ii; <b>PDBTitle:</b> crystal structure of e. coli uvrd
113	<a href="#">c1gm5A_</a>	Alignment	not modelled	79.5	19	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> recg; <b>PDBTitle:</b> structure of recg bound to three-way dna junction
114	<a href="#">d1p3da3</a>	Alignment	not modelled	79.4	24	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> MurD-like peptide ligases, catalytic domain <b>Family:</b> MurCDEF
115	<a href="#">c3lk7A_</a>	Alignment	not modelled	79.2	26	<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-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
116	<a href="#">d4tmka_</a>	Alignment	not modelled	78.9	39	<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="#">c1pjrA_</a>	Alignment	not modelled	78.7	23	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> pcra; <b>PDBTitle:</b> structure of dna helicase
118	<a href="#">c2dclB_</a>	Alignment	not modelled	78.4	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical upf0166 protein ph1503; <b>PDBTitle:</b> structure of ph1503 protein from pyrococcus horikoshii ot3
119	<a href="#">c2npiB_</a>	Alignment	not modelled	78.4	25	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein clp1; <b>PDBTitle:</b> clp1-atp-pcf11 complex
120	<a href="#">d1f0ka_</a>	Alignment	not modelled	78.2	21	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG