Phyre^2

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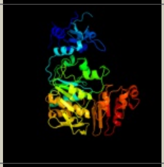
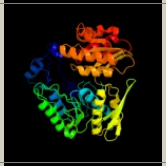
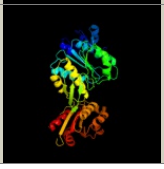
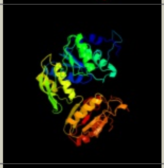
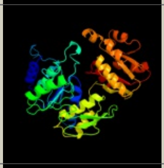
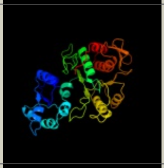
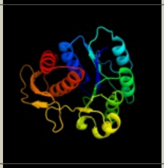
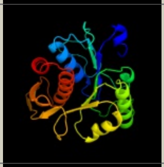
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gg4A_	Alignment		100.0	98	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamyl-2,6- **PDBTitle:** crystal structure of escherichia coli udpmurnac-tripeptide2 d-alanyl-d-alanine-adding enzyme (murf) at 2.3 angstrom3 resolution
2	c2am1A_	Alignment		100.0	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- **PDBTitle:** sp protein ligand 1
3	c2wtzC_	Alignment		100.0	26	**PDB header:**ligase **Chain:** C: **PDB Molecule:**udp-n-acetylmuramoyl-l-alanyl-d-glutamate- **PDBTitle:** mure ligase of mycobacterium tuberculosis
4	c1e8cB_	Alignment		100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamate--2,6- **PDBTitle:** structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
5	c3lk7A_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine--d-glutamate ligase; **PDBTitle:** the crystal structure of udp-n-acetylmuramoylalanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
6	c2f00A_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
7	c3hn7A_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
8	c3uagA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (udp-n-acetylmuramoyl-l-alanine:d- **PDBTitle:** udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
9	c1j6uA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
10	c2vosA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
11	c1gqqA_	Alignment		100.0	19	**PDB header:**cell wall biosynthesis **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-l-alanine ligase; **PDBTitle:** murc - crystal structure of the apo-enzyme from haemophilus2 influenzae

12	c1w78A_	Alignment		100.0	18	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
13	c2gc6A_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase; **PDBTitle:** s73a mutant of l. casei fpgs
14	c1o5zA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
15	c3n2aA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**bifunctional folylpolyglutamate synthase/dihydrofolate **PDBTitle:** crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
16	c3eagA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- **PDBTitle:** the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
17	d1gg4a4	Alignment		100.0	90	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
18	d1e8ca3	Alignment		100.0	21	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
19	d1p3da3	Alignment		100.0	23	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
20	d2jfga3	Alignment		100.0	23	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
21	d2gc6a2	Alignment	not modelled	100.0	21	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
22	d1j6ua3	Alignment	not modelled	100.0	20	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**MurCDEF
23	d1o5za2	Alignment	not modelled	100.0	22	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
24	d1gg4a1	Alignment	not modelled	100.0	97	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
25	d1gg4a3	Alignment	not modelled	99.9	99	**Fold:**MurF and HprK N-domain-like **Superfamily:**MurE/MurF N-terminal domain **Family:**MurE/MurF N-terminal domain
26	d2jfga2	Alignment	not modelled	99.9	19	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
27	d1e8ca1	Alignment	not modelled	99.8	24	**Fold:**MurF and HprK N-domain-like **Superfamily:**MurE/MurF N-terminal domain **Family:**MurE/MurF N-terminal domain
28	d1e8ca2	Alignment	not modelled	99.7	15	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
29	d1p3da2	Alignment	not modelled	99.7	15	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain

						Family: MurCDEF C-terminal domain
30	c3mvnA_	Alignment	not modelled	99.7	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
31	d1j6ua2	Alignment	not modelled	99.6	15	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
32	d1o5za1	Alignment	not modelled	99.4	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
33	d2gc6a1	Alignment	not modelled	99.3	21	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
34	c3pmoA_	Alignment	not modelled	98.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; **PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
35	c3eh0C_	Alignment	not modelled	98.3	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
36	c2iu9C_	Alignment	not modelled	96.9	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
37	d1a7ja_	Alignment	not modelled	96.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
38	c3fmfA_	Alignment	not modelled	96.1	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
39	c3tqcB_	Alignment	not modelled	95.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
40	c2og2A_	Alignment	not modelled	95.5	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
41	c3of5A_	Alignment	not modelled	95.5	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
42	c3b9qA_	Alignment	not modelled	95.2	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
43	d1sq5a_	Alignment	not modelled	95.1	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
44	c2cnwF_	Alignment	not modelled	95.1	16	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
45	c2qy9A_	Alignment	not modelled	95.0	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
46	c2yhsA_	Alignment	not modelled	95.0	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
47	d2g0ta1	Alignment	not modelled	95.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
48	c2ozeA_	Alignment	not modelled	94.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf delta'; **PDBTitle:** the crystal structure of delta protein of psm19035 from2 streptoccocus pyogenes
49	d1byia_	Alignment	not modelled	94.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
50	c3c8uA_	Alignment	not modelled	94.9	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
51	c3cioA_	Alignment	not modelled	94.8	22	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
52	d1vmaa2	Alignment	not modelled	94.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
53	c1zu4A_	Alignment	not modelled	94.7	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212

54	d2qy9a2	Alignment	not modelled	94.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
55	d1okkd2	Alignment	not modelled	94.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
56	c2bekB_	Alignment	not modelled	94.2	29	**PDB header:**chromosome segregation **Chain:** B: **PDB Molecule:**segregation protein; **PDBTitle:** structure of the bacterial chromosome segregation protein2 soj
57	c2qmoA_	Alignment	not modelled	94.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
58	c1hyqA_	Alignment	not modelled	93.8	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
59	d1hyqa_	Alignment	not modelled	93.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
60	c2f1rA_	Alignment	not modelled	93.8	27	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
61	d1rz3a_	Alignment	not modelled	93.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
62	d2afhe1	Alignment	not modelled	93.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
63	c2j37W_	Alignment	not modelled	93.4	13	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
64	c2vedA_	Alignment	not modelled	93.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
65	c2gesA_	Alignment	not modelled	93.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase; **PDBTitle:** pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
66	c2iy3A_	Alignment	not modelled	93.1	14	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
67	c3la6P_	Alignment	not modelled	92.9	26	**PDB header:**transferase **Chain:** P: **PDB Molecule:**tyrosine-protein kinase wzc; **PDBTitle:** octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
68	c1qzwC_	Alignment	not modelled	92.8	13	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
69	c2ph1A_	Alignment	not modelled	92.8	19	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**nucleotide-binding protein; **PDBTitle:** crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
70	d1nksa_	Alignment	not modelled	92.8	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
71	c3endA_	Alignment	not modelled	92.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
72	c2xj9B_	Alignment	not modelled	92.7	21	**PDB header:**replication **Chain:** B: **PDB Molecule:**mipz; **PDBTitle:** dimer structure of the bacterial cell division regulator mipz
73	c1vmaA_	Alignment	not modelled	92.6	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
74	c3dmdA_	Alignment	not modelled	92.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
75	d1cp2a_	Alignment	not modelled	92.4	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
76	d1iona_	Alignment	not modelled	92.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
77	c2j7pA_	Alignment	not modelled	92.2	14	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy

78	c2v3cC_	Alignment	not modelled	91.9	14	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
79	d1np6a_	Alignment	not modelled	91.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
80	d1deka_	Alignment	not modelled	91.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
81	d2ioja1	Alignment	not modelled	91.7	18	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
82	d1g3qa_	Alignment	not modelled	91.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
83	c2wwiC_	Alignment	not modelled	91.5	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidilate kinase, putative; **PDBTitle:** plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
84	c3k9gA_	Alignment	not modelled	91.3	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**pf-32 protein; **PDBTitle:** crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
85	c3lv8A_	Alignment	not modelled	91.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp
86	c3dm5A_	Alignment	not modelled	91.3	13	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
87	c3zq6D_	Alignment	not modelled	91.1	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative arsenical pump-driving atpase; **PDBTitle:** adp-alf4 complex of m. therm. trc40
88	d1uj2a_	Alignment	not modelled	91.1	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
89	d1qzxa3	Alignment	not modelled	90.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
90	c3ibgF_	Alignment	not modelled	90.5	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
91	c2w0sB_	Alignment	not modelled	90.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
92	c3q9lB_	Alignment	not modelled	90.3	33	**PDB header:**cell cycle, hydrolase **Chain:** B: **PDB Molecule:**septum site-determining protein mind; **PDBTitle:** the structure of the dimeric e.coli mind-atp complex
93	c2plrB_	Alignment	not modelled	90.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thymidylate kinase; **PDBTitle:** crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7
94	c2z0hA_	Alignment	not modelled	90.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
95	c2gksB_	Alignment	not modelled	89.7	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
96	c3asyB_	Alignment	not modelled	89.7	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine kinase; **PDBTitle:** ligand-free structure of uridine kinase from thermus thermophilus hb8
97	d1khta_	Alignment	not modelled	89.4	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
98	c3fkqA_	Alignment	not modelled	89.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntrc-like two-domain protein; **PDBTitle:** crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
99	c2grjH_	Alignment	not modelled	89.1	28	**PDB header:**transferase **Chain:** H: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
100	d1nn5a_	Alignment	not modelled	89.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
101	d1odfa_	Alignment	not modelled	89.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
102	d1ckea_	Alignment	not modelled	88.9	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
						Fold:P-loop containing nucleoside triphosphate hydrolases

103	d1ki9a_	Alignment	not modelled	88.5	26	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
104	c1ueiB_	Alignment	not modelled	88.5	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine-cytidine kinase 2; **PDBTitle:** crystal structure of human uridine-cytidine kinase 22 complexed with a feedback-inhibitor, utp
105	c3ch4B_	Alignment	not modelled	88.5	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution
106	c2wooC_	Alignment	not modelled	88.5	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atpase get3; **PDBTitle:** nucleotide-free form of s. pombe get3
107	d1ls1a2	Alignment	not modelled	88.4	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
108	c1m8pB_	Alignment	not modelled	88.2	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of p. chrysogenum atp sulfurylase in the t-state
109	c3akcA_	Alignment	not modelled	88.2	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
110	c2f6rA_	Alignment	not modelled	87.9	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional coenzyme a synthase; **PDBTitle:** crystal structure of bifunctional coenzyme a synthase (coa synthase):2 (18044849) from mus musculus at 1.70 a resolution
111	c3ug7D_	Alignment	not modelled	87.7	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of get3 from methanocaldococcus jannaschii
112	d1tmka_	Alignment	not modelled	87.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
113	d1m8pa3	Alignment	not modelled	87.4	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
114	d4tmka_	Alignment	not modelled	87.3	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
115	d1xjca_	Alignment	not modelled	87.1	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
116	c3ea0B_	Alignment	not modelled	86.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase, para family; **PDBTitle:** crystal structure of para family atpase from chlorobium tepidum tls
117	d1x6va3	Alignment	not modelled	86.8	34	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
118	c3hdtB_	Alignment	not modelled	86.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
119	d1qf9a_	Alignment	not modelled	86.4	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
120	c3io3A_	Alignment	not modelled	86.1	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**deha2d07832p; **PDBTitle:** get3 with adp from d. hansenii in closed form