

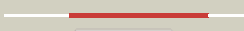





























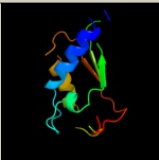




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2afhe1</a>	 Alignment		100.0	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
2	<a href="#">c2ph1A</a>	 Alignment		100.0	41	<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
3	<a href="#">c3endA</a>	 Alignment		100.0	21	<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
4	<a href="#">d1cp2a</a>	 Alignment		100.0	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
5	<a href="#">d1iona</a>	 Alignment		100.0	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
6	<a href="#">d1g3qa</a>	 Alignment		100.0	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
7	<a href="#">c3q9lB</a>	 Alignment		100.0	19	<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
8	<a href="#">c1hyqA</a>	 Alignment		100.0	24	<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
9	<a href="#">d1hyqa</a>	 Alignment		100.0	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
10	<a href="#">c3ea0B</a>	 Alignment		100.0	17	<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
11	<a href="#">c3kigB</a>	 Alignment		100.0	17	<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

12	<a href="#">c2bekB_</a>	Alignment		100.0	24	<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
13	<a href="#">c2ozeA_</a>	Alignment		100.0	12	<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="#">c3ez6B_</a>	Alignment		100.0	17	<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
15	<a href="#">c2xj9B_</a>	Alignment		100.0	18	<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
16	<a href="#">c3fkqA_</a>	Alignment		100.0	17	<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
17	<a href="#">c3zq6D_</a>	Alignment		100.0	21	<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
18	<a href="#">c3cwqB_</a>	Alignment		100.0	22	<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
19	<a href="#">c2wooc_</a>	Alignment		100.0	21	<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
20	<a href="#">c3ug7D_</a>	Alignment		100.0	22	<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
21	<a href="#">c3k9gA_</a>	Alignment	not modelled	100.0	17	<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
22	<a href="#">c1ii0A_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">c3ezfA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
24	<a href="#">c3pg5A_</a>	Alignment	not modelled	100.0	18	<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
25	<a href="#">c2wojD_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c3ibgF_</a>	Alignment	not modelled	100.0	24	<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
27	<a href="#">c3cioA_</a>	Alignment	not modelled	100.0	16	<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
28	<a href="#">d1byia_</a>	Alignment	not modelled	100.0	13	<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

29	<a href="#">c3la6P_</a>	Alignment		100.0	15	<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
30	<a href="#">c3of5A_</a>	Alignment	not modelled	100.0	12	<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
31	<a href="#">dlihua2</a>	Alignment	not modelled	100.0	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
32	<a href="#">c2vedA_</a>	Alignment	not modelled	100.0	19	<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
33	<a href="#">c3io3A_</a>	Alignment	not modelled	100.0	18	<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
34	<a href="#">dlihua1</a>	Alignment	not modelled	100.0	17	<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
35	<a href="#">c3igfB_</a>	Alignment	not modelled	100.0	18	<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
36	<a href="#">c2qmoA_</a>	Alignment	not modelled	99.9	9	<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
37	<a href="#">c3fmfA_</a>	Alignment	not modelled	99.9	15	<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
38	<a href="#">c3lnoA_</a>	Alignment		99.7	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of domain of unknown function duf59 from2 bacillus anthracis
39	<a href="#">d2cu6a1</a>	Alignment		99.6	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
40	<a href="#">d1uwda_</a>	Alignment		99.6	13	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
41	<a href="#">c1zu4A_</a>	Alignment	not modelled	99.6	15	<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
42	<a href="#">c2qy9A_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsyt; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsyt
43	<a href="#">c1vmaA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsyt; <b>PDBTitle:</b> crystal structure of cell division protein ftsyt (tm0570) from2 thermotoga maritima at 1.60 a resolution
44	<a href="#">c3dm5A_</a>	Alignment	not modelled	99.5	15	<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.
45	<a href="#">c2iy3A_</a>	Alignment	not modelled	99.4	18	<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
46	<a href="#">c2cnwF_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsyt; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsyt
47	<a href="#">c2og2A_</a>	Alignment	not modelled	99.4	16	<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 ftsyt from arabidopsis2 thaliana
48	<a href="#">c2j37W_</a>	Alignment	not modelled	99.4	17	<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
49	<a href="#">c2j7pA_</a>	Alignment	not modelled	99.4	17	<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 ftsyt

50	<a href="#">c3b9qA</a>	Alignment	not modelled	99.4	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 cpftsyt from arabidopsis thaliana
51	<a href="#">c2v3cC</a>	Alignment	not modelled	99.3	21	<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
52	<a href="#">c2yhsA</a>	Alignment	not modelled	99.3	18	<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
53	<a href="#">c1qzwC</a>	Alignment	not modelled	99.3	17	<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
54	<a href="#">c2j289</a>	Alignment	not modelled	99.1	18	<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
55	<a href="#">c3dmdA</a>	Alignment	not modelled	99.1	17	<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
56	<a href="#">d1vmaa2</a>	Alignment	not modelled	98.7	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
57	<a href="#">d1qzxa3</a>	Alignment	not modelled	98.7	19	<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="#">d1j8yf2</a>	Alignment	not modelled	98.4	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
59	<a href="#">c1j8yF</a>	Alignment	not modelled	98.3	17	<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
60	<a href="#">c2px0D</a>	Alignment	not modelled	98.3	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+)
61	<a href="#">d1okkd2</a>	Alignment	not modelled	98.2	19	<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
62	<a href="#">d1ls1a2</a>	Alignment	not modelled	98.0	19	<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	98.0	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
64	<a href="#">c2npiB</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein clp1; <b>PDBTitle:</b> clp1-atp-pcf11 complex
65	<a href="#">c2h5eB</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor rf-3; <b>PDBTitle:</b> crystal structure of e.coli polypeptide release factor rf3
66	<a href="#">d2qm8a1</a>	Alignment	not modelled	97.8	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
67	<a href="#">c2recB</a>	Alignment	not modelled	97.6	24	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
68	<a href="#">d1x6va3</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Adenosine-5'phosphosulfate kinase (APS kinase)
69	<a href="#">c1xp8A</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> "deinococcus radiodurans reca in complex with atp-gamma-s"
70	<a href="#">c2ywfA</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> crystal structure of gmppnp-bound lepa from aquifex aeolicus
71	<a href="#">d1mo6a1</a>	Alignment	not modelled	97.3	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
72	<a href="#">c2zroA</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
73	<a href="#">c1xnjB</a>	Alignment	not modelled	97.2	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
74	<a href="#">c2f1rA</a>	Alignment	not modelled	97.2	19	<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)
75	<a href="#">c3hr8A</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca

76	<a href="#">c1zunB_</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylate transferase, subunit <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
77	<a href="#">d1n0ua2</a>	Alignment	not modelled	97.1	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
78	<a href="#">c3b8hA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> biosynthetic protein/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> structure of the eef2-exoa(e546a)-nad+ complex
79	<a href="#">d1nija1</a>	Alignment	not modelled	97.1	11	<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
80	<a href="#">d1xjca_</a>	Alignment	not modelled	97.1	29	<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
81	<a href="#">c3bgwD_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> the structure of a dnab-like replicative helicase and its interactions2 with primase
82	<a href="#">d1u94a1</a>	Alignment	not modelled	96.9	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
83	<a href="#">c2q6tB_</a>	Alignment	not modelled	96.8	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dnab replication fork helicase; <b>PDBTitle:</b> crystal structure of the thermus aquaticus dnab monomer
84	<a href="#">c3tr5C_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
85	<a href="#">d1np6a_</a>	Alignment	not modelled	96.8	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
86	<a href="#">d1nlfa_</a>	Alignment	not modelled	96.8	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
87	<a href="#">c2gksB_</a>	Alignment	not modelled	96.8	34	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional sat/aps kinase; <b>PDBTitle:</b> crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
88	<a href="#">d1ubea1</a>	Alignment	not modelled	96.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
89	<a href="#">c1d2eA_</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu (ef-tu); <b>PDBTitle:</b> crystal structure of mitochondrial ef-tu in complex with gdp
90	<a href="#">c2vyeA_</a>	Alignment	not modelled	96.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnac-ssdna complex
91	<a href="#">c3cr8C_</a>	Alignment	not modelled	96.7	33	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenyltranferase, adenylsulfate <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
92	<a href="#">c3bh0A_</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
93	<a href="#">d1xp8a1</a>	Alignment	not modelled	96.6	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
94	<a href="#">d1rz3a_</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
95	<a href="#">c2dy1A_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> signaling protein, translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of ef-g-2 from thermus thermophilus
96	<a href="#">c2ztsB_</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ph0186; <b>PDBTitle:</b> crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
97	<a href="#">c2w0mA_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus2 p2
98	<a href="#">c1zn0B_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> translation/biosynthetic protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf
99	<a href="#">c2xexA_</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of staphylococcus aureus elongation factor2 g
100	<a href="#">c2dr3A_</a>	Alignment	not modelled	96.4	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0273 protein ph0284; <b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
101	<a href="#">c3do6B_</a>	Alignment	not modelled	96.4	29	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> formate--tetrahydrofolate ligase; <b>PDBTitle:</b> crystal structure of putative formyltetrahydrofolate2 synthetase (tm1766) from thermotoga maritima at 1.85 a3 resolution



102	<a href="#">d1tf7a2</a>	Alignment	not modelled	96.4	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
103	<a href="#">c3c8uA</a>	Alignment	not modelled	96.3	30	<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
104	<a href="#">d2p67a1</a>	Alignment	not modelled	96.3	19	<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="#">d1eg7a</a>	Alignment	not modelled	96.3	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
106	<a href="#">d1knqa</a>	Alignment	not modelled	96.3	34	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Gluconate kinase
107	<a href="#">c2i1vB</a>	Alignment	not modelled	96.3	17	<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
108	<a href="#">d1g64b</a>	Alignment	not modelled	96.2	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
109	<a href="#">c3tqcB</a>	Alignment	not modelled	96.2	30	<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
110	<a href="#">d1yrba1</a>	Alignment	not modelled	96.2	14	<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
111	<a href="#">c2bm0A</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> elongation factor <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
112	<a href="#">d1sq5a</a>	Alignment	not modelled	96.1	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
113	<a href="#">d1ki9a</a>	Alignment	not modelled	96.0	22	<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
114	<a href="#">c2gesA</a>	Alignment	not modelled	95.9	39	<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)
115	<a href="#">c3cb4D</a>	Alignment	not modelled	95.9	11	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> the crystal structure of lepa
116	<a href="#">c2wwwB</a>	Alignment	not modelled	95.9	22	<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
117	<a href="#">c3cmvG</a>	Alignment	not modelled	95.9	25	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
118	<a href="#">d1odfa</a>	Alignment	not modelled	95.9	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
119	<a href="#">c1fnnB</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum
120	<a href="#">d1k6ma1</a>	Alignment	not modelled	95.9	16	<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