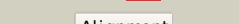
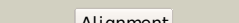
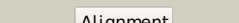
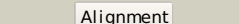
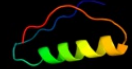


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iutA_	 Alignment		100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
2	c2iuuE_	 Alignment		100.0	21	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
3	d1e9ra_	 Alignment		100.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
4	c2iusB_	 Alignment		100.0	20	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
5	d2ve8a1	 Alignment		99.4	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
6	d2j5pa1	 Alignment		99.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
7	c2r2aB_	 Alignment		98.4	16	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
8	c3b9pA_	 Alignment		97.9	24	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
9	c3l9oA_	 Alignment		97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: crystal structure of ntr4, a co-factor of the nuclear exosome
10	c2w0mA_	 Alignment		97.5	24	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
11	d1byia_	 Alignment		97.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

12	d2i3ba1	Alignment		97.4	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
13	c3hu2C_	Alignment		97.3	28	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
14	c1xwiA_	Alignment		97.3	22	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
15	d1vmaa2	Alignment		97.3	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
16	d1cr2a_	Alignment		97.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
17	c2d3wB_	Alignment		97.1	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcd; PDBTitle: crystal structure of escherichia coli sufcd, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
18	d2qy9a2	Alignment		97.1	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
19	c3of5A_	Alignment		97.1	25	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
20	d1g6oa_	Alignment		97.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
21	d1okkd2	Alignment	not modelled	97.0	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
22	c1zu4A_	Alignment	not modelled	97.0	39	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
23	c2cnwF_	Alignment	not modelled	97.0	33	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsyt; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsyt
24	c3jvvA_	Alignment	not modelled	97.0	26	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-pcp
25	c2j7pA_	Alignment	not modelled	97.0	30	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsyt
26	d1p9ra_	Alignment	not modelled	97.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
27	c2ja1A_	Alignment	not modelled	97.0	16	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
28	c3d8bB_	Alignment	not modelled	97.0	24	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
						PDB header: protein transport

29	c1vmaA	Alignment	not modelled	97.0	36	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
30	d1qzxa3	Alignment	not modelled	96.9	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
31	d1np6a	Alignment	not modelled	96.9	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
32	c3u5zM	Alignment	not modelled	96.9	20	PDB header: dna binding protein/dna Chain: M: PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
33	c3b9qA	Alignment	not modelled	96.9	45	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
34	c1s3sA	Alignment	not modelled	96.9	28	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
35	c3bh0A	Alignment	not modelled	96.9	18	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
36	c2qy9A	Alignment	not modelled	96.9	39	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
37	c2yhsA	Alignment	not modelled	96.9	39	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
38	c2qmoA	Alignment	not modelled	96.8	25	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
39	c2og2A	Alignment	not modelled	96.8	42	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
40	c2gzaB	Alignment	not modelled	96.8	23	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein virb11; PDBTitle: crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
41	d1ls1a2	Alignment	not modelled	96.8	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
42	c3dmdA	Alignment	not modelled	96.8	41	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
43	c3bgwD	Alignment	not modelled	96.8	19	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
44	c2f1rA	Alignment	not modelled	96.7	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
45	d1l7vc	Alignment	not modelled	96.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
46	c2oaq1	Alignment	not modelled	96.7	20	PDB header: hydrolase Chain: 1: PDB Molecule: type ii secretion system protein; PDBTitle: crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
47	c2gszE	Alignment	not modelled	96.7	24	PDB header: protein transport Chain: E: PDB Molecule: twitching motility protein pilt; PDBTitle: structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
48	c2iy3A	Alignment	not modelled	96.7	30	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
49	c3a4mB	Alignment	not modelled	96.6	29	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
50	c3dm5A	Alignment	not modelled	96.6	36	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.
51	c2eyuA	Alignment	not modelled	96.6	21	PDB header: protein transport Chain: A: PDB Molecule: twitching motility protein pilt; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
52	d1cp2a	Alignment	not modelled	96.6	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
53	c2j37W	Alignment	not modelled	96.6	31	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein

					PDBTitle: model of mammalian srp bound to 80s rncs PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
54	c1xx6B_	Alignment	not modelled	96.6	14
55	c2hydB_	Alignment	not modelled	96.6	18
56	c2vyeA_	Alignment	not modelled	96.6	21
57	c2b92A_	Alignment	not modelled	96.5	27
58	c3c8uA_	Alignment	not modelled	96.4	33
59	d1rz3a_	Alignment	not modelled	96.3	26
60	c3fmfA_	Alignment	not modelled	96.3	35
61	d1pjra1	Alignment	not modelled	96.3	26
62	c1zuiA_	Alignment	not modelled	96.3	31
63	c3oiyB_	Alignment	not modelled	96.3	21
64	d1l8qa2	Alignment	not modelled	96.3	31
65	d2qm8a1	Alignment	not modelled	96.3	33
66	c2q6tB_	Alignment	not modelled	96.3	18
67	d1u94a1	Alignment	not modelled	96.2	19
68	c3bosA_	Alignment	not modelled	96.2	14
69	c2xgjA_	Alignment	not modelled	96.2	19
70	c2px0D_	Alignment	not modelled	96.2	34
71	c1ii0A_	Alignment	not modelled	96.2	30
72	d1uaaa1	Alignment	not modelled	96.2	20
73	c3lfuA_	Alignment	not modelled	96.2	20
74	c1xp8A_	Alignment	not modelled	96.2	19
75	d1xjca_	Alignment	not modelled	96.2	22
76	c3h1tA_	Alignment	not modelled	96.2	32
77	c3tqcB_	Alignment	not modelled	96.1	28
					Fold: P-loop containing nucleoside triphosphate hydrolases PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the pantothenate kinase (coaA) from coxiella burnetii

78	d2afhe1	Alignment	not modelled	96.1	37	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
79	c3hr8A	Alignment	not modelled	96.1	19	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
80	dlg41a	Alignment	not modelled	96.1	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
81	d1khta	Alignment	not modelled	96.1	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
82	c2qq0B	Alignment	not modelled	96.1	26	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + apnhp
83	dlgkub1	Alignment	not modelled	96.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
84	dlgl9b1	Alignment	not modelled	96.1	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
85	c3nxsA	Alignment	not modelled	96.1	39	PDB header: transport protein Chain: A: PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
86	c1pjrA	Alignment	not modelled	96.0	26	PDB header: helicase Chain: A: PDB Molecule: pcra; PDBTitle: structure of dna helicase
87	c2v3cC	Alignment	not modelled	96.0	34	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
88	dlubea1	Alignment	not modelled	96.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
89	c2ce7B	Alignment	not modelled	96.0	32	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
90	dlmo6a1	Alignment	not modelled	96.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
91	dlxp8a1	Alignment	not modelled	96.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
92	dlyrba1	Alignment	not modelled	96.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
93	c2kjqA	Alignment	not modelled	96.0	25	PDB header: replication Chain: A: PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
94	dlodfa	Alignment	not modelled	96.0	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
95	c2recB	Alignment	not modelled	96.0	19	PDB header: helicase PDB COMPND:
96	c2gesA	Alignment	not modelled	95.9	22	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)
97	c3endA	Alignment	not modelled	95.9	27	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
98	c3b85A	Alignment	not modelled	95.9	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
99	d2p67a1	Alignment	not modelled	95.9	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	d1viaa	Alignment	not modelled	95.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
101	d1sq5a	Alignment	not modelled	95.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
102	d1f5na2	Alignment	not modelled	95.9	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins PDB header: protein binding

103	c3pxiB_	Alignment	not modelled	95.9	28	Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mecc; PDBTitle: structure of meca108:clpc
104	d1c4oa1	Alignment	not modelled	95.9	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
105	d2bmfa2	Alignment	not modelled	95.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
106	c4a4zA_	Alignment	not modelled	95.8	14	PDB header: hydrolase Chain: A: PDB Molecule: antiviral helicase ski2; PDBTitle: crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
107	c3asyB_	Alignment	not modelled	95.8	40	PDB header: transferase Chain: B: PDB Molecule: uridine kinase; PDBTitle: ligand-free structure of uridine kinase from thermophilus hb8
108	d1fnna2	Alignment	not modelled	95.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
109	d1in4a2	Alignment	not modelled	95.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
110	c1ojlf_	Alignment	not modelled	95.8	24	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
111	c2w58B_	Alignment	not modelled	95.8	26	PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dnaI
112	c2c99A_	Alignment	not modelled	95.7	28	PDB header: transcription regulation Chain: A: PDB Molecule: psp operon transcriptional activator; PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
113	c2is6B_	Alignment	not modelled	95.7	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrd-dna-adpmgf3 ternary complex
114	c2hbcC_	Alignment	not modelled	95.7	33	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
115	c1gl9B_	Alignment	not modelled	95.7	20	PDB header: topoisomerase Chain: B: PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp
116	c2zroA_	Alignment	not modelled	95.7	19	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
117	d1ny5a2	Alignment	not modelled	95.7	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
118	c3tbkA_	Alignment	not modelled	95.7	22	PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
119	c1wp9D_	Alignment	not modelled	95.7	28	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent rna helicase, putative; PDBTitle: crystal structure of pyrococcus furiosus hef helicase domain
120	c2qgzA_	Alignment	not modelled	95.7	31	PDB header: hydrolase Chain: A: PDB Molecule: putative primosome component; PDBTitle: crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58