Phyre2

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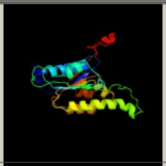
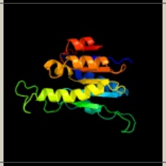
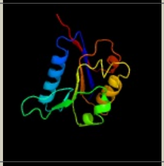
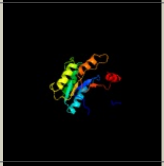
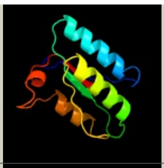
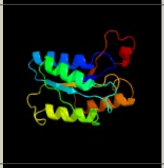
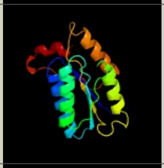
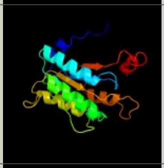
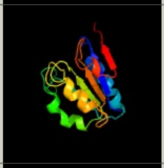
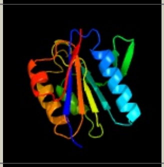
Description	RVBD2849c_(cobO)_3157531_3158154
Date	Wed Aug 7 12:50:51 BST 2019
Unique Job ID	e8a2e17883b627de

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g64b_	Alignment		100.0	42	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
2	d1g5ta_	Alignment		100.0	42	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
3	c2b8tA_	Alignment		97.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
4	c4uxjB_	Alignment		97.2	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** leishmania major thymidine kinase in complex with dttp
5	c2cnwF_	Alignment		97.2	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
6	c1xx6B_	Alignment		97.2	24	**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.
7	c5l3qB_	Alignment		97.1	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**signal recognition particle receptor subunit alpha; **PDBTitle:** structure of the gtpase heterodimer of human srp54 and sralpha
8	c6bs5B_	Alignment		97.0	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**anion transporter; **PDBTitle:** crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
9	d2b8ta1	Alignment		97.0	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
10	c2ja1A_	Alignment		96.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
11	c5bq5A_	Alignment		96.8	18	**PDB header:**atp-binding protein **Chain:** A: **PDB Molecule:**insertion sequence is5376 putative atp-binding protein; **PDBTitle:** crystal structure of the istb aaa+ domain bound to adp-bef3

12	c2qy9A_	Alignment		96.8	21	**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
13	c2j37W_	Alignment		96.8	20	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein (srp54); **PDBTitle:** model of mammalian srp bound to 80s rncs
14	c5l3rC_	Alignment		96.7	22	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**signal recognition particle 54 kda protein, chloroplastic; **PDBTitle:** structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
15	c2orvB_	Alignment		96.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** human thymidine kinase 1 in complex with tp4a
16	c3b9qA_	Alignment		96.6	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
17	c3dmdA_	Alignment		96.6	19	**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
18	c1w4rC_	Alignment		96.5	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine kinase; **PDBTitle:** structure of a type ii thymidine kinase with bound dttp
19	d1xx6a1	Alignment		96.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
20	c4ydsA_	Alignment		96.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagella-related protein h; **PDBTitle:** flah from sulfolobus acidocaldarius with atp and mg-ion
21	c3ibgF_	Alignment	not modelled	96.2	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
22	c3igfB_	Alignment	not modelled	96.2	23	**PDB header:**atp binding protein **Chain:** B: **PDB Molecule:**all4481 protein; **PDBTitle:** crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
23	c3dm5A_	Alignment	not modelled	96.1	24	**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 assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
24	c1vmaA_	Alignment	not modelled	96.1	23	**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
25	c3gp8A_	Alignment	not modelled	96.1	28	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd, putative; **PDBTitle:** crystal structure of the binary complex of recd2 with dna
26	c1xp8A_	Alignment	not modelled	96.1	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** deinococcus radiodurans reca in complex with atp-gamma-s
27	c2recB_	Alignment	not modelled	96.1	13	**PDB header:**helicase **PDB COMPND:**
28	c2j7pA_	Alignment	not modelled	96.0	16	**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

29	c2vbcA_	Alignment	not modelled	96.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
30	c2qq0B_	Alignment	not modelled	96.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
31	c2og2A_	Alignment	not modelled	95.8	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
32	c2w0mA_	Alignment	not modelled	95.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus p2
33	c1zu4A_	Alignment	not modelled	95.8	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
34	d1mo6a1	Alignment	not modelled	95.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
35	c2q9cA_	Alignment	not modelled	95.7	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of ftsy:gmppnp with mgcl complex
36	c2ph1A_	Alignment	not modelled	95.7	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
37	c2j87D_	Alignment	not modelled	95.6	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thymidine kinase; **PDBTitle:** structure of vaccinia virus thymidine kinase in complex2 with dttp: insights for drug design
38	c2iy3A_	Alignment	not modelled	95.6	18	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein,signal recognition **PDBTitle:** structure of the e. coli signal regognition particle
39	c3b85A_	Alignment	not modelled	95.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
40	d1xp8a1	Alignment	not modelled	95.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
41	d1ubea1	Alignment	not modelled	95.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
42	c5fuvB_	Alignment	not modelled	95.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymdine kinase; **PDBTitle:** catalytic domain of thymidine kinase from trypanosoma2 brucei with dthd
43	c3e2iA_	Alignment	not modelled	95.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** crystal structure of thymidine kinase from s. aureus
44	d1xbta1	Alignment	not modelled	95.4	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
45	c2ozeA_	Alignment	not modelled	95.3	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf delta'; **PDBTitle:** the crystal structure of delta protein of psm19035 from2 streptoccocus pyogenes
46	c3e1sA_	Alignment	not modelled	95.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
47	c5he8J_	Alignment	not modelled	95.0	16	**PDB header:**protein binding **Chain:** J: **PDB Molecule:**helicase loader; **PDBTitle:** bacterial initiation protein
48	c5l3sF_	Alignment	not modelled	95.0	19	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**signal recognition particle receptor ftsy; **PDBTitle:** structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
49	c3fkqA_	Alignment	not modelled	94.8	15	**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
50	c6cy1B_	Alignment	not modelled	94.7	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor ftsy; **PDBTitle:** crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
51	c2zroA_	Alignment	not modelled	94.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
52	c5gafi_	Alignment	not modelled	94.6	15	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l10; **PDBTitle:** rnc in complex with srp
53	c2wooC_	Alignment	not modelled	94.6	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atpase get3; **PDBTitle:** nucleotide-free form of s. pombe get3
54	c3hr8A_	Alignment	not modelled	94.5	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca

55	c2yhsA_	Alignment	not modelled	94.5	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
56	c4pfsA_	Alignment	not modelled	94.5	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cobyrinic acid a,c-diamide synthase; **PDBTitle:** crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
57	c2w58B_	Alignment	not modelled	94.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
58	c3of5A_	Alignment	not modelled	94.4	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
59	d1cr2a_	Alignment	not modelled	94.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
60	c6bs3A_	Alignment	not modelled	94.3	38	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative atpase rv3679; **PDBTitle:** crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
61	c5lklB_	Alignment	not modelled	94.3	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**genome polyprotein; **PDBTitle:** crystal structure of full-lengh csfv ns3/4a
62	d1u94a1	Alignment	not modelled	94.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
63	c1qzwC_	Alignment	not modelled	94.2	22	**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
64	c6g2gA_	Alignment	not modelled	94.0	20	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**cytosolic fe-s cluster assembly factor cfd1; **PDBTitle:** fe-s assembly cfd1
65	c5j1jA_	Alignment	not modelled	94.0	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**site-determining protein; **PDBTitle:** structure of flen-amppnp complex
66	c3q9lB_	Alignment	not modelled	93.9	15	**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
67	d1ihua1	Alignment	not modelled	93.9	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
68	c6nonB_	Alignment	not modelled	93.8	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**cobyrinic acid ac-diamide synthase; **PDBTitle:** structure of cyanthece apo mcda
69	c1ii0A_	Alignment	not modelled	93.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of the escherichia coli arsenite-translocating2 atpase
70	c3endA_	Alignment	not modelled	93.8	13	**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
71	d1iona_	Alignment	not modelled	93.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
72	d1tf7a1	Alignment	not modelled	93.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
73	c3cmvG_	Alignment	not modelled	93.4	16	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
74	c3pihA_	Alignment	not modelled	93.4	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
75	c2px0D_	Alignment	not modelled	93.3	10	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
76	c1u9iA_	Alignment	not modelled	93.2	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
77	c5jwqA_	Alignment	not modelled	93.1	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**circadian clock protein kinase kaic; **PDBTitle:** crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
78	c3zq6D_	Alignment	not modelled	93.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative arsenical pump-driving atpase; **PDBTitle:** adp-alf4 complex of m. therm. trc40
79	c5zmfA_	Alignment	not modelled	92.9	22	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**atpase arsa1; **PDBTitle:** amppnp complex of c. reinhardtii arsa1
80	c2j289_	Alignment	not modelled	92.6	14	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
81	c4nh0A_	Alignment	not modelled	92.5	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell divisionftsk/spoiiie;

81	c4nn0A_	Alignment	not modelled	92.5	18	**PDBTitle:** cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
82	d1yksa1	Alignment	not modelled	92.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
83	c3vx3A_	Alignment	not modelled	92.4	15	**PDB header:**adp binding protein **Chain:** A: **PDB Molecule:**atpase involved in chromosome partitioning, para/mind **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
84	c3qf4B_	Alignment	not modelled	92.2	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized abc transporter atp-binding protein **PDBTitle:** crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
85	c5mkkB_	Alignment	not modelled	92.0	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance abc transporter atp-binding and **PDBTitle:** crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
86	c3cioA_	Alignment	not modelled	92.0	13	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
87	c3ug7D_	Alignment	not modelled	92.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of get3 from methanocaldococcus jannaschii
88	d1w36d1	Alignment	not modelled	91.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
89	c3berA_	Alignment	not modelled	91.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx47; **PDBTitle:** human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
90	c2vedA_	Alignment	not modelled	91.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
91	c4n1aE_	Alignment	not modelled	91.3	18	**PDB header:**protein binding/protein binding **Chain:** E: **PDB Molecule:**cell divisionftsk/spoiiie; **PDBTitle:** thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
92	c4zc0A_	Alignment	not modelled	91.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** structure of a dodecameric bacterial helicase
93	c5x5yB_	Alignment	not modelled	90.6	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable atp-binding component of abc transporter; **PDBTitle:** a membrane protein complex
94	c5ochH_	Alignment	not modelled	90.5	17	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**atp-binding cassette sub-family b member 8, mitochondrial; **PDBTitle:** the crystal structure of human abcb8 in an outward-facing state
95	c3k9gA_	Alignment	not modelled	90.3	23	**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
96	c3la6P_	Alignment	not modelled	90.2	11	**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
97	c2ztsB_	Alignment	not modelled	90.1	12	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
98	c2vf7B_	Alignment	not modelled	90.0	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
99	d1ihua2	Alignment	not modelled	90.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
100	c4kfuC_	Alignment	not modelled	90.0	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**genome packaging ntpase b204; **PDBTitle:** structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
101	c4wiaA_	Alignment	not modelled	90.0	10	**PDB header:**atp-binding protein **Chain:** A: **PDB Molecule:**putative flagella-related protein h; **PDBTitle:** crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
102	c2hydB_	Alignment	not modelled	90.0	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
103	c4nmnA_	Alignment	not modelled	90.0	22	**PDB header:**replication **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
104	c4lyaA_	Alignment	not modelled	89.9	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
105	d2afhe1	Alignment	not modelled	89.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
						PDB header:hydrolase

106	c5gvrA_	Alignment	not modelled	89.8	10	**Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx41; **PDBTitle:** crystal structure of the ddx41 dead domain in an apo closed form
107	c2q6tB_	Alignment	not modelled	89.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
108	c5ochF_	Alignment	not modelled	89.8	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atp-binding cassette sub-family b member 8, mitochondrial; **PDBTitle:** the crystal structure of human abcb8 in an outward-facing state
109	c1j8yF_	Alignment	not modelled	89.7	18	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
110	d1byia_	Alignment	not modelled	89.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
111	c3wmeA_	Alignment	not modelled	89.4	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette, sub-family b, member 1; **PDBTitle:** crystal structure of an inward-facing eukaryotic abc multidrug2 transporter
112	c3b5xB_	Alignment	not modelled	89.4	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
113	c5c76D_	Alignment	not modelled	89.4	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**wlab protein; **PDBTitle:** atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
114	c5u1dA_	Alignment	not modelled	89.2	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**antigen peptide transporter 1; **PDBTitle:** cryo-em structure of the human tap atp-binding cassette transporter
115	c4aa3A_	Alignment	not modelled	89.2	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter,2 abcb10 (plate form)
116	d1cp2a_	Alignment	not modelled	89.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
117	c2qmoA_	Alignment	not modelled	89.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
118	c5mkkA_	Alignment	not modelled	88.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multidrug resistance abc transporter atp-binding and **PDBTitle:** crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
119	c6qelB_	Alignment	not modelled	88.7	20	**PDB header:**replication **Chain:** B: **PDB Molecule:**replicative dna helicase; **PDBTitle:** e. coli dnabc apo complex
120	c4p31B_	Alignment	not modelled	88.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipopolysaccharide export system atp-binding protein lptb; **PDBTitle:** crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magensium