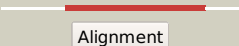
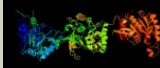

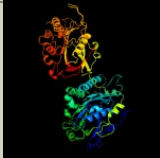




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1783 (- )_2019264_2023439
Date	Fri Aug 2 13:30:39 BST 2019
Unique Job ID	1ea50f6cd48498f3

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4nh0A_</a>	 Alignment		100.0	37	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell divisionftsks/poiiiie; <b>PDBTitle:</b> cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
2	<a href="#">c4n1aE_</a>	 Alignment		100.0	36	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> cell divisionftsks/poiiiie; <b>PDBTitle:</b> thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
3	<a href="#">c4lyaA_</a>	 Alignment		100.0	21	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
4	<a href="#">c2iuuE_</a>	 Alignment		100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> p. aeruginosa ftsk motor domain, hexamer
5	<a href="#">c2iutA_</a>	 Alignment		100.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> p. aeruginosa ftsk motor domain, dimeric
6	<a href="#">c2iusB_</a>	 Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> e. coli ftsk motor domain
7	<a href="#">c4kfuC_</a>	 Alignment		99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> genome packaging ntpase b204; <b>PDBTitle:</b> structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
8	<a href="#">c4d2iB_</a>	 Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hera; <b>PDBTitle:</b> crystal structure of the hera hexameric dna translocase2 from sulfolobus solfataricus bound to amp-pnp
9	<a href="#">c4ag5A_</a>	 Alignment		99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type iv secretory pathway virb4 components-like protein; <b>PDBTitle:</b> structure of virb4 of thermoanaerobacter pseudethanolicus
10	<a href="#">d1e9ra_</a>	 Alignment		99.5	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)
11	<a href="#">c6matE_</a>	 Alignment		99.3	25	<b>PDB header:</b> ribosomal protein <b>Chain:</b> E: <b>PDB Molecule:</b> rix7 mutant; <b>PDBTitle:</b> cryo-em structure of the essential ribosome assembly aaa-atpase rix7

12	<a href="#">c5g4gF_</a>	Alignment		99.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> structure of the atpgs-bound vat complex
13	<a href="#">c5ifwB_</a>	Alignment		99.2	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
14	<a href="#">c3cf1C_</a>	Alignment		99.2	17	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
15	<a href="#">c3cf2B_</a>	Alignment		99.2	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/amp-pnp
16	<a href="#">c5e7pA_</a>	Alignment		99.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
17	<a href="#">c4ag5D_</a>	Alignment		99.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> type iv secretory pathway virb4 components-like protein; <b>PDBTitle:</b> structure of virb4 of thermoanaerobacter pseudethanolicus
18	<a href="#">c6opcf_</a>	Alignment		98.9	19	<b>PDB header:</b> motor protein <b>Chain:</b> F: <b>PDB Molecule:</b> cell division control protein 48; <b>PDBTitle:</b> cdc48 hexamer in a complex with substrate and shp1(ubx domain)
19	<a href="#">c1u9iA_</a>	Alignment		98.8	14	<b>PDB header:</b> circadian clock protein <b>Chain:</b> A: <b>PDB Molecule:</b> kaic; <b>PDBTitle:</b> crystal structure of circadian clock protein kaic with phosphorylation2 sites
20	<a href="#">c3j96F_</a>	Alignment		98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vesicle-fusing atpase; <b>PDBTitle:</b> structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
21	<a href="#">c5jwqA_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> circadian clock protein kinase kaic; <b>PDBTitle:</b> crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
22	<a href="#">c1r6bX_</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
23	<a href="#">c5kneA_</a>	Alignment	not modelled	98.6	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
24	<a href="#">c1yqtA_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
25	<a href="#">c6djvE_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpggammas and casein, conformer 2
26	<a href="#">c5vq9D_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> pachytene checkpoint protein 2 homolog; <b>PDBTitle:</b> structure of human trip13, apo form
27	<a href="#">c1xwiA_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
28	<a href="#">c4b4tj_</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s protease regulatory subunit 8 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome <b>PDB header:</b> protein transport

29	<a href="#">c2zamA</a>	Alignment	not modelled	98.2	22	<b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
30	<a href="#">c6b5cA</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> katanin p60 atpase-containing subunit a-like 1; <b>PDBTitle:</b> structural basis for katanin self-assembly
31	<a href="#">c4xguB</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> putative pachytene checkpoint protein 2; <b>PDBTitle:</b> structure of c. elegans pch-2
32	<a href="#">c3d8bB</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of human fidgetin-like protein 1 in complex with adp
33	<a href="#">c3b9pA</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
34	<a href="#">c5w0tA</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein msp1; <b>PDBTitle:</b> crystal structure of monomeric msp1 from s. cerevisiae
35	<a href="#">c4finA</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> etta (yijk) abcf family protein; <b>PDBTitle:</b> crystal structure of etta (formerly yijk) - an e. coli abc-type atpase
36	<a href="#">c6nyyC</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> translocase <b>Chain:</b> C; <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
37	<a href="#">c4z8xC</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> truncated ftsh from a. aeolicus
38	<a href="#">c6epcJ</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> J; <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
39	<a href="#">c3cmvG</a>	Alignment	not modelled	98.1	17	<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-ssdna/dsdna2 structures
40	<a href="#">c5wc0D</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> motor protein <b>Chain:</b> D; <b>PDB Molecule:</b> meiotic spindle formation protein mei-1; <b>PDBTitle:</b> katanin hexamer in spiral conformation
41	<a href="#">c3j16B</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> ribosome <b>Chain:</b> B; <b>PDB Molecule:</b> rli1p; <b>PDBTitle:</b> models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
42	<a href="#">c5udbD</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> replication <b>Chain:</b> D; <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
43	<a href="#">c4b4tH</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> 26s protease regulatory subunit 7 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
44	<a href="#">c3hu2C</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
45	<a href="#">c3vfdA</a>	Alignment	not modelled	98.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
46	<a href="#">c4xgcD</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
47	<a href="#">c1s3sA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter) <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
48	<a href="#">c5kzfJ</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> J; <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
49	<a href="#">c4i16A</a>	Alignment	not modelled	98.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
50	<a href="#">c4b4tK</a>	Alignment	not modelled	97.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> K; <b>PDB Molecule:</b> 26s protease regulatory subunit 6b homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
51	<a href="#">c4kxfF</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> immune system <b>Chain:</b> F; <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> crystal structure of nlr4 reveals its autoinhibition mechanism
52	<a href="#">c5vy9C</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> chaperone <b>Chain:</b> C; <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> s. cerevisiae hsp104:casein complex, middle domain conformation
53	<a href="#">c6hecH</a>	Alignment	not modelled	97.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
54	<a href="#">c3eihB</a>	Alignment	not modelled	97.9	25	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4;

						<b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas
55	<a href="#">c2dhrC</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ftsh; <b>PDBTitle:</b> whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
56	<a href="#">c4b4tM</a>	Alignment	not modelled	97.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s protease regulatory subunit 6a; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
57	<a href="#">c5mpaL</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> 26s proteasome in presence of atp (s2)
58	<a href="#">c5gjqL</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease regulatory subunit 10b; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
59	<a href="#">c4lcbA</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein cdvc, vps4; <b>PDBTitle:</b> structure of vps4 homolog from acidianus hospitalis
60	<a href="#">c4xgcE</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
61	<a href="#">c2ce7B</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
62	<a href="#">d1fna2</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
63	<a href="#">c6epdM</a>	Alignment	not modelled	97.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 6a; <b>PDBTitle:</b> substrate processing state 26s proteasome (sps1)
64	<a href="#">c4b4tL</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
65	<a href="#">c5uj7C</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
66	<a href="#">c1iy2A</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh; <b>PDBTitle:</b> crystal structure of the ftsh atpase domain from thermus2 thermophilus
67	<a href="#">c3bk7A</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abc1/rnaase-i inhibitor protein from2 pyrococcus abyssi
68	<a href="#">c5t0gA</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 26s protease regulatory subunit 7; <b>PDBTitle:</b> structural basis for dynamic regulation of the human 26s proteasome
69	<a href="#">c2r2aB</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
70	<a href="#">c4ypnA</a>	Alignment	not modelled	97.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
71	<a href="#">d2ce7a2</a>	Alignment	not modelled	97.7	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
72	<a href="#">c4ciuA</a>	Alignment	not modelled	97.7	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> crystal structure of e. coli clpb
73	<a href="#">c3l0oB</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transcription termination factor rho; <b>PDBTitle:</b> structure of rna-free rho transcription termination factor from2 thermotoga maritima
74	<a href="#">c5x06G</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
75	<a href="#">c3pvsA</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
76	<a href="#">d1nlfa</a>	Alignment	not modelled	97.6	16	<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)
77	<a href="#">c3l0oA</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination factor rho; <b>PDBTitle:</b> structure of rna-free rho transcription termination factor from2 thermotoga maritima
78	<a href="#">c2x8aA</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear valosin-containing protein-like; <b>PDBTitle:</b> human nuclear valosin containing protein like (nv1), c-2 terminal aaa-atpase domain
79	<a href="#">d1jbka</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
80	<a href="#">c3ldaA</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> yeast rad51 h352y filament interface mutant

81	<a href="#">d1w5sa2</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
82	<a href="#">d1qvra2</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
83	<a href="#">c5l3rC_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
84	<a href="#">c4kxfP_</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> crystal structure of nlr4 reveals its autoinhibition mechanism
85	<a href="#">c3sylB_</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein cbbx; <b>PDBTitle:</b> crystal structure of the aaa+ protein cbbx, native structure
86	<a href="#">c5uj7B_</a>	Alignment	not modelled	97.5	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
87	<a href="#">c6mdnF_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vesicle-fusing atpase; <b>PDBTitle:</b> the 20s supercomplex engaging the snap-25 n-terminus (class 2)
88	<a href="#">c2v1uA_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog; <b>PDBTitle:</b> structure of the aeropyrum pernix orc1 protein in complex2 with dna
89	<a href="#">c4b4tl_</a>	Alignment	not modelled	97.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 26s protease regulatory subunit 4 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
90	<a href="#">c6azyA_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp104; <b>PDBTitle:</b> crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
91	<a href="#">d1d2na_</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
92	<a href="#">c6e11l_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> 1: <b>PDB Molecule:</b> heat shock protein 101; <b>PDBTitle:</b> ptex core complex in the resetting (compact) state
93	<a href="#">c3pfiB_</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
94	<a href="#">c1szpC_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> a crystal structure of the rad51 filament
95	<a href="#">c2qbyA_</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog 1; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
96	<a href="#">d1lixza_</a>	Alignment	not modelled	97.4	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
97	<a href="#">c3bh0A_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
98	<a href="#">c1fnnB_</a>	Alignment	not modelled	97.4	13	<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
99	<a href="#">c2ja1A_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
100	<a href="#">c1nsfA_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide sensitive factor; <b>PDBTitle:</b> d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
101	<a href="#">c2qz4A_</a>	Alignment	not modelled	97.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> paraplegin; <b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp
102	<a href="#">c2r65A_</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protease ftsH homolog; <b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsH2 adp complex
103	<a href="#">c1xpuB_</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> transcription/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rho transcription termination factor; <b>PDBTitle:</b> structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
104	<a href="#">d1tf7a2</a>	Alignment	not modelled	97.4	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)
105	<a href="#">d1xpua3</a>	Alignment	not modelled	97.4	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)

106	<a href="#">c2eyuA</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> twitching motility protein pilt; <b>PDBTitle:</b> the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
107	<a href="#">c6nyyA</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> translocase <b>Chain:</b> A: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
108	<a href="#">c2recB</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
109	<a href="#">d1r6bx3</a>	Alignment	not modelled	97.4	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
110	<a href="#">c6az0A</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial inner membrane i-aaa protease supercomplex <b>PDBTitle:</b> mitochondrial atpase protease yme1
111	<a href="#">c1iqpF</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rfcs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
112	<a href="#">c5d4wB</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
113	<a href="#">c3pxiB</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca108:clpc
114	<a href="#">c5zr1A</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
115	<a href="#">c2vyeA</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dna-ssdna complex
116	<a href="#">c4ydsA</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagella-related protein h; <b>PDBTitle:</b> flah from sulfolobus acidocaldarius with atp and mg-ion
117	<a href="#">c1q57G</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
118	<a href="#">d1szpa2</a>	Alignment	not modelled	97.2	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)
119	<a href="#">c3te6A</a>	Alignment	not modelled	97.2	9	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain
120	<a href="#">d2qy9a2</a>	Alignment	not modelled	97.2	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