Phyre^2

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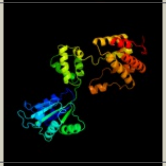
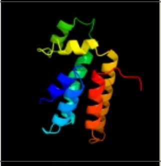
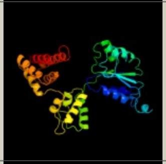
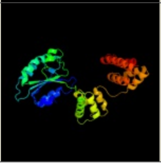
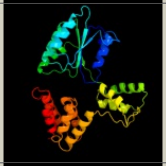
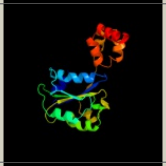
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xxiF_	Alignment		100.0	100	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna polymerase iii, delta subunit; **PDBTitle:** adp bound e. coli clamp loader complex
2	d1jr3d2	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
3	c1xxhB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
4	d1jqlb_	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
5	c1jr3E_	Alignment		99.9	17	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna polymerase iii, delta' subunit; **PDBTitle:** crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
6	d1jr3d1	Alignment		99.9	100	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
7	c1iqpF_	Alignment		99.7	16	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
8	c2gnoA_	Alignment		99.7	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna polymerase iii, gamma subunit-related protein; **PDBTitle:** crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution
9	c3pvsA_	Alignment		99.7	11	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
10	c1sxjD_	Alignment		99.7	13	**PDB header:**replication **Chain:** D: **PDB Molecule:**activator 1 41 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
11	c3u5zM_	Alignment		99.7	12	**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

12	c2chvE_	Alignment		99.6	14	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
13	c1sxjE_	Alignment		99.6	17	**PDB header:**replication **Chain:** E: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
14	c1sxjC_	Alignment		99.6	13	**PDB header:**replication **Chain:** C: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
15	c1sxjB_	Alignment		99.6	11	**PDB header:**replication **Chain:** B: **PDB Molecule:**activator 1 37 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
16	d1jr3a1	Alignment		99.5	17	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
17	c2chgB_	Alignment		99.4	9	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
18	d2gnoa2	Alignment		99.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
19	d1sxjb2	Alignment		99.3	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
20	d1iqpa2	Alignment		99.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
21	d1sxjc2	Alignment	not modelled	99.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
22	d1njfa_	Alignment	not modelled	99.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
23	c1sxjA_	Alignment	not modelled	99.2	15	**PDB header:**replication **Chain:** A: **PDB Molecule:**activator 1 95 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
24	d1sxje2	Alignment	not modelled	99.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
25	d1sxjd2	Alignment	not modelled	99.1	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
26	c3bosA_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase regulator,dna binding protein **Chain:** A: **PDB Molecule:**putative dna replication factor; **PDBTitle:** crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
27	d1a5ta2	Alignment	not modelled	99.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
28	d1sxja2	Alignment	not modelled	98.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

28	d1sxja2	Alignment	not modelled	98.9	14	hydrolases **Family:**Extended AAA-ATPase domain
29	d1in4a2	Alignment	not modelled	98.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
30	c3pfiB_	Alignment	not modelled	98.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 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
31	c2z4rB_	Alignment	not modelled	98.6	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
32	c1in8A_	Alignment	not modelled	98.6	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
33	d1ixsb2	Alignment	not modelled	98.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
34	d1l8qa2	Alignment	not modelled	97.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
35	c2c9oC_	Alignment	not modelled	97.6	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
36	c3te6A_	Alignment	not modelled	97.6	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
37	d1ny5a2	Alignment	not modelled	97.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
38	d1w5sa2	Alignment	not modelled	97.5	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
39	d1r6bx2	Alignment	not modelled	97.1	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
40	c1ny5A_	Alignment	not modelled	97.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
41	d1fnna2	Alignment	not modelled	96.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
42	c3h4mC_	Alignment	not modelled	96.9	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
43	c2ce7B_	Alignment	not modelled	96.8	12	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
44	d1sxjd1	Alignment	not modelled	96.8	16	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
45	d1ixza_	Alignment	not modelled	96.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
46	c3b9pA_	Alignment	not modelled	95.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
47	c1ojlF_	Alignment	not modelled	95.8	16	**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
48	c2c99A_	Alignment	not modelled	95.8	14	**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
49	d2ce7a2	Alignment	not modelled	95.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
50	c2zamA_	Alignment	not modelled	95.4	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
51	c1hqcB_	Alignment	not modelled	95.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
52	c3d8bB_	Alignment	not modelled	95.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
53	c2dhrC_	Alignment	not modelled	95.1	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh;

53	c2dhrC_	Alignment	not modelled	95.1	15	**PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
54	c1r6bX_	Alignment	not modelled	95.0	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
55	d1iqpa1	Alignment	not modelled	94.8	18	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
56	c1iy2A_	Alignment	not modelled	94.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
57	d1qvra2	Alignment	not modelled	94.5	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
58	c2r65A_	Alignment	not modelled	94.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
59	c2v1uA_	Alignment	not modelled	94.1	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**cell division control protein 6 homolog; **PDBTitle:** structure of the aeropyrum pernix orc1 protein in complex2 with dna
60	c1qvrB_	Alignment	not modelled	93.6	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
61	d1jbka_	Alignment	not modelled	93.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
62	c1xwiA_	Alignment	not modelled	93.1	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
63	c2hcbC_	Alignment	not modelled	92.7	14	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
64	c1fnnB_	Alignment	not modelled	91.5	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
65	c3hteC_	Alignment	not modelled	91.1	17	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
66	d1id3b_	Alignment	not modelled	90.8	8	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
67	c3dzdA_	Alignment	not modelled	90.7	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
68	d1qvra3	Alignment	not modelled	90.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
69	d1hiod_	Alignment	not modelled	89.2	8	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
70	d1sxjc1	Alignment	not modelled	89.2	11	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
71	d2huec1	Alignment	not modelled	88.7	8	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
72	c2kjqA_	Alignment	not modelled	88.7	11	**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.
73	d1e32a2	Alignment	not modelled	87.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
74	d1r6bx3	Alignment	not modelled	87.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
75	d1lv7a_	Alignment	not modelled	86.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
76	d1tafb_	Alignment	not modelled	86.2	15	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
77	d1sxjb1	Alignment	not modelled	85.9	19	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
78	d1kx5b_	Alignment	not modelled	85.7	8	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
79	c2v6zM_	Alignment	not modelled	85.4	22	**PDB header:**transferase **Chain:** M: **PDB Molecule:**dna polymerase epsilon subunit 2; **PDBTitle:** solution structure of amino terminal domain of human

						dna2 polymerase epsilon subunit b
80	c2qz4A_	Alignment	not modelled	85.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
81	d1a5ta1	Alignment	not modelled	83.6	22	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
82	d1g41a_	Alignment	not modelled	81.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
83	d1r7ra3	Alignment	not modelled	80.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
84	c2qbyB_	Alignment	not modelled	78.9	12	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**cell division control protein 6 homolog 3; **PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
85	c3pxiB_	Alignment	not modelled	77.8	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
86	c3pxgA_	Alignment	not modelled	76.5	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
87	c2qbyA_	Alignment	not modelled	75.4	13	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cell division control protein 6 homolog 1; **PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
88	d1htaa_	Alignment	not modelled	71.5	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
89	d1a7wa_	Alignment	not modelled	69.9	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
90	c3eihB_	Alignment	not modelled	68.8	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
91	d1ofha_	Alignment	not modelled	67.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
92	d1ku5a_	Alignment	not modelled	67.1	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
93	c3ctdB_	Alignment	not modelled	65.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative atpase, aaa family; **PDBTitle:** crystal structure of a putative aaa family atpase from2 prochlorococcus marinus subsp. pastoris
94	d1p3mh_	Alignment	not modelled	64.5	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
95	d1hiob_	Alignment	not modelled	64.1	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
96	d1id3d_	Alignment	not modelled	63.8	12	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
97	d1tzyb_	Alignment	not modelled	62.5	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
98	c1w5sB_	Alignment	not modelled	62.4	11	**PDB header:**replication **Chain:** B: **PDB Molecule:**origin recognition complex subunit 2 orc2; **PDBTitle:** structure of the aeropyrum pernix orc2 protein (adp form)
99	c1s3sA_	Alignment	not modelled	61.3	16	**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
100	d3ctda1	Alignment	not modelled	60.9	14	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
101	c2jssA_	Alignment	not modelled	51.7	12	**PDB header:**chaperone/nuclear protein **Chain:** A: **PDB Molecule:**chimera of histone h2b.1 and histone h2a.z; **PDBTitle:** nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
102	d3bgea1	Alignment	not modelled	50.0	14	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**MgsA/YrvN C-terminal domain-like
103	d1um8a_	Alignment	not modelled	48.9	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
104	d1kx5d_	Alignment	not modelled	45.4	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
105	d2b5ea3	Alignment	not modelled	42.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like

						Family:PDI-like
106	c3cf1C_	Alignment	not modelled	42.5	18	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
107	d1d2na_	Alignment	not modelled	42.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
108	c2x8aA_	Alignment	not modelled	40.9	10	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear valosin-containing protein-like; **PDBTitle:** human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
109	d1tafa_	Alignment	not modelled	40.1	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
110	d1s32d_	Alignment	not modelled	38.0	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
111	d1h3oa_	Alignment	not modelled	37.9	22	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
112	c1h3oA_	Alignment	not modelled	37.9	22	**PDB header:**transcription/tbp-associated factors **Chain:** A: **PDB Molecule:**transcription initiation factor tfiid 135 kda **PDBTitle:** crystal structure of the human taf4-taf122 (tafii135-tafii20) complex
113	c3iuoA_	Alignment	not modelled	37.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase recq; **PDBTitle:** the crystal structure of the c-terminal domain of the atp-dependent2 dna helicase recq from porphyromonas gingivalis to 1.6a
114	d1eqzb_	Alignment	not modelled	37.2	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
115	d2fnaa2	Alignment	not modelled	37.1	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
116	d3bula1	Alignment	not modelled	35.5	10	**Fold:**Methionine synthase domain-like **Superfamily:**Methionine synthase domain **Family:**Methionine synthase domain
117	c2krkA_	Alignment	not modelled	34.8	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**26s protease regulatory subunit 8; **PDBTitle:** solution nmr structure of 26s protease regulatory subunit 82 from h.sapiens, northeast structural genomics consortium3 target target hr3102a
118	d1zl8a1	Alignment	not modelled	34.6	24	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
119	d1a9xa1	Alignment	not modelled	32.8	11	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
120	d1y74a1	Alignment	not modelled	31.8	35	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain