Phyre^2

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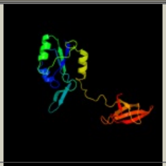
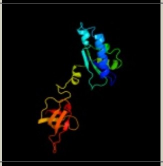
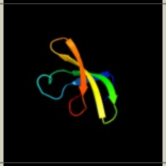
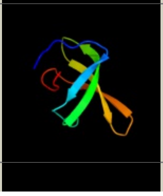
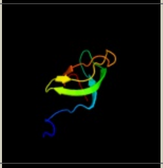
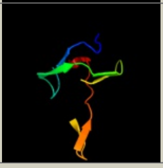
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m1gB_	Alignment		100.0	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
2	c2ougC_	Alignment		100.0	98	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional activator rfah; **PDBTitle:** crystal structure of the rfah transcription factor at 2.1a2 resolution
3	c2xhcA_	Alignment		100.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
4	c3p8bB_	Alignment		99.9	21	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
5	c2k06A_	Alignment		99.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of the aminoterminal domain of e. coli2 nusg
6	d1nz8a_	Alignment		99.9	26	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
7	d1m1ha2	Alignment		99.9	18	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
8	d1nppa2	Alignment		99.4	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
9	d1nz9a_	Alignment		99.4	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
10	c2jvvA_	Alignment		99.4	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
11	c2kvqG_	Alignment		99.4	20	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex

12	c3ewgA_	Alignment		97.2	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription antitermination protein nusg; **PDBTitle:** crystal structure of the n-terminal domain of nusg (ngn) from2 methanocaldococcus jannaschii
13	c2e6zA_	Alignment		97.0	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
14	c2exuA_	Alignment		96.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
15	d2do3a1	Alignment		96.1	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
16	c3h7hB_	Alignment		95.9	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
17	c2ckkA_	Alignment		95.8	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**kin17; **PDBTitle:** high resolution crystal structure of the human kin172 c-terminal domain containing a kow motif3 kin17.
18	c2e70A_	Alignment		95.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the fifth kow motif of human2 transcription elongation factor spt5
19	d1vqot1	Alignment		95.5	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
20	c3iz5Y_	Alignment		95.3	8	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
21	c2zkrt_	Alignment	not modelled	95.3	10	**PDB header:**ribosomal protein/rna **Chain:** T: **PDB Molecule:**rna expansion segment es39 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
22	c4a1cS_	Alignment	not modelled	95.1	16	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
23	d2gycs1	Alignment	not modelled	93.3	16	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
24	d2zjrr1	Alignment	not modelled	93.2	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
25	c2jz2A_	Alignment	not modelled	90.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
26	c1s1iU_	Alignment	not modelled	85.9	14	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l26-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
27	c3bboW_	Alignment	not modelled	83.7	17	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**ribosomal protein l24; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
						PDB header:ribosome

28	c3iz5N_	Alignment	not modelled	81.4	13	**Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
29	d2j01y1	Alignment	not modelled	79.1	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
30	c3izcN_	Alignment	not modelled	79.0	23	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
31	d2joya1	Alignment	not modelled	77.8	9	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
32	c4a19F_	Alignment	not modelled	69.9	17	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl14; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
33	c2ftcN_	Alignment	not modelled	67.9	32	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**mitochondrial ribosomal protein l24; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
34	d1ib8a1	Alignment	not modelled	63.0	10	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
35	d1nxza1	Alignment	not modelled	51.0	9	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
36	d1vqoq1	Alignment	not modelled	46.4	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
37	c3kbgA_	Alignment	not modelled	37.8	18	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
38	c4a18N_	Alignment	not modelled	36.9	17	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**rpl27; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
39	c3qiiA_	Alignment	not modelled	36.5	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
40	d1rkia1	Alignment	not modelled	31.3	10	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**PAE0736-like
41	d2vv5a1	Alignment	not modelled	29.8	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
42	d2pu9b1	Alignment	not modelled	29.0	18	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
43	d1vhka1	Alignment	not modelled	28.0	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
44	d2zgwa1	Alignment	not modelled	27.9	34	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
45	d1h3ga1	Alignment	not modelled	25.2	36	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
46	c2dxcG_	Alignment	not modelled	24.0	19	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
47	c3ikmD_	Alignment	not modelled	23.0	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
48	c3iz6D_	Alignment	not modelled	22.5	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
49	c3pifD_	Alignment	not modelled	21.4	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**5'->3' exoribonuclease (xrn1); **PDBTitle:** crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
50	c2gpzC_	Alignment	not modelled	21.1	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** transthyretin-like protein from salmonella dublin
51	c3j04A_	Alignment	not modelled	17.9	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**myosin-11; **PDBTitle:** em structure of the heavy meromyosin subfragment of chick smooth2 muscle myosin with regulatory light chain in phosphorylated state
52	d1a8pa1	Alignment	not modelled	17.7	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
53	c3d8tB_	Alignment	not modelled	17.5	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase;

						PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
54	c2h1xB_	Alignment	not modelled	17.3	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
55	c2vc8A_	Alignment	not modelled	16.6	20	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of the lsm domain of human edc3 (enhancer2 of decapping 3)
56	d1yt8a4	Alignment	not modelled	16.6	12	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
57	d1ugpb_	Alignment	not modelled	15.5	24	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
58	d1wd7a_	Alignment	not modelled	15.4	17	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
59	c2k3aA_	Alignment	not modelled	15.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chap domain protein; **PDBTitle:** nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
60	c2equA_	Alignment	not modelled	14.9	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
61	d1v29b_	Alignment	not modelled	14.7	10	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
62	c2xzmW_	Alignment	not modelled	14.2	14	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
63	d2hqha1	Alignment	not modelled	14.0	14	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
64	c3izcG_	Alignment	not modelled	13.9	18	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein rpl6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
65	c2vv5D_	Alignment	not modelled	13.6	14	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
66	c3p8dB_	Alignment	not modelled	13.4	7	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**medulloblastoma antigen mu-mb-50.72; **PDBTitle:** crystal structure of the second tudor domain of human phf20 (homodimer2 form)
67	d1jr2a_	Alignment	not modelled	12.3	24	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
68	c1jr2A_	Alignment	not modelled	12.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
69	d1ixda_	Alignment	not modelled	12.3	20	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
70	c1x60A_	Alignment	not modelled	12.1	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
71	d1f86a_	Alignment	not modelled	12.1	0	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
72	d2qdyb1	Alignment	not modelled	12.0	15	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
73	d1s7ia_	Alignment	not modelled	11.9	29	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
74	d1kgia_	Alignment	not modelled	11.5	0	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
75	d2coya1	Alignment	not modelled	11.3	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
76	c2hqxB_	Alignment	not modelled	10.7	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**p100 co-activator tudor domain; **PDBTitle:** crystal structure of human p100 tudor domain conserved2 region
77	d2hqxa1	Alignment	not modelled	10.7	11	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
78	c2rm4A_	Alignment	not modelled	10.6	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**cg6311-pb; **PDBTitle:** solution structure of the lsm domain of dm edc3 (enhancer2 of decapping 3)

79	d1e0ta3	Alignment	not modelled	10.5	12	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
80	d2diqa1	Alignment	not modelled	10.3	11	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
81	c2ky9A_	Alignment	not modelled	10.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ydhk; **PDBTitle:** solution nmr structure of ydhk c-terminal domain from b.subtilis,2 northeast structural genomics consortium target target sr518
82	c3qz9D_	Alignment	not modelled	10.1	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**co-type nitrile hydratase beta subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
83	d2p3ha1	Alignment	not modelled	10.1	10	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
84	d2hlja1	Alignment	not modelled	10.0	11	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
85	c1nwxN_	Alignment	not modelled	9.5	20	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**ribosomal protein l19; **PDBTitle:** complex of the large ribosomal subunit from deinococcus2 radiodurans with abt-773
86	c3izca_	Alignment	not modelled	9.4	18	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein rpl1 (l1p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
87	d1fdra1	Alignment	not modelled	9.4	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
88	d1ttaa_	Alignment	not modelled	9.3	0	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
89	d2zjrm1	Alignment	not modelled	9.2	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
90	c3izbD_	Alignment	not modelled	9.1	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
91	c1vhkA_	Alignment	not modelled	9.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
92	c2eqmA_	Alignment	not modelled	9.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
93	d1rw1a_	Alignment	not modelled	8.9	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
94	c1i84V_	Alignment	not modelled	8.9	14	**PDB header:**contractile protein **Chain:** V: **PDB Molecule:**smooth muscle myosin heavy chain; **PDBTitle:** cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.
95	d1oo2a_	Alignment	not modelled	8.8	6	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
96	c3nnhA_	Alignment	not modelled	8.5	17	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**cugbp elav-like family member 1; **PDBTitle:** crystal structure of the cugbp1 rrm1 with guuguuuuguuu rna
97	c3q1jA_	Alignment	not modelled	8.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
98	c2k3yA_	Alignment	not modelled	8.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**chromatin modification-related protein eaf3; **PDBTitle:** solution structure of eaf3 chromo barrel domain bound to2 histone h3 with a dimethyllysine analog h3k36me2
99	c2pmzV_	Alignment	not modelled	8.3	13	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus