



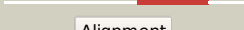










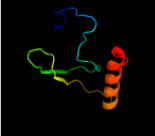
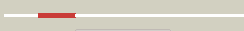






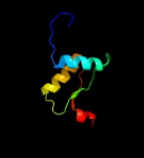
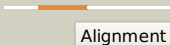

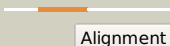







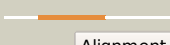



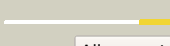

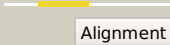




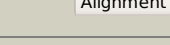
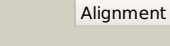
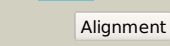
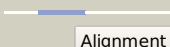


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3446c (- )_3863496_3864710
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	a989a3703e6aa27f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xb3A_</a>	 Alignment		97.2	14	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> psbp protein; <b>PDBTitle:</b> the structure of cyanobacterial psbp
2	<a href="#">c2lnjA_</a>	 Alignment		96.4	12	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sll1418; <b>PDBTitle:</b> solution structure of cyanobacterial psbp (cyanop) from synechocystis2 sp. pcc 6803
3	<a href="#">d1v2ba_</a>	 Alignment		95.9	14	<b>Fold:</b> Mog1p/PsbP-like <b>Superfamily:</b> Mog1p/PsbP-like <b>Family:</b> PsbP-like
4	<a href="#">d1jcea1</a>	 Alignment		94.8	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
5	<a href="#">c4ol4A_</a>	 Alignment		94.6	19	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> proline-rich 28 kda antigen; <b>PDBTitle:</b> crystal structure of secreted proline rich antigen mtc28 (rv0040c)2 from mycobacterium tuberculosis
6	<a href="#">d1dkgd1</a>	 Alignment		94.3	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
7	<a href="#">c2vu4A_</a>	 Alignment		93.5	13	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> oxygen-evolving enhancer protein 2; <b>PDBTitle:</b> structure of psbp protein from spinacia oleracea at 1.98 a2 resolution
8	<a href="#">c6e8aA_</a>	 Alignment		92.6	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> duf1795 domain-containing protein; <b>PDBTitle:</b> crystal structure of dcrb from salmonella enterica at 1.92 angstroms2 resolution
9	<a href="#">d2e8aa1</a>	 Alignment		92.6	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
10	<a href="#">c2v7yA_</a>	 Alignment		92.5	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
11	<a href="#">d1tu1a_</a>	 Alignment		91.4	13	<b>Fold:</b> Mog1p/PsbP-like <b>Superfamily:</b> Mog1p/PsbP-like <b>Family:</b> PA0094-like

12	<a href="#">d1bupa1</a>	 Alignment		91.3	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
13	<a href="#">c4j8fA</a>	 Alignment		87.0	9	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock 70 kda protein 1a/1b, hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
14	<a href="#">c5obuA</a>	 Alignment		85.0	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
15	<a href="#">c2khoA</a>	 Alignment		83.8	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 70; <b>PDBTitle:</b> nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate
16	<a href="#">c3d2fC</a>	 Alignment		83.1	11	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein homolog sse1; <b>PDBTitle:</b> crystal structure of a complex of sse1p and hsp70
17	<a href="#">c4rtfD</a>	 Alignment		82.3	16	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
18	<a href="#">c3h1qB</a>	 Alignment		81.5	12	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutj; <b>PDBTitle:</b> crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrus hydrogenoformans
19	<a href="#">c5mb9B</a>	 Alignment		77.2	16	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
20	<a href="#">c3lydA</a>	 Alignment		73.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative uncharacterized protein from jonesia2 denitrificans
21	<a href="#">c1jcgA</a>	 Alignment	not modelled	72.4	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> mreB from thermotoga maritima, amppnp
22	<a href="#">c3c7nB</a>	 Alignment	not modelled	68.9	11	<b>PDB header:</b> chaperone/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock cognate; <b>PDBTitle:</b> structure of the hsp110:hsc70 nucleotide exchange complex
23	<a href="#">c4gniA</a>	 Alignment	not modelled	68.0	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> structure of the ssz1 atpase bound to atp and magnesium
24	<a href="#">c5e84B</a>	 Alignment	not modelled	67.6	12	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> 78 kda glucose-regulated protein; <b>PDBTitle:</b> atp-bound state of bip
25	<a href="#">c5jygA</a>	 Alignment	not modelled	65.0	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin-like atpase; <b>PDBTitle:</b> cryo-em structure of the mamk filament at 6.5 a
26	<a href="#">c5tkyA</a>	 Alignment	not modelled	49.6	9	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
27	<a href="#">c1dkgD</a>	 Alignment	not modelled	33.4	14	<b>PDB header:</b> complex (hsp24/hsp70) <b>Chain:</b> D: <b>PDB Molecule:</b> molecular chaperone dnak; <b>PDBTitle:</b> crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
28	<a href="#">c4pl7B</a>	 Alignment	not modelled	29.8	13	<b>PDB header:</b> structural protein, contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin,thymosin beta-4; <b>PDBTitle:</b> structure of komagataella pastoris actin-thymosin beta4 hybrid
						<b>PDB header:</b> chaperone

29	<a href="#">c6gfaA</a>	Alignment	not modelled	29.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 105 kda; <b>PDBTitle:</b> structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
30	<a href="#">c3iucC</a>	Alignment	not modelled	28.4	11	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock 70kda protein 5 (glucose-regulated <b>PDBTitle:</b> crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
31	<a href="#">c2if0A</a>	Alignment	not modelled	20.6	55	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yib1; <b>PDBTitle:</b> solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scattering, nesg4 target sfr339/ocsp target sf3636
32	<a href="#">c5afuB</a>	Alignment	not modelled	15.8	15	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein; <b>PDBTitle:</b> cryo-em structure of dynein tail-dynein-bicd2n complex
33	<a href="#">c6igmG</a>	Alignment	not modelled	15.8	9	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> actin-related protein 6; <b>PDBTitle:</b> cryo-em structure of human srcap complex
34	<a href="#">c5tt2D</a>	Alignment	not modelled	15.0	38	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> cystathionine gamma-lyase; <b>PDBTitle:</b> inactive conformation of engineered human cystathionine gamma lyase2 (e59n, r119l, e339v) to depleting methionine
35	<a href="#">c4czeA</a>	Alignment	not modelled	14.5	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> c. crescentus mreB, double filament, empty
36	<a href="#">c1o1f4</a>	Alignment	not modelled	13.6	13	<b>PDB header:</b> contractile protein <b>Chain:</b> 4: <b>PDB Molecule:</b> skeletal muscle actin; <b>PDBTitle:</b> molecular models of averaged rigor crossbridges from tomograms of2 insect flight muscle
37	<a href="#">c6e5fA</a>	Alignment	not modelled	12.8	19	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid binding protein lpqn; <b>PDBTitle:</b> crystal structure of lpqn involved in cell envelope biogenesis of2 mycobacterium tuberculosis
38	<a href="#">c5yk2A</a>	Alignment	not modelled	12.4	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable conserved atp-binding protein abc transporter; <b>PDBTitle:</b> the complex structure of rv3197-erythromycin from mycobacterium2 tuberculosis
39	<a href="#">c4jd2B</a>	Alignment	not modelled	10.9	15	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-related protein 2; <b>PDBTitle:</b> crystal structure of bos taurus arp2/3 complex binding with mus2 musculus gmf
40	<a href="#">d1n8pa</a>	Alignment	not modelled	10.8	32	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
41	<a href="#">c4pedA</a>	Alignment	not modelled	10.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone activity of bc1 complex-like, mitochondrial; <b>PDBTitle:</b> mitochondrial adck3 employs an atypical protein kinase-like fold to2 enable coenzyme q biosynthes
42	<a href="#">c2nmpC</a>	Alignment	not modelled	9.6	37	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> cystathionine gamma-lyase; <b>PDBTitle:</b> crystal structure of human cystathionine gamma lyase
43	<a href="#">c2bsjB</a>	Alignment	not modelled	9.6	25	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone protein syct; <b>PDBTitle:</b> native crystal structure of the type iii secretion chaperone syct from2 yersinia enterocolitica
44	<a href="#">d1w96a1</a>	Alignment	not modelled	9.5	20	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
45	<a href="#">c3u7iB</a>	Alignment	not modelled	9.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase 1; <b>PDBTitle:</b> the crystal structure of fmn-dependent nadh-azoreductase 1 (gbaa0966)2 from bacillus anthracis str. ames ancestor
46	<a href="#">c4mtkD</a>	Alignment	not modelled	9.0	19	<b>PDB header:</b> toxin <b>Chain:</b> D: <b>PDB Molecule:</b> vgrg1; <b>PDBTitle:</b> crystal structure of pa0091 vgrg1, the central spike of the type vi2 secretion system
47	<a href="#">c3lcmB</a>	Alignment	not modelled	8.9	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159
48	<a href="#">d2p5zx1</a>	Alignment	not modelled	8.9	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> gp5 N-terminal domain-like <b>Family:</b> gp4 N-terminal domain-like
49	<a href="#">c6aufB</a>	Alignment	not modelled	8.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase-like protein; <b>PDBTitle:</b> crystal structure of metallo beta lactamases mim-1 from novosphingobium2 pentaromativorans
50	<a href="#">c4kboA</a>	Alignment	not modelled	8.3	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> stress-70 protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the human mortalin (grp75) atpase domain in the2 apo form
51	<a href="#">c2khrA</a>	Alignment	not modelled	7.7	69	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein mbth; <b>PDBTitle:</b> solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
52	<a href="#">c5jn6A</a>	Alignment	not modelled	7.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the nmr solution structure of rpa3313
53	<a href="#">d1w96c1</a>	Alignment	not modelled	7.5	20	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like <b>PDB header:</b> hydrolase

54	<a href="#">c6e0sA</a>	Alignment	not modelled	7.5	15	<b>Chain:</b> A: <b>PDB Molecule:</b> mem-a1; <b>PDBTitle:</b> crystal structure of mem-a1, a subclass b3 metallo-beta-lactamase2 isolated from a soil metagenome library
55	<a href="#">c2v9cA</a>	Alignment	not modelled	7.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase 1; <b>PDBTitle:</b> x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
56	<a href="#">d1ig4a</a>	Alignment	not modelled	7.1	20	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> Methyl-CpG-binding domain, MBD
57	<a href="#">c2lpdA</a>	Alignment	not modelled	7.0	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b
58	<a href="#">c5u89B</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> mbth domain protein; <b>PDBTitle:</b> crystal structure of a cross-module fragment from the dimodular nrps2 dhhbf
59	<a href="#">d1ei5a2</a>	Alignment	not modelled	6.8	31	<b>Fold:</b> Streptavidin-like <b>Superfamily:</b> D-aminopeptidase, middle and C-terminal domains <b>Family:</b> D-aminopeptidase, middle and C-terminal domains
60	<a href="#">d1dy2a</a>	Alignment	not modelled	6.6	27	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Endostatin
61	<a href="#">c5oqml</a>	Alignment	not modelled	6.6	22	<b>PDB header:</b> transcription <b>Chain:</b> L: <b>PDB Molecule:</b> dna-directed rna polymerases i, ii, and iii subunit rpabc4; <b>PDBTitle:</b> structure of yeast transcription pre-initiation complex with tfiih and2 core mediator
62	<a href="#">d1hc8a</a>	Alignment	not modelled	6.4	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
63	<a href="#">d1mmsa1</a>	Alignment	not modelled	6.4	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
64	<a href="#">c2ky8A</a>	Alignment	not modelled	6.3	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 2; <b>PDBTitle:</b> solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
65	<a href="#">d1xbpg1</a>	Alignment	not modelled	6.2	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
66	<a href="#">d1rlia</a>	Alignment	not modelled	6.2	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Hypothetical protein YwqN
67	<a href="#">c5f4bB</a>	Alignment	not modelled	6.2	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p)h dehydrogenase (quinone); <b>PDBTitle:</b> structure of b. abortus wrba-related protein a (wrpa)
68	<a href="#">c3rpeA</a>	Alignment	not modelled	6.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> modulator of drug activity b; <b>PDBTitle:</b> 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
69	<a href="#">d2gycg1</a>	Alignment	not modelled	5.7	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
70	<a href="#">d1vqoi1</a>	Alignment	not modelled	5.5	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Ribosomal protein L11, C-terminal domain <b>Family:</b> Ribosomal protein L11, C-terminal domain
71	<a href="#">c1vq8L</a>	Alignment	not modelled	5.5	18	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l11p; <b>PDBTitle:</b> the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
72	<a href="#">d1d4aa</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
73	<a href="#">c5iqkB</a>	Alignment	not modelled	5.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase rm3; <b>PDBTitle:</b> rm3 metallo-beta-lactamase
74	<a href="#">d2qwxal</a>	Alignment	not modelled	5.3	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
75	<a href="#">c4r81C</a>	Alignment	not modelled	5.2	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
76	<a href="#">c2zkiH</a>	Alignment	not modelled	5.2	21	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 199aa long hypothetical trp repressor binding <b>PDBTitle:</b> crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
77	<a href="#">c5o5oD</a>	Alignment	not modelled	5.1	31	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> rnase adapter protein rapz; <b>PDBTitle:</b> x-ray crystal structure of rapz from escherichia coli (p32 space2 group)
78	<a href="#">d1c3ga1</a>	Alignment	not modelled	5.1	2	<b>Fold:</b> HSP40/Dnaj peptide-binding domain <b>Superfamily:</b> HSP40/Dnaj peptide-binding domain <b>Family:</b> HSP40/Dnaj peptide-binding domain
79	<a href="#">c2lazA</a>	Alignment	not modelled	5.1	21	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase smurf1; <b>PDBTitle:</b> structure of the first ww domain of human smurf1 in

