




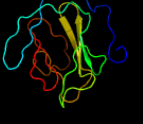


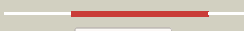















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0019c (-)_23270_23737
Date	Tue Jul 23 14:50:04 BST 2019
Unique Job ID	57c777a28fa1ab18

Detailed template
information

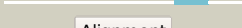
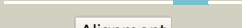
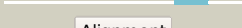





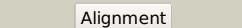

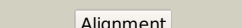

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kkIA_	 Alignment		99.9	30	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein mb1858; PDBTitle: solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
2	c2kfuA_	 Alignment		99.9	29	PDB header: protein binding Chain: A; PDB Molecule: rv1827 pthr 22; PDBTitle: pknb-phosphorylated rv1827
3	c2n84A_	 Alignment		99.9	25	PDB header: isomerase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the fha domain of tbpar42
4	c4h87A_	 Alignment		99.8	28	PDB header: peptide binding protein Chain: A; PDB Molecule: kanadaptn; PDBTitle: crystal structure of a fha domain of kanadaptn (slc4a1ap) from homo2 sapiens at 1.55 a resolution
5	c3vpyA_	 Alignment		99.8	23	PDB header: protein binding Chain: A; PDB Molecule: fha domain-containing protein ddl; PDBTitle: crystal structure of arabidopsis ddl fha domain
6	d1mzka_	 Alignment		99.8	28	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
7	c3gqsB_	 Alignment		99.8	28	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: adenylate cyclase-like protein; PDBTitle: crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
8	d2affa1	 Alignment		99.8	19	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
9	c3poaA_	 Alignment		99.8	29	PDB header: peptide binding protein Chain: A; PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
10	c3ouaA_	 Alignment		99.8	30	PDB header: protein binding/transferase Chain: A; PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: crystal structure of the fhaa fha domain complexed with the2 intracellular domain of rv3910
11	c1r21A_	 Alignment		99.8	19	PDB header: cell cycle Chain: A; PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain

12	c4a0eB_	Alignment		99.8	16	PDB header: transport protein Chain: B; PDB Molecule: type iii secretion protein; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of yersinia2 pestis yscd
13	d2ff4a3	Alignment		99.8	26	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
14	d1uhta_	Alignment		99.8	25	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
15	c4jonA_	Alignment		99.8	28	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: centrosomal protein of 170 kda; PDBTitle: crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
16	c3hx1B_	Alignment		99.8	21	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: slr1951 protein; PDBTitle: crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
17	c6ccdA_	Alignment		99.8	29	PDB header: protein binding Chain: A; PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: the crystal structure of mycobacterium tuberculosis rv1747 fha-1
18	c2ff4B_	Alignment		99.8	23	PDB header: transcription Chain: B; PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low affinity2 phosphopeptide
19	c3uotB_	Alignment		99.8	20	PDB header: cell cycle Chain: B; PDB Molecule: mediator of dna damage checkpoint protein 1; PDBTitle: crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
20	c6cahA_	Alignment		99.8	30	PDB header: protein binding Chain: A; PDB Molecule: abc transporter atp-binding/permease protein rv1747; PDBTitle: nmr-based structure of the fha-2 domain from mycobacterium2 tuberculosis abc transporter rv1747
21	c5a8iA_	Alignment	not modelled	99.8	27	PDB header: transcription Chain: A; PDB Molecule: arna; PDBTitle: crystal structure of the fha domain of arna from sulfolobus2 acidocaldarius
22	c2jpeA_	Alignment	not modelled	99.8	19	PDB header: transcription Chain: A; PDB Molecule: nuclear inhibitor of protein phosphatase 1; PDBTitle: fha domain of nipp1
23	c5yyxA_	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A; PDB Molecule: meiosis-specific serine/threonine-protein kinase mek1; PDBTitle: crystal structure of the mek1 fha domain
24	c3fm8A_	Alignment	not modelled	99.7	15	PDB header: transport protein/hydrolase activator Chain: A; PDB Molecule: kinesin-like protein kif13b; PDBTitle: crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
25	c6ar2B_	Alignment	not modelled	99.7	21	PDB header: membrane protein Chain: B; PDB Molecule: sarcolemmal membrane-associated protein; PDBTitle: structure of human slmap fha domain in complex with pmst2
26	c2jqIA_	Alignment	not modelled	99.7	17	PDB header: cell cycle Chain: A; PDB Molecule: dna damage response protein kinase dun1; PDBTitle: nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
27	c2jkdB_	Alignment	not modelled	99.7	22	PDB header: gene regulation Chain: B; PDB Molecule: pre-mrna leakage protein 1; PDBTitle: structure of the yeast pm11 splicing factor and its2 integration into the res complex
						PDB header: splicing

28	c3elsA	Alignment	not modelled	99.7	22	Chain: A; PDB Molecule: pre-mrna leakage protein 1; PDBTitle: crystal structure of yeast pml1p, residues 51-204
29	d2piea1	Alignment	not modelled	99.7	22	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
30	d1g6ga	Alignment	not modelled	99.7	22	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
31	c5t2sA	Alignment	not modelled	99.7	21	PDB header: cell cycle Chain: A; PDB Molecule: ddk kinase regulatory subunit dbf4,serine/threonine-protein PDBTitle: structure of the fha1 domain of rad53 bound simultaneously to the brct2 domain of dbf4 and a phosphopeptide.
32	d1lgpa	Alignment	not modelled	99.7	19	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
33	d1wlna1	Alignment	not modelled	99.7	13	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
34	c5djoB	Alignment	not modelled	99.6	8	PDB header: transport protein Chain: B; PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the cc1-fha tandem of kinesin-3 kif13a
35	d1g3ga	Alignment	not modelled	99.6	22	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
36	c6a8wA	Alignment	not modelled	99.6	26	PDB header: protein binding Chain: A; PDB Molecule: vacuolar protein sorting-associated protein 64; PDBTitle: crystal structure of the fha domain of far9
37	d1dmza	Alignment	not modelled	99.6	20	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
38	c5e50A	Alignment	not modelled	99.6	20	PDB header: lyase Chain: A; PDB Molecule: aprataxin and pnk-like factor; PDBTitle: aplf/xrcc4 complex
39	d2q1la1	Alignment	not modelled	99.6	16	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
40	d1yjma1	Alignment	not modelled	99.6	16	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
41	d1gxca	Alignment	not modelled	99.6	14	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
42	c1gxcA	Alignment	not modelled	99.6	14	PDB header: phosphoprotein-binding domain Chain: A; PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide PDB header: transferase Chain: C; PDB Molecule: 5' polynucleotide kinase-3' phosphatase fha domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
43	c1yj5C	Alignment	not modelled	99.6	14	PDB header: transport protein Chain: A; PDB Molecule: kinesin-like protein kif1b; PDBTitle: solution structure of the fha domain from human kinesin-2 like protein kif1b
44	c2eh0A	Alignment	not modelled	99.6	16	PDB header: transport protein Chain: A; PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem
45	c4eqxA	Alignment	not modelled	99.6	16	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
46	d1qu5a	Alignment	not modelled	99.6	18	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
47	d1ujxa	Alignment	not modelled	99.5	16	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
48	c3kt9A	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A; PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain
49	d2brfa1	Alignment	not modelled	99.5	18	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
50	c5z58X	Alignment	not modelled	99.5	21	PDB header: splicing Chain: X; PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
51	c4ejqB	Alignment	not modelled	99.4	17	PDB header: transport protein Chain: B; PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha
52	c3i0mA	Alignment	not modelled	99.1	25	PDB header: cell cycle Chain: A; PDB Molecule: dna repair and telomere maintenance protein nbs1; PDBTitle: structure of the s. pombe nbs1 fha/brct-repeat domain
53	c5xzvB	Alignment	not modelled	99.0	24	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase rad53; PDBTitle: crystal structure of rad53 1-466 in complex with amp-pnp
54	c3i6uA	Alignment	not modelled	98.8	18	PDB header: transferase Chain: A; PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: structure and activation mechanism of the chk2 dna-damage checkpoint2 kinase

55	c3i6wB_	Alignment	not modelled	98.6	19	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase chk2; PDBTitle: structure and activation mechanism of the chk2 dna-damage checkpoint2 kinase
56	c5fwhA_	Alignment	not modelled	98.3	12	PDB header: structural protein Chain: A: PDB Molecule: essc; PDBTitle: n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
57	c4zgiA_	Alignment	not modelled	97.4	16	PDB header: signaling protein Chain: A: PDB Molecule: traf-interacting protein with fha domain-containing protein PDBTitle: structure of truncated human tifa
58	c3uv0B_	Alignment	not modelled	95.9	19	PDB header: protein binding Chain: B: PDB Molecule: mutator 2, isoform b; PDBTitle: crystal structure of the drosophila mu2 fha domain
59	d1dm9a_	Alignment	not modelled	86.1	6	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd
60	c1dm9A_	Alignment	not modelled	86.1	6	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
61	c5z81A_	Alignment	not modelled	77.7	12	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 15; PDBTitle: trimeric structure of vibrio cholerae heat shock protein 15 at 2.32 angstrom resolution
62	c3egbA_	Alignment	not modelled	72.5	21	PDB header: protein binding Chain: A: PDB Molecule: protein pellino homolog 2; PDBTitle: structure of pellino2 fha domain at 3.3 angstroms resolution.
63	c3hvvB_	Alignment	not modelled	71.6	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
64	d1c06a_	Alignment	not modelled	71.2	19	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
65	c3j1wU_	Alignment	not modelled	69.0	15	PDB header: cell invasion Chain: U: PDB Molecule: protein prgh; PDBTitle: a refined model of the prototypical salmonella typhimurium t3ss basal2 body reveals the molecular basis for its assembly
66	d2uubd1	Alignment	not modelled	68.8	15	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
67	d1p9ka_	Alignment	not modelled	67.7	17	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
68	c5o5jD_	Alignment	not modelled	64.1	19	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
69	c2kmmA_	Alignment	not modelled	64.0	17	PDB header: hydrolase Chain: A: PDB Molecule: guanosine-3',5'-bis(diphosphate) 3'- PDBTitle: solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
70	c2k6pA_	Alignment	not modelled	63.4	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
71	c3bbnD_	Alignment	not modelled	63.2	8	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s4; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
72	c3dwmA_	Alignment	not modelled	62.9	27	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
73	c3po0A_	Alignment	not modelled	61.7	5	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
74	d1wxqa2	Alignment	not modelled	61.3	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
75	c3dh3C_	Alignment	not modelled	60.7	20	PDB header: isomerase/rna Chain: C: PDB Molecule: ribosomal large subunit pseudouridine synthase f; PDBTitle: crystal structure of rluf in complex with a 22 nucleotide rna2 substrate
76	d1fm0d_	Alignment	not modelled	60.6	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
77	d1vjka_	Alignment	not modelled	59.6	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
78	d1vioa2	Alignment	not modelled	57.7	8	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
79	d1xo3a_	Alignment	not modelled	56.6	5	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
80	c2qieB_	Alignment	not modelled	55.0	9	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in

						complex with precursor2 z
81	c1v8cA_	Alignment	not modelled	54.9	14	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
82	c3mmfE_	Alignment	not modelled	54.8	14	PDB header: hydrolase Chain: E: PDB Molecule: allophanate hydrolase subunit 2; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
83	d2gy9d1	Alignment	not modelled	54.7	23	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
84	d1h3fa2	Alignment	not modelled	54.3	21	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
85	c4xmmE_	Alignment	not modelled	50.6	11	PDB header: transport protein/immune system Chain: E: PDB Molecule: nucleoporin nup120; PDBTitle: structure of the yeast coat nucleoporin complex, space group c2
86	c2qjIA_	Alignment	not modelled	47.9	9	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
87	d1tkea1	Alignment	not modelled	46.4	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
88	c2k9xA_	Alignment	not modelled	46.0	9	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
89	c4n6eB_	Alignment	not modelled	45.8	21	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
90	d1jh3a_	Alignment	not modelled	45.8	18	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
91	c1kskA_	Alignment	not modelled	45.5	20	PDB header: lyase Chain: A: PDB Molecule: ribosomal small subunit pseudouridine synthase a; PDBTitle: structure of rsua
92	c6jzbD_	Alignment	not modelled	45.2	23	PDB header: transferase Chain: D: PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
93	d1v8ca1	Alignment	not modelled	44.7	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
94	d1wgka_	Alignment	not modelled	43.2	5	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: C9orf74 homolog
95	d1ryja_	Alignment	not modelled	43.2	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
96	c2g1eA_	Alignment	not modelled	42.2	7	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
97	c3hxrA_	Alignment	not modelled	42.1	11	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin nup120; PDBTitle: nucleoporin nup120 from s.cerevisiae (aa 1-757)
98	d1udxa3	Alignment	not modelled	41.7	44	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
99	c6jc0A_	Alignment	not modelled	41.4	15	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
100	c5dudA_	Alignment	not modelled	40.4	16	PDB header: unknown function Chain: A: PDB Molecule: ybgk; PDBTitle: crystal structure of e. coli ybgk
101	c1h3eA_	Alignment	not modelled	39.6	21	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from thermus thermophilus complexed with wild-2 type trnatyr(gua) and with atp and tyrosinol
102	c2m19A_	Alignment	not modelled	38.4	14	PDB header: protein binding Chain: A: PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
103	c4oudA_	Alignment	not modelled	38.1	21	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2,4,4-biphenylalanine
104	c3oepA_	Alignment	not modelled	37.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
105	c5mpoA_	Alignment	not modelled	36.1	9	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
106	c5i2rA_	Alignment	not modelled	34.8	28	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of fumarate hydratase from leishmania major

107	c3u7zA_	 Alignment	not modelled	33.8	19	PDB header: metal binding protein Chain: A: PDB Molecule: putative metal binding protein rumgna_00854; PDBTitle: crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
108	c2istA_	 Alignment	not modelled	33.1	16	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase d; PDBTitle: crystal structure of rlud from e. coli
109	d1o65a_	 Alignment	not modelled	31.2	31	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: MOSC (MOCO sulphurase C-terminal) domain
110	c2l52A_	 Alignment	not modelled	29.2	5	PDB header: protein binding Chain: A: PDB Molecule: methanosarcina acetivorans samp1 homolog; PDBTitle: solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
111	c5yhhA_	 Alignment	not modelled	27.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized conserved protein yiiim; PDBTitle: crystal structure of yiiim from geobacillus stearothermophilus
112	c2ekiA_	 Alignment	not modelled	27.0	16	PDB header: signaling protein Chain: A: PDB Molecule: developmentally-regulated gtp-binding protein 1; PDBTitle: solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
113	c5lo7B_	 Alignment	not modelled	26.2	17	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein myfa,fimbrial protein myfa; PDBTitle: crystal structure of self-complemented myfa, the major subunit of myf2 fimbriae from yersinia enterocolitica
114	d2je8a4	 Alignment	not modelled	25.7	14	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
115	d1jz8a3	 Alignment	not modelled	23.9	11	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
116	c3rpfC_	 Alignment	not modelled	23.2	9	PDB header: transferase Chain: C: PDB Molecule: molybdopterin converting factor, subunit 1 (moad); PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
117	c2janD_	 Alignment	not modelled	23.0	18	PDB header: ligase Chain: D: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
118	d1nyra2	 Alignment	not modelled	21.9	9	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain