

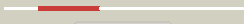



















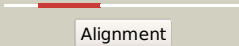







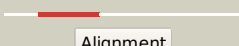

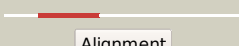

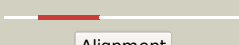




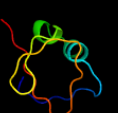



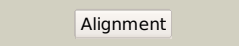
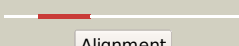
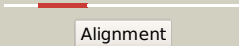



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0579 (-) _676241_676999
Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	e78cac8558fa98e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3po0A_	 Alignment		98.9	29	PDB header: protein binding Chain: A; PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
2	d1vjka_	 Alignment		98.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
3	c6jzbD_	 Alignment		98.6	24	PDB header: transferase Chain: D; PDB Molecule: moad/this family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
4	c2qieB_	 Alignment		98.6	17	PDB header: transferase Chain: B; PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
5	d1fm0d_	 Alignment		98.6	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: MoaD
6	c6jc0A_	 Alignment		98.5	18	PDB header: transferase Chain: A; PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
7	c5mpoA_	 Alignment		98.5	16	PDB header: transferase Chain: A; PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
8	c2qjlA_	 Alignment		98.4	24	PDB header: signaling protein Chain: A; PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
9	c4n6eB_	 Alignment		98.4	17	PDB header: lyase/biosynthetic protein Chain: B; PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
10	c2m19A_	 Alignment		98.4	23	PDB header: protein binding Chain: A; PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein
11	c3dwmA_	 Alignment		98.4	28	PDB header: transferase Chain: A; PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen

12	c2g1eA_	 Alignment		98.3	28	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
13	d1xo3a_	 Alignment		98.2	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
14	d1wgka_	 Alignment		98.1	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
15	c3rpfC_	 Alignment		98.0	20	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
16	c1v8cA_	 Alignment		98.0	18	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
17	c2I52A_	 Alignment		97.9	29	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
18	c2k9xA_	 Alignment		97.8	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
19	d1v8ca1	 Alignment		97.7	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: Moad
20	d1zud21	 Alignment		97.4	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
21	c3cwiA_	 Alignment	not modelled	96.8	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
22	c2kmmA_	 Alignment	not modelled	96.5	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)
23	c2hj1A_	 Alignment	not modelled	96.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
24	d2hj1a1	 Alignment	not modelled	96.5	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: HI0395-like
25	c3hvvB_	 Alignment	not modelled	96.5	20	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
26	c2ki0A_	 Alignment	not modelled	96.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
27	d2cu3a1	 Alignment	not modelled	96.3	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
						Fold: beta-Grasp (ubiquitin-like)

28	d1rwsa_	Alignment	not modelled	95.9	23	Superfamily: MoaD/ThiS Family: ThiS
29	d1tygb_	Alignment	not modelled	95.8	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
30	c1tygG_	Alignment	not modelled	95.1	14	PDB header: biosynthetic protein Chain: G; PDB Molecule: cyjbs; PDBTitle: structure of the thiazole synthase/this complex
31	d1wxqa2	Alignment	not modelled	94.8	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
32	d1tkea1	Alignment	not modelled	93.9	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
33	c3na7A_	Alignment	not modelled	93.8	32	PDB header: gene regulation, chaperone Chain: A; PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
34	c2k5cA_	Alignment	not modelled	92.8	21	PDB header: metal binding protein Chain: A; PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
35	c4dlpA_	Alignment	not modelled	91.7	15	PDB header: ligase Chain: A; PDB Molecule: aminoacyl-trna synthetase, class i:aminoacyl-trna PDBTitle: crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
36	c5gl7A_	Alignment	not modelled	91.3	19	PDB header: ligase Chain: A; PDB Molecule: methionine--trna ligase, cytoplasmic; PDBTitle: crystal structure of a truncated human cytosolic methionyl-trna2 synthetase
37	c5ghaF_	Alignment	not modelled	91.0	11	PDB header: transferase/transport protein Chain: F; PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
38	c2ekiA_	Alignment	not modelled	90.8	19	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
39	c3gn5B_	Alignment	not modelled	90.6	17	PDB header: dna binding protein Chain: B; PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
40	c5y3tC_	Alignment	not modelled	90.6	17	PDB header: ligase Chain: C; PDB Molecule: sharpin; PDBTitle: crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
41	c5xgqB_	Alignment	not modelled	90.6	21	PDB header: ligase Chain: B; PDB Molecule: methionine-trna ligase; PDBTitle: crystal structure of apo form (free-state) mycobacterium tuberculosis2 methionyl-trna synthetase
42	d1nyra2	Alignment	not modelled	89.8	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
43	c5urbB_	Alignment	not modelled	89.6	13	PDB header: ligase Chain: B; PDB Molecule: methionine--trna ligase; PDBTitle: crystal structure of methionyl-trna synthetase (metrs) from2 acinetobacter baumannii with bound l-methionine
44	c3kflA_	Alignment	not modelled	89.6	13	PDB header: ligase Chain: A; PDB Molecule: methionyl-trna synthetase; PDBTitle: leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
45	d1v5oa_	Alignment	not modelled	89.6	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
46	c2jxxA_	Alignment	not modelled	89.2	16	PDB header: protein binding Chain: A; PDB Molecule: nfatc2-interacting protein; PDBTitle: nmr solution structure of ubiquitin-like domain of2 nfatc2ip. northeast structural genomics consortium target3 hr5627
47	c5z81A_	Alignment	not modelled	88.7	25	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
48	c1rqgA_	Alignment	not modelled	88.6	22	PDB header: ligase Chain: A; PDB Molecule: methionyl-trna synthetase; PDBTitle: methionyl-trna synthetase from pyrococcus abyssi
49	c1tkeA_	Alignment	not modelled	88.2	15	PDB header: ligase Chain: A; PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
50	d1dm9a_	Alignment	not modelled	87.9	12	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kD
51	c1dm9A_	Alignment	not modelled	87.9	12	PDB header: structural genomics Chain: A; PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
52	c1wwtA_	Alignment	not modelled	87.4	8	PDB header: ligase Chain: A; PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
53	c2k6pA_	Alignment	not modelled	87.3	33	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein hp_1423; PDBTitle: solution structure of hypothetical protein, hp1423
54	c2ietA_	Alignment	not modelled	87.1	18	PDB header: isomerase Chain: A; PDB Molecule: ribosomal large subunit pseudouridine

54	c2b5A_	Alignment	not modelled	87.1	18	synthase d; PDB header: crystal structure of rlud from e. coli
55	c1pfuA_	Alignment	not modelled	86.9	15	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
56	d1wm3a_	Alignment	not modelled	86.7	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
57	c5jp1B_	Alignment	not modelled	86.6	15	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
58	c4iloA_	Alignment	not modelled	86.0	32	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
59	c5y3tA_	Alignment	not modelled	85.3	23	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hetero-trimeric core of lubac: hoip double-uba2 complexed with hoil-1l ubl and sharpin ubl
60	c1u0bB_	Alignment	not modelled	84.1	26	PDB header: ligase/rna Chain: B: PDB Molecule: cysteiny l trna; PDBTitle: crystal structure of cysteiny l-trna synthetase binary2 complex with trnacys
61	c2k5rA_	Alignment	not modelled	83.5	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein xf2673; PDBTitle: solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
62	d1ryja_	Alignment	not modelled	83.4	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: This
63	c3c8zB_	Alignment	not modelled	83.2	16	PDB header: ligase Chain: B: PDB Molecule: cysteiny l-trna synthetase; PDBTitle: the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
64	c2js4A_	Alignment	not modelled	82.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein bb2007; PDBTitle: solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
65	c2ekeC_	Alignment	not modelled	82.8	15	PDB header: ligase/protein binding Chain: C: PDB Molecule: ubiquitin-like protein smt3; PDBTitle: structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
66	c1woyA_	Alignment	not modelled	82.4	18	PDB header: ligase Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
67	c2gb5B_	Alignment	not modelled	82.3	18	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
68	d2uyzb1	Alignment	not modelled	81.7	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
69	d1we7a_	Alignment	not modelled	81.5	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
70	c2jr6A_	Alignment	not modelled	81.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein nma0874; PDBTitle: solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
71	d1wjua_	Alignment	not modelled	81.4	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
72	d1wgga_	Alignment	not modelled	80.9	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
73	c2mqjA_	Alignment	not modelled	80.0	19	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like protein; PDBTitle: solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
74	c5f4hF_	Alignment	not modelled	79.8	11	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
75	d2uubd1	Alignment	not modelled	79.7	46	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
76	d1c06a_	Alignment	not modelled	79.7	42	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
77	c4k95G_	Alignment	not modelled	79.4	13	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
78	d2jnva1	Alignment	not modelled	78.8	21	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
79	c2n7dA_	Alignment	not modelled	78.6	21	PDB header: unknown function Chain: A: PDB Molecule: protein ddi1 homolog 2; PDBTitle: solution structure of the ubl domain of human ddi2

80	c4eqxA	Alignment	not modelled	78.6	27	PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a cc1-fha tandem
81	c6f5zC	Alignment	not modelled	78.3	11	PDB header: transferase Chain: C: PDB Molecule: upf0434 family protein; PDBTitle: complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
82	c4dbgA	Alignment	not modelled	78.3	21	PDB header: ligase Chain: A: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of hoil-1-ubl complexed with a hoip-uba derivative
83	c3bbnD	Alignment	not modelled	78.2	46	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.
84	d1wz0a1	Alignment	not modelled	78.0	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
85	c3goeA	Alignment	not modelled	77.5	21	PDB header: recombination, replication Chain: A: PDB Molecule: dna repair protein rad60; PDBTitle: molecular mimicry of sumo promotes dna repair
86	c2hu9B	Alignment	not modelled	77.4	22	PDB header: metal transport Chain: B: PDB Molecule: mercuric transport protein periplasmic component; PDBTitle: x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
87	c4dlpB	Alignment	not modelled	77.0	25	PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase, class i:aminoacyl-trna PDBTitle: crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
88	d1ud7a	Alignment	not modelled	77.0	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
89	d1j8ca	Alignment	not modelled	77.0	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
90	c4qrdA	Alignment	not modelled	76.7	22	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: structure of methionyl-trna synthetase in complex with n-(1h-2 benzimidazol-2-ylmethyl)-n'-(2,4-dichlorophenyl)-6-(morpholin-4-yl)-3,1,3,5-triazine-2,4-diamine
91	c5ijlA	Alignment	not modelled	76.5	32	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
92	c3a44D	Alignment	not modelled	76.3	23	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
93	c3m62B	Alignment	not modelled	76.3	17	PDB header: ligase/protein binding Chain: B: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
94	d2g1la1	Alignment	not modelled	76.2	27	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
95	c3a4rB	Alignment	not modelled	76.2	13	PDB header: transcription Chain: B: PDB Molecule: nfatc2-interacting protein; PDBTitle: the crystal structure of sumo-like domain 2 in nip45
96	c5gjlA	Alignment	not modelled	75.7	21	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sumo from plasmodium falciparum
97	c5xmjl	Alignment	not modelled	75.7	12	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
98	c5ywwA	Alignment	not modelled	75.6	12	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
99	c2eh0A	Alignment	not modelled	75.6	27	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
100	c3twkB	Alignment	not modelled	75.5	7	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
101	c5djoB	Alignment	not modelled	75.4	32	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the cc1-fha tandem of kinesin-3 kif13a
102	d1p9ka	Alignment	not modelled	75.0	20	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: YbcJ-like
103	d1z2ma1	Alignment	not modelled	74.9	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
104	c1nyqA	Alignment	not modelled	74.8	13	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase 1; PDBTitle: structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna

105	c6hmsB_	Alignment	not modelled	74.8	29	polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
106	c1wxqA_	Alignment	not modelled	74.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
107	c5o5jD_	Alignment	not modelled	74.7	38	PDB header: ribosome Chain: D: PDB Molecule: 30s ribosomal protein s4; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
108	c4idiA_	Alignment	not modelled	74.4	14	PDB header: protein binding Chain: A: PDB Molecule: oryza sativa rum1-related; PDBTitle: crystal structure of rum1-related protein from plasmodium yoelii,2 py06420
109	c4ejqB_	Alignment	not modelled	73.8	23	PDB header: transport protein Chain: B: PDB Molecule: kinesin-like protein kif1a; PDBTitle: crystal structure of kif1a c-cc1-fha
110	d1ileA3	Alignment	not modelled	73.6	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
111	c3tixA_	Alignment	not modelled	73.4	11	PDB header: gene regulation/protein binding Chain: A: PDB Molecule: ubiquitin-like protein smt3,rna-induced transcriptional PDBTitle: crystal structure of the chp1-tas3 complex core
112	c1yx5B_	Alignment	not modelled	73.4	22	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
113	c5xqmA_	Alignment	not modelled	73.2	12	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin-related modifier; PDBTitle: nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
114	d1wx7a1	Alignment	not modelled	73.0	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
115	c2kd0A_	Alignment	not modelled	72.9	19	PDB header: signaling protein Chain: A: PDB Molecule: lrr repeats and ubiquitin-like domain-containing PDBTitle: nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
116	c3ziuB_	Alignment	not modelled	72.7	25	PDB header: ligase Chain: B: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site
117	d2gy9d1	Alignment	not modelled	72.5	29	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ribosomal protein S4
118	d1o4wa_	Alignment	not modelled	72.5	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
119	c2x1lC_	Alignment	not modelled	72.5	31	PDB header: ligase Chain: C: PDB Molecule: methionyl-trna synthetase; PDBTitle: crystal structure of mycobacterium smegmatis methionyl-trna synthetase2 in complex with methionine and adenosine
120	c1v8pK_	Alignment	not modelled	72.3	26	PDB header: structural genomics, unknown function Chain: K: PDB Molecule: hypothetical protein pae2754; PDBTitle: crystal structure of pae2754 from pyrobaculum aerophilum