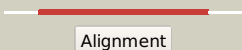







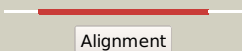

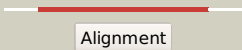



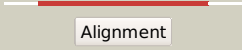


















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2683 (-)_3000122_3000619
Date	Wed Aug 7 12:50:33 BST 2019
Unique Job ID	9428e0d59fc7553d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nocA_	 Alignment		100.0	53	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein with cbs domains; PDBTitle: the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
2	d2d4za3	 Alignment		99.9	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
3	c6cozB_	 Alignment		99.9	14	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
4	c2d4zB_	 Alignment		99.9	14	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
5	d2j9la1	 Alignment		99.9	11	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
6	c4esyB_	 Alignment		99.9	19	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain containing membrane protein; PDBTitle: crystal structure of the cbs domain of cbs domain containing membrane2 protein from sphaerobacter thermophilus
7	c3fwrB_	 Alignment		99.9	13	PDB header: transcription Chain: B: PDB Molecule: yqzb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
8	c4l3vB_	 Alignment		99.9	17	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
9	c2qh1B_	 Alignment		99.9	24	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ta0289; PDBTitle: structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
10	d2ooxe1	 Alignment		99.9	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
11	c4o9kB_	 Alignment		99.9	21	PDB header: isomerase Chain: B: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: crystal structure of the cbs pair of a putative d-arabinose 5-2 phosphate isomerase from methylococcus capsulatus in complex with3 cmp-kdo

12	d3ddja1	Alignment		99.9	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
13	d2yzia1	Alignment		99.9	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
14	c5tr1A_	Alignment		99.9	15	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein; PDBTitle: cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation
15	d2v8qe2	Alignment		99.9	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
16	c6qvcB_	Alignment		99.9	18	PDB header: membrane protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
17	c2v8qE_	Alignment		99.9	18	PDB header: transferase Chain: E: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
18	d1o50a3	Alignment		99.9	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
19	c2qlvF_	Alignment		99.9	21	PDB header: transferase/protein binding Chain: F: PDB Molecule: nuclear protein snf4; PDBTitle: crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1
20	c6h1wA_	Alignment		99.9	13	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii
21	c2qr1E_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: E: PDB Molecule: protein c1556.08c; PDBTitle: crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
22	c2pfiA_	Alignment	not modelled	99.9	10	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein clc-ka; PDBTitle: crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
23	c5aweA_	Alignment	not modelled	99.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetoin utilization protein, acetoin PDBTitle: crystal structure of a hypothetical protein, ttha0829 from thermus2 thermophilus hb8, composed of cystathionine-beta-synthase (cbs) and3 aspartate-kinase chorismate-mutase tyra (act) domains
24	d1y5ha3	Alignment	not modelled	99.9	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
25	c5nmuC_	Alignment	not modelled	99.9	22	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
26	c3pc3A_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
27	c5ohxB_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
28	c3sl7B_	Alignment	not modelled	99.9	19	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from

						arabidopsis thaliana
29	c4fryA	Alignment	not modelled	99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: putative signal-transduction protein with cbs domains; PDBTitle: the structure of a putative signal-transduction protein with cbs2 domains from burkholderia ambifaria mc40-6
30	c2emqA	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
31	d2ooxe2	Alignment	not modelled	99.9	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
32	d2yzqa1	Alignment	not modelled	99.9	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
33	c2p9mD	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0922; PDBTitle: crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
34	d2rc3a1	Alignment	not modelled	99.9	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
35	c3lfrB	Alignment	not modelled	99.9	14	PDB header: transport protein Chain: B: PDB Molecule: putative metal ion transporter; PDBTitle: the crystal structure of a cbs domain from a putative metal ion2 transporter bound to amp from pseudomonas syringae to 1.55a
36	d2o16a3	Alignment	not modelled	99.9	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
37	d1pvma4	Alignment	not modelled	99.9	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
38	c3kh5A	Alignment	not modelled	99.9	25	PDB header: unknown function Chain: A: PDB Molecule: protein mj1225; PDBTitle: crystal structure of protein mj1225 from methanocaldococcus2 jannaschii, a putative archaeal homolog of g-ampk.
39	c3fnaA	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: A: PDB Molecule: possible arabinose 5-phosphate isomerase; PDBTitle: crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
40	c3hf7A	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cbs-domain protein; PDBTitle: the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
41	c2ouxB	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
42	d1vr9a3	Alignment	not modelled	99.9	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
43	c1zfa	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
44	c3i8nB	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp2912; PDBTitle: a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
45	d1pbja3	Alignment	not modelled	99.9	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
46	c3lhaA	Alignment	not modelled	99.9	18	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
47	d2v8qe1	Alignment	not modelled	99.9	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
48	c3fhmD	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function, n Chain: D: PDB Molecule: uncharacterized protein atu1752; PDBTitle: crystal structure of the cbs-domain containing protein atu1752 from2 agrobacterium tumefaciens
49	c1vr9B	Alignment	not modelled	99.9	17	PDB header: unknown function Chain: B: PDB Molecule: cbs domain protein/act domain protein; PDBTitle: crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
50	c3gbyA	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ct1051; PDBTitle: crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
51	c3lqnA	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
52	c3orgB	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
53	c3lv9A	Alignment	not modelled	99.9	18	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630 PDB header: oxidoreductase

54	c4z87B_	Alignment	not modelled	99.8	21	Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
55	c3ocmA_	Alignment	not modelled	99.8	21	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
56	c3l31B_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: B: PDB Molecule: probable manganase-dependent inorganic PDBTitle: crystal structure of the cbs and drtg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
57	c5ks7A_	Alignment	not modelled	99.8	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: carnitine transport atp-binding protein opuca; PDBTitle: crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
58	c3jtfB_	Alignment	not modelled	99.8	13	PDB header: transport protein Chain: B: PDB Molecule: magnesium and cobalt efflux protein; PDBTitle: the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
59	c3ctuB_	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
60	c1yavB_	Alignment	not modelled	99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein ykul2 from bacillus subtilis
61	d1yava3	Alignment	not modelled	99.8	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
62	d2nyca1	Alignment	not modelled	99.8	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
63	c5x8oA_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
64	d2ef7a1	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
65	d2ouxax2	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
66	c3nqrD_	Alignment	not modelled	99.8	15	PDB header: transport protein Chain: D: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: a putative cbs domain-containing protein from salmonella typhimurium2 lt2
67	c3tsdA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
68	c4gqvA_	Alignment	not modelled	99.8	25	PDB header: protein binding Chain: A: PDB Molecule: cbs domain-containing protein cbsx1, chloroplastic; PDBTitle: crystal structure of cbs-pair protein, cbsx1 from arabidopsis thaliana
69	c3kpbA_	Alignment	not modelled	99.8	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0100; PDBTitle: crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
70	c4iy3B_	Alignment	not modelled	99.8	15	PDB header: metal transport Chain: B: PDB Molecule: metal transporter cnm4; PDBTitle: structural and ligand binding properties of the bateman domain of2 human magnesium transporters cnm2 and cnm4
71	c2yvzA_	Alignment	not modelled	99.8	25	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
72	c5iipA_	Alignment	not modelled	99.8	15	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
73	c3ocoB_	Alignment	not modelled	99.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hemolysin-like protein containing cbs domains; PDBTitle: the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
74	c3ocmB_	Alignment	not modelled	99.8	23	PDB header: membrane protein Chain: B: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
75	d2riha1	Alignment	not modelled	99.8	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	c2yvxD_	Alignment	not modelled	99.8	26	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
77	c4hg0A_	Alignment	not modelled	99.8	14	PDB header: transport protein Chain: A: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40 PDB header: hydrolase

78	c5g5rA_	Alignment	not modelled	99.8	18	Chain: A: PDB Molecule: site-2 protease; PDBTitle: cbs domain tandem of site-2 protease from archaeoglobus fulgidus in2 complex with llama nanobody - apo form
79	c4qfsC_	Alignment	not modelled	99.8	13	PDB header: signaling protein/inhibitor/activator Chain: C: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: structure of ampk in complex with br2-a769662core activator and2 staurosporine inhibitor
80	d1zfja4	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
81	c3kxrA_	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: A: PDB Molecule: magnesium transporter, putative; PDBTitle: structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
82	c3ddja_	Alignment	not modelled	99.8	19	PDB header: amp-binding protein Chain: A: PDB Molecule: cbs domain-containing protein; PDBTitle: crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
83	d3ddja2	Alignment	not modelled	99.8	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
84	c4dqwb_	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
85	c3oi8B_	Alignment	not modelled	99.7	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
86	d2yvxa2	Alignment	not modelled	99.7	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
87	c2yzqA_	Alignment	not modelled	99.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
88	d2yzqa2	Alignment	not modelled	99.7	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
89	c4fxsA_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
90	c3fioB_	Alignment	not modelled	99.2	17	PDB header: nucleotide binding protein, metal bindin Chain: B: PDB Molecule: a cystathionine beta-synthase domain protein PDBTitle: crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
91	d1jcna4	Alignment	not modelled	99.0	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
92	d1jr1a4	Alignment	not modelled	98.4	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
93	d2a29a1	Alignment	not modelled	73.8	22	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
94	d1lcy2	Alignment	not modelled	60.4	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
95	c3nziA_	Alignment	not modelled	58.8	10	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
96	c3stiC_	Alignment	not modelled	56.3	10	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli
97	c3nwuB_	Alignment	not modelled	55.6	10	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
98	d2qf3a1	Alignment	not modelled	54.4	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
99	d1ky9a2	Alignment	not modelled	53.4	10	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
100	c3k6zA_	Alignment	not modelled	53.3	15	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
101	c2w5eB_	Alignment	not modelled	52.1	19	PDB header: hydrolase Chain: B: PDB Molecule: putative serine protease; PDBTitle: structural and biochemical analysis of human pathogenic2 astrovirus serine protease at 2.0 angstrom resolution
102	d2z9ia2	Alignment	not modelled	52.0	10	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
103	d1p0za_	Alignment	not modelled	50.5	13	Fold: Profilin-like Superfamily: Sensory domain-like

						Family: Sensory domain of two-component sensor kinase
104	c5y28B_	Alignment	not modelled	50.0	10	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
105	c6o6dA_	Alignment	not modelled	48.4	7	PDB header: ligase Chain: A: PDB Molecule: translation initiation factor if-3; PDBTitle: n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
106	d1l1ja_	Alignment	not modelled	47.2	10	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
107	c4mjsQ_	Alignment	not modelled	45.0	25	PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
108	c5hmaA_	Alignment	not modelled	44.1	10	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like serine protease; PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
109	c4ic5B_	Alignment	not modelled	43.5	15	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
110	c2arfA_	Alignment	not modelled	42.8	16	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
111	c3faoA_	Alignment	not modelled	40.3	33	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein; PDBTitle: crystal structure of s118a mutant 3clsp of prrsv
112	d3by8a1	Alignment	not modelled	40.1	19	Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
113	c5ilaA_	Alignment	not modelled	39.4	18	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
114	c2rcel_	Alignment	not modelled	39.2	12	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
115	c2vidA_	Alignment	not modelled	37.6	12	PDB header: hydrolase Chain: A: PDB Molecule: serine protease splb; PDBTitle: serine protease splb from staphylococcus aureus at 1.8a resolution
116	c5mm8A_	Alignment	not modelled	36.1	15	PDB header: hydrolase Chain: A: PDB Molecule: serine protease sple; PDBTitle: atomic resolution structure of sple protease from staphylococcus2 aureus
117	c5c2zA_	Alignment	not modelled	35.8	12	PDB header: toxin Chain: A: PDB Molecule: exfoliative toxin d2; PDBTitle: molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
118	c2w7uC_	Alignment	not modelled	35.1	15	PDB header: hydrolase Chain: C: PDB Molecule: serine protease spla; PDBTitle: spla serine protease of staphylococcus aureus (2.4a)
119	d1tifa_	Alignment	not modelled	34.7	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
120	c2as9B_	Alignment	not modelled	34.5	18	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus