

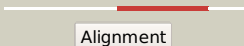

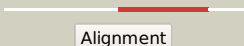



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1841c (-) _2089688_2090725
Date	Fri Aug 2 13:30:45 BST 2019
Unique Job ID	72bcfb4e1d807da0

Detailed template information

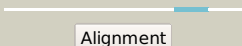
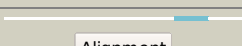
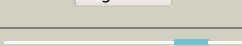
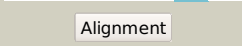
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hg0A_	 Alignment		100.0	25	PDB header: transport protein Chain: A: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40
2	c3ocmA_	 Alignment		100.0	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
3	c3ocmB_	 Alignment		100.0	21	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
4	c3oi8B_	 Alignment		99.9	25	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
5	c3ocoB_	 Alignment		99.9	25	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
6	c3lhhA_	 Alignment		99.9	23	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
7	c3lv9A_	 Alignment		99.9	22	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
8	c4iy3B_	 Alignment		99.9	28	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
9	c3lfrB_	 Alignment		99.9	30	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
10	c3jtfB_	 Alignment		99.9	31	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
11	c3i8nB_	 Alignment		99.9	28	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.

12	c3hf7A_	Alignment		99.9	23	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
13	c3kxrA_	Alignment		99.9	14	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.
14	c6qvcB_	Alignment		99.9	16	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
15	c2yvxD_	Alignment		99.9	22	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
16	c5tr1A_	Alignment		99.9	17	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
17	c2ouxB_	Alignment		99.9	16	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
18	c6h1wA_	Alignment		99.9	17	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii
19	c3ctuB_	Alignment		99.9	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
20	c3orgB_	Alignment		99.9	15	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
21	c2yvzA_	Alignment	not modelled	99.8	20	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
22	c3nqrD_	Alignment	not modelled	99.8	26	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
23	c1yavB_	Alignment	not modelled	99.8	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yku12 from bacillus subtilis
24	c1zfvA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
25	c3sl7B_	Alignment	not modelled	99.8	22	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
26	c3lqnA_	Alignment	not modelled	99.8	17	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
27	d2ooxe1	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
28	d2nyca1	Alignment	not modelled	99.8	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair PDB header: lyase

29	c4l3vB_	Alignment	not modelled	99.8	20	Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
30	c2qh1B_	Alignment	not modelled	99.8	20	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
31	c2emqA_	Alignment	not modelled	99.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
32	c3tsdA_	Alignment	not modelled	99.8	15	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
33	c6cozB_	Alignment	not modelled	99.8	23	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
34	d1yava3	Alignment	not modelled	99.8	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
35	c4gqvA_	Alignment	not modelled	99.8	20	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
36	d2ouxax2	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
37	c4z87B_	Alignment	not modelled	99.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
38	d1vr9a3	Alignment	not modelled	99.8	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
39	d2d4za3	Alignment	not modelled	99.8	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
40	c1vr9B_	Alignment	not modelled	99.8	22	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
41	c4o9kB_	Alignment	not modelled	99.8	18	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
42	d1zfja4	Alignment	not modelled	99.8	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
43	c3fnaA_	Alignment	not modelled	99.8	13	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
44	d2j9la1	Alignment	not modelled	99.8	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
45	c5x8oA_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
46	d3ddja1	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
47	c3pc3A_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
48	d2yzia1	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
49	c5nmuC_	Alignment	not modelled	99.8	10	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
50	d2v8qe2	Alignment	not modelled	99.8	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
51	c3fwrB_	Alignment	not modelled	99.7	20	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
52	c2d4zB_	Alignment	not modelled	99.7	24	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
53	c5ks7A_	Alignment	not modelled	99.7	13	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
54	d2v8qe1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
55	d2yzqa1	Alignment	not modelled	99.7	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
56	c2p9mD_	Alignment	not modelled	99.7	16	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
57	c3kpbA_	Alignment	not modelled	99.7	21	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.
58	d2ooxe2	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
59	d2ef7a1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
60	d1y5ha3	Alignment	not modelled	99.7	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	d1pvma4	Alignment	not modelled	99.7	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
62	d1o50a3	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
63	c4esyB_	Alignment	not modelled	99.7	23	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
64	c2qr1E_	Alignment	not modelled	99.7	18	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
65	c4frvA_	Alignment	not modelled	99.7	16	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
66	c3gbyA_	Alignment	not modelled	99.7	17	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
67	d2rc3a1	Alignment	not modelled	99.7	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
68	d2o16a3	Alignment	not modelled	99.7	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
69	c2qlvF_	Alignment	not modelled	99.7	22	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
70	c4nocA_	Alignment	not modelled	99.7	21	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.
71	d2yvxa2	Alignment	not modelled	99.7	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
72	c5ohxB_	Alignment	not modelled	99.7	11	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
73	c2v8qE_	Alignment	not modelled	99.7	22	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
74	c5aweA_	Alignment	not modelled	99.7	19	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
75	c4dqwb_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
76	d2riha1	Alignment	not modelled	99.7	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
77	d1pbja3	Alignment	not modelled	99.6	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
78	c2pfiA_	Alignment	not modelled	99.6	12	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

79	c3fhmD_	Alignment	not modelled	99.6	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
80	c5iipA_	Alignment	not modelled	99.6	16	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
81	c5g5rA_	Alignment	not modelled	99.6	21	PDB header: hydrolase 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
82	d3ddja2	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
83	d2yzqa2	Alignment	not modelled	99.5	22	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
84	c3kh5A_	Alignment	not modelled	99.5	22	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.
85	c3ddja_	Alignment	not modelled	99.5	14	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
86	c4qfsC_	Alignment	not modelled	99.5	18	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
87	c2yzqA_	Alignment	not modelled	99.5	19	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	c3l31B_	Alignment	not modelled	99.4	19	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
89	c4fxsA_	Alignment	not modelled	99.4	18	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	98.1	14	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	98.0	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
92	d1jr1a4	Alignment	not modelled	97.6	29	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
93	d1lcya2	Alignment	not modelled	56.5	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
94	c3k6zA_	Alignment	not modelled	54.8	36	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
95	c3nwuB_	Alignment	not modelled	54.6	21	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
96	c3nziA_	Alignment	not modelled	52.6	20	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
97	c2rceI_	Alignment	not modelled	51.5	14	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
98	d2qf3a1	Alignment	not modelled	51.0	14	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
99	c5y28B_	Alignment	not modelled	50.1	21	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
100	d1p0za_	Alignment	not modelled	49.1	12	Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
101	d1ky9a2	Alignment	not modelled	48.3	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
102	d1l1ja_	Alignment	not modelled	47.7	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
103	c4ic5B_	Alignment	not modelled	47.4	14	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5

104	c3stiC_	 Alignment	not modelled	45.8	21	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli
105	c3ia1A_	 Alignment	not modelled	45.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thio-disulfide isomerase/thioredoxin; PDBTitle: crystal structure of thio-disulfide isomerase from thermus2 thermophilus
106	c3lwaA_	 Alignment	not modelled	41.0	13	PDB header: isomerase Chain: A: PDB Molecule: secreted thiol-disulfide isomerase; PDBTitle: the crystal structure of a secreted thiol-disulfide isomerase from2 corynebacterium glutamicum to 1.75a
107	d3by8a1	 Alignment	not modelled	40.0	25	Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
108	c2arfA_	 Alignment	not modelled	39.7	26	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
109	c1ky9A_	 Alignment	not modelled	39.6	21	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
110	c5hmaA_	 Alignment	not modelled	39.4	21	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like serine protease; PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
111	d2z9ia2	 Alignment	not modelled	39.0	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
112	c2w5eB_	 Alignment	not modelled	38.2	20	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
113	c6o6dA_	 Alignment	not modelled	37.7	24	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
114	c4ic6A_	 Alignment	not modelled	36.8	14	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
115	d2a29a1	 Alignment	not modelled	36.1	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
116	c2ejbA_	 Alignment	not modelled	34.3	15	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
117	d1y0na_	 Alignment	not modelled	33.9	13	Fold: YehU-like Superfamily: YehU-like Family: YehU-like
118	c2r3yC_	 Alignment	not modelled	33.2	14	PDB header: hydrolase/hydrolase activator Chain: C: PDB Molecule: protease degs; PDBTitle: crystal structure of the degs protease in complex with the2 ywf activating peptide
119	c3otpF_	 Alignment	not modelled	33.1	21	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
120	c5ilaA_	 Alignment	not modelled	33.0	29	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain