

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0362_(mgtE)_439872_441254
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yvxD_	Alignment		100.0	36	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgtE; PDBTitle: crystal structure of magnesium transporter mgtE
2	c2ouxB_	Alignment		100.0	27	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
3	d2yvxa3	Alignment		100.0	46	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
4	c2yvzA_	Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgtE; PDBTitle: crystal structure of magnesium transporter mgtE cytosolic domain,2 mg2+-free form
5	c3kxrA_	Alignment		100.0	17	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.
6	d2oux2	Alignment		99.9	35	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
7	d2yvxa2	Alignment		99.9	36	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
8	d2oux1	Alignment		99.8	18	Fold: alpha-alpha superhelix Superfamily: MgtE N-terminal domain-like Family: MgtE N-terminal domain-like
9	d1vr9a3	Alignment		99.8	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
10	c5x8oA_	Alignment		99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
11	c1vr9B_	Alignment		99.8	20	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

12	c2qh1B_	Alignment		99.8	21	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
13	c3ocmB_	Alignment		99.8	16	PDB header: membrane protein Chain: B: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of f2 bordetella parapertussis
14	c3ocmA_	Alignment		99.8	16	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of f2 bordetella parapertussis
15	c3oi8B_	Alignment		99.8	15	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
16	d1pvma4	Alignment		99.8	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
17	d3ddja1	Alignment		99.8	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
18	c4hg0A_	Alignment		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
19	c4l3vB_	Alignment		99.8	15	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
20	c1zfa_	Alignment		99.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (imph; ec 1.1.1.205) from2 streptococcus pyogenes
21	c5nmuC_	Alignment	not modelled	99.7	20	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
22	c3jtfB_	Alignment	not modelled	99.7	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
23	c4z87B_	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
24	d2yvxa1	Alignment	not modelled	99.7	20	Fold: alpha-alpha superhelix Superfamily: MgtE N-terminal domain-like Family: MgtE N-terminal domain-like
25	d2d4za3	Alignment	not modelled	99.7	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
26	d2ef7a1	Alignment	not modelled	99.7	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
27	c5ks7A_	Alignment	not modelled	99.7	23	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
28	c6cozB_	Alignment	not modelled	99.7	19	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic

					domain
29	c3ocoB	Alignment	not modelled	99.7	16 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
30	c3tsdA	Alignment	not modelled	99.7	17 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
31	c3i8nB	Alignment	not modelled	99.7	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.
32	c3sl7B	Alignment	not modelled	99.7	27 PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
33	c3lv9A	Alignment	not modelled	99.7	19 PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
34	c5tr1A	Alignment	not modelled	99.7	16 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
35	c3lhhA	Alignment	not modelled	99.7	14 PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
36	c3gbyA	Alignment	not modelled	99.7	15 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
37	d2j9la1	Alignment	not modelled	99.7	24 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
38	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.
39	d1y5ha3	Alignment	not modelled	99.7	24 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
40	c3hf7A	Alignment	not modelled	99.7	13 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	c4qqvA	Alignment	not modelled	99.7	31 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
42	c3kpbA	Alignment	not modelled	99.7	19 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.
43	c4esyB	Alignment	not modelled	99.7	18 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
44	c3fnaA	Alignment	not modelled	99.7	16 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
45	c4iy3B	Alignment	not modelled	99.7	13 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
46	d2yzqa1	Alignment	not modelled	99.7	18 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
47	c3fwrB	Alignment	not modelled	99.7	16 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
48	c2d4zB	Alignment	not modelled	99.7	16 PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
49	d2yzia1	Alignment	not modelled	99.7	15 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
50	c5aweA	Alignment	not modelled	99.7	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
51	d1o50a3	Alignment	not modelled	99.7	20 Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
52	c3nc3A	Alignment	not modelled	99.7	16 PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a;

52	c3pcaA	Alignment	not modelled	99.7	10	PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
53	d2o16a3	Alignment	not modelled	99.7	26	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
54	c3nqrD	Alignment	not modelled	99.7	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
55	c3lfrB	Alignment	not modelled	99.7	11	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
56	c1yavB	Alignment	not modelled	99.7	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yukul2 from bacillus subtilis
57	d2nyca1	Alignment	not modelled	99.7	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
58	d1zfa4	Alignment	not modelled	99.7	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
59	c6qvcB	Alignment	not modelled	99.7	15	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
60	c4o9kB	Alignment	not modelled	99.7	17	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
61	d1yava3	Alignment	not modelled	99.6	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
62	c3orgB	Alignment	not modelled	99.6	20	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
63	c2p9mD	Alignment	not modelled	99.6	17	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
64	c5ohxB	Alignment	not modelled	99.6	13	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
65	c2emqA	Alignment	not modelled	99.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
66	c5g5rA	Alignment	not modelled	99.6	28	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
67	c4fryA	Alignment	not modelled	99.6	20	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
68	d1pbja3	Alignment	not modelled	99.6	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
69	c2qlvF	Alignment	not modelled	99.6	15	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	c2v8qE	Alignment	not modelled	99.6	15	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
71	d2ooxe1	Alignment	not modelled	99.6	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
72	c3lqnA	Alignment	not modelled	99.6	16	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
73	c2qr1E	Alignment	not modelled	99.6	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
74	c3ctuB	Alignment	not modelled	99.6	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
75	d2ooxe2	Alignment	not modelled	99.6	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
76	d2rc3a1	Alignment	not modelled	99.6	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
77	d2v8qe1	Alignment	not modelled	99.6	13	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair

78	c5iipA_	Alignment	not modelled	99.6	27	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
79	d2v8qe2	Alignment	not modelled	99.6	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
80	d2riha1	Alignment	not modelled	99.6	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
81	d3ddja2	Alignment	not modelled	99.5	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
82	c4dqwb_	Alignment	not modelled	99.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
83	c3ddjA_	Alignment	not modelled	99.5	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
84	c2pfiA_	Alignment	not modelled	99.5	17	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
85	c3kh5A_	Alignment	not modelled	99.5	37	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.
86	c3l31B_	Alignment	not modelled	99.5	27	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
87	d2yzqa2	Alignment	not modelled	99.5	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
88	c3fhmD_	Alignment	not modelled	99.5	28	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
89	c2yzqA_	Alignment	not modelled	99.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
90	c4qfsC_	Alignment	not modelled	99.4	19	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
91	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
92	d1lkvx_	Alignment	not modelled	99.3	13	Fold: alpha-alpha superhelix Superfamily: FlIG Family: FlIG
93	c3pkrA_	Alignment	not modelled	99.3	11	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 86-343) from h. pylori
94	c3pl4A_	Alignment	not modelled	98.7	14	PDB header: motor protein Chain: A: PDB Molecule: flagellar motor switch protein; PDBTitle: crystal structure of flig (residue 116-343) from h. pylori
95	d1jcna4	Alignment	not modelled	98.2	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
96	c3hjlA_	Alignment	not modelled	98.2	18	PDB header: proton transport Chain: A: PDB Molecule: flagellar motor switch protein flig; PDBTitle: the structure of full-length flig from aquifex aeolicus
97	c3fioB_	Alignment	not modelled	98.0	22	PDB header: nucleotide binding protein, metal bindin Chain: B: PDB Molecule: z 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
98	d1jr1a4	Alignment	not modelled	97.5	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
99	c5wujB_	Alignment	not modelled	96.2	16	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: crystal structure of flif-flig complex from h. pylori
100	c3sohB_	Alignment	not modelled	92.9	17	PDB header: motor protein Chain: B: PDB Molecule: flagellar motor switch protein flig; PDBTitle: architecture of the flagellar rotor
101	c6ajjA_	Alignment	not modelled	88.2	15	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmpl3 from mycobacterium2 smegmatis complexed with ica38
102	d1qc7b_	Alignment	not modelled	85.1	15	Fold: alpha-alpha superhelix Superfamily: FlIG Family: FlIG

103	d1qc7a_	Alignment	not modelled	84.1	15	Fold: alpha-alpha superhelix Superfamily: FliG Family: FliG
104	c5tdyD_	Alignment	not modelled	84.0	15	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
105	c3aaqB_	Alignment	not modelled	82.9	13	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus
106	c5lj7B_	Alignment	not modelled	82.3	15	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
107	c5nikK_	Alignment	not modelled	82.2	20	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
108	c5ws4A_	Alignment	not modelled	81.7	17	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
109	d3by8a1	Alignment	not modelled	80.4	14	Fold: Profilin-like Superfamily: Sensory domain-like Family: Sensory domain of two-component sensor kinase
110	c5mg3D_	Alignment	not modelled	77.4	10	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
111	c5mg3F_	Alignment	not modelled	76.7	13	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
112	c6fo1G_	Alignment	not modelled	72.0	17	PDB header: chaperone Chain: G: PDB Molecule: rna polymerase ii-associated protein 3; PDBTitle: human r2tp subcomplex containing 1 ruvbl1-ruvbl2 hexamer bound to 12 rbd domain from rpap3.
113	c4ic5B_	Alignment	not modelled	70.8	25	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
114	c5lq3F_	Alignment	not modelled	69.6	14	PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
115	c1oy8A_	Alignment	not modelled	69.4	14	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
116	c5xu1M_	Alignment	not modelled	68.8	23	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
117	c6o6dA_	Alignment	not modelled	66.1	33	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
118	d1cya2	Alignment	not modelled	65.1	29	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
119	c3nwb_	Alignment	not modelled	64.6	36	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
120	c5bz3A_	Alignment	not modelled	64.5	14	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of sodium proton antiporter napa in outward-facing2 conformation.