Phyre^2

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Description	P0AAM3
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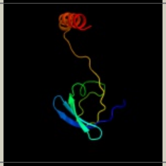
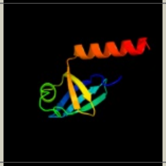
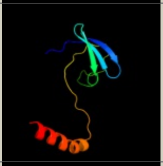
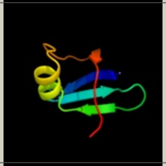
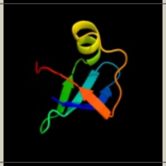
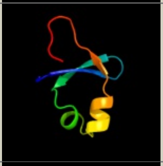
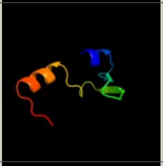
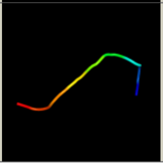
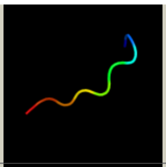
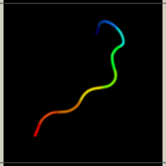
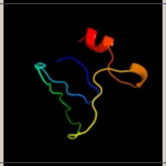
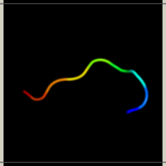
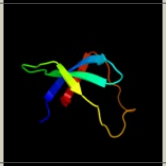
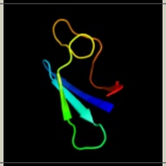
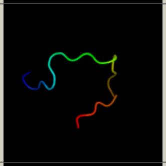
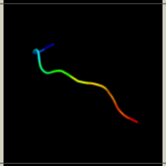
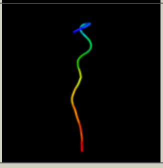
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ot2a1	Alignment		100.0	100	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
2	c3d3rA_	Alignment		100.0	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
3	d2z1ca1	Alignment		99.9	35	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
4	d3d3ra1	Alignment		99.9	29	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
5	c2rcnA_	Alignment		79.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
6	c4a2iV_	Alignment		78.7	19	**PDB header:**ribosome/hydrolase **Chain:** V: **PDB Molecule:**putative ribosome biogenesis gtpase rsga; **PDBTitle:** cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
7	c2yv5A_	Alignment		70.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
8	c2hc8A_	Alignment		48.3	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
9	d1rl2a2	Alignment		46.6	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	c1xnil_	Alignment		46.1	20	**PDB header:**cell cycle **Chain:** I: **PDB Molecule:**tumor suppressor p53-binding protein 1; **PDBTitle:** tandem tudor domain of 53bp1
11	c1g0dA_	Alignment		44.2	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** crystal structure of red sea bream transglutaminase

12	c1kv3F_	Alignment		43.6	33	**PDB header:**transferase **Chain:** F: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** human tissue transglutaminase in gdp bound form
13	c1l9mB_	Alignment		43.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-glutamine glutamyltransferase e3; **PDBTitle:** three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
14	d1vfsa1	Alignment		42.7	11	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
15	c1f13A_	Alignment		40.8	44	**PDB header:**coagulation factor **Chain:** A: **PDB Molecule:**cellular coagulation factor xiii zymogen; **PDBTitle:** recombinant human cellular coagulation factor xiii
16	c1u0lB_	Alignment		40.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
17	c2rhsB_	Alignment		39.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
18	d1njjb1	Alignment		37.0	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
19	d1g0da4	Alignment		37.0	40	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
20	d2q3za4	Alignment		34.7	40	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
21	d1u0la1	Alignment	not modelled	34.4	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	c2e8gB_	Alignment	not modelled	34.2	19	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**hypothetical protein ph0536; **PDBTitle:** the structure of protein from p. horikoshii at 1.7 angstrom2 resolution
23	d1ex0a4	Alignment	not modelled	33.8	50	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
24	d1d7ka1	Alignment	not modelled	32.1	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
25	d1vjja4	Alignment	not modelled	31.9	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
26	c2opkC_	Alignment	not modelled	31.5	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
27	c3mxnB_	Alignment	not modelled	30.6	18	**PDB header:**replication **Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2; **PDBTitle:** crystal structure of the rmi core complex
28	c2fhdA_	Alignment	not modelled	30.1	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains

29	d2toda1	Alignment	not modelled	30.0	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
30	d2nn6h1	Alignment	not modelled	30.0	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	c2dbiA_	Alignment	not modelled	29.4	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
32	c2nvaH_	Alignment	not modelled	28.4	16	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
33	d2csga1	Alignment	not modelled	27.5	26	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
34	c3m9bK_	Alignment	not modelled	26.7	15	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
35	c1njjC_	Alignment	not modelled	26.1	33	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
36	d1tt2a_	Alignment	not modelled	25.5	27	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
37	d2soba_	Alignment	not modelled	25.4	25	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
38	d1f3ta1	Alignment	not modelled	24.8	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
39	c2oqkA_	Alignment	not modelled	24.6	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
40	c3fp9E_	Alignment	not modelled	24.4	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
41	d1hh2p1	Alignment	not modelled	24.1	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	c2pljA_	Alignment	not modelled	23.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
43	c1ltlE_	Alignment	not modelled	23.0	15	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
44	d1pqwa_	Alignment	not modelled	22.6	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
45	d2gy9q1	Alignment	not modelled	22.6	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
46	c3bu2B_	Alignment	not modelled	22.6	26	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**putative trna-binding protein; **PDBTitle:** crystal structure of a trna-binding protein from2 staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target syr77
47	c3j09A_	Alignment	not modelled	22.3	29	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
48	d2fzwa2	Alignment	not modelled	22.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
49	c2qghA_	Alignment	not modelled	22.1	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
50	c2vl6C_	Alignment	not modelled	21.6	18	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
51	d7odca1	Alignment	not modelled	20.4	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
52	d1v3va2	Alignment	not modelled	20.2	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
53	d1ltla_	Alignment	not modelled	19.8	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
54	d1knwa1	Alignment	not modelled	19.6	17	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like

55	c2p1gA_	Alignment	not modelled	18.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis
56	c2p3eA_	Alignment	not modelled	18.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus
57	d1vqoa2	Alignment	not modelled	18.0	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
58	d1e3ia2	Alignment	not modelled	17.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
59	d2rcfa1	Alignment	not modelled	17.6	31	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
60	c3bbnQ_	Alignment	not modelled	17.5	27	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
61	c1knwA_	Alignment	not modelled	17.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
62	d1yb5a2	Alignment	not modelled	17.4	38	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
63	d1p0fa2	Alignment	not modelled	17.4	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
64	c1oy5B_	Alignment	not modelled	17.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
65	c2a7yA_	Alignment	not modelled	16.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2302/mt2359; **PDBTitle:** solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
66	d2a7ya1	Alignment	not modelled	16.9	30	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Rv2302-like
67	d1oy5a_	Alignment	not modelled	16.9	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
68	d1fr3a_	Alignment	not modelled	16.8	11	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
69	c2yxxA_	Alignment	not modelled	16.8	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa)
70	d1twia1	Alignment	not modelled	16.8	17	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
71	d1d1ta2	Alignment	not modelled	16.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
72	d1t9ha1	Alignment	not modelled	16.6	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	d1rkna_	Alignment	not modelled	16.0	25	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
74	d1qora2	Alignment	not modelled	15.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
75	d2q07a1	Alignment	not modelled	15.8	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
76	d2uubq1	Alignment	not modelled	15.5	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
77	c3rfuC_	Alignment	not modelled	15.4	27	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
78	d1gu7a2	Alignment	not modelled	15.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
79	c1s1hQ_	Alignment	not modelled	15.3	23	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s11; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
80	c3knuD_	Alignment	not modelled	15.1	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
81	d1f8fa2	Alignment	not modelled	15.0	0	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Alcohol dehydrogenase-like, C-terminal domain
82	c3pcoD_	Alignment	not modelled	14.9	27	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phenylalanyl-trna synthetase, beta chain; **PDBTitle:** crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
83	d2qamc2	Alignment	not modelled	14.6	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
84	d1p9pa_	Alignment	not modelled	14.4	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
85	c3ky7A_	Alignment	not modelled	14.2	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
86	d1pl8a2	Alignment	not modelled	14.1	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
87	c1vftA_	Alignment	not modelled	14.0	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
88	c3iefA_	Alignment	not modelled	13.9	18	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
89	d1uala_	Alignment	not modelled	13.8	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
90	d2jhfa2	Alignment	not modelled	13.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
91	c1w4sA_	Alignment	not modelled	13.5	50	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**polybromo 1 protein; **PDBTitle:** crystal structure of the proximal bah domain of polybromo
92	c2zkqq_	Alignment	not modelled	13.5	18	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
93	d1cdoa2	Alignment	not modelled	13.3	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
94	c3mt1B_	Alignment	not modelled	13.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
95	c3n29A_	Alignment	not modelled	12.9	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase; **PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
96	d2qw7a1	Alignment	not modelled	12.7	33	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
97	c3smaD_	Alignment	not modelled	12.7	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
98	c2dgyA_	Alignment	not modelled	12.7	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
99	d1rcqa1	Alignment	not modelled	12.7	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase