Phyre2

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Description	P77173
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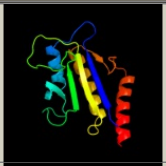
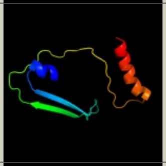
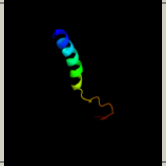
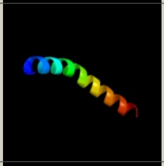
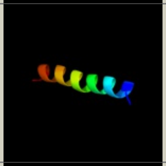
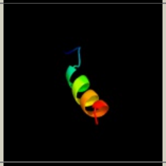
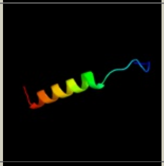
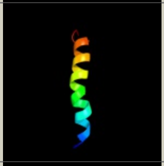
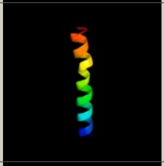
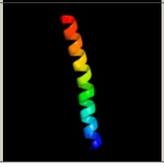
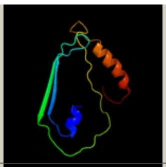
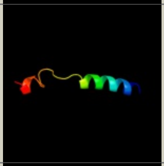
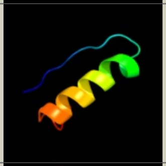
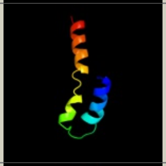
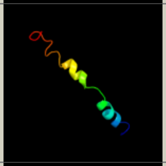
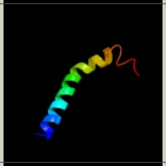
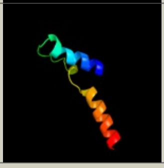
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f46a_	Alignment		100.0	99	**Fold:**TBP-like **Superfamily:**Cell-division protein ZipA, C-terminal domain **Family:**Cell-division protein ZipA, C-terminal domain
2	c1qmiC_	Alignment		79.0	13	**PDB header:**rna 3'-terminal phosphate cyclase **Chain:** C: **PDB Molecule:**rna 3'-terminal phosphate cyclase; **PDBTitle:** crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
3	c2kncA_	Alignment		75.4	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
4	c3sokB_	Alignment		55.5	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
5	d2pila_	Alignment		48.9	32	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
6	c2kncB_	Alignment		45.6	35	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
7	d2axtj1	Alignment		45.0	33	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
8	c1afoB_	Alignment		43.6	36	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures
9	c2k21A_	Alignment		41.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
10	c2jwaA_	Alignment		40.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
11	d1oqwa_	Alignment		39.3	29	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin

12	c3pqvD_	Alignment		38.3	17	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**rcl1 protein; **PDBTitle:** cyclase homolog
13	c2l9uA_	Alignment		38.1	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
14	c2it3B_	Alignment		33.2	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0130 protein ph1069; **PDBTitle:** structure of ph1069 protein from pyrococcus horikoshii
15	c2dvkA_	Alignment		32.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0130 protein ape0816; **PDBTitle:** crystal structure of hypothetical protein from aeropyrum pernix
16	d2o02a1	Alignment		31.3	14	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
17	c2qg3B_	Alignment		31.0	32	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0130 protein af_2059; **PDBTitle:** crystal structure of a tyw3 methyltransferase-like protein (af_2059)2 from archaeoglobus fulgidus dsm 4304 at 1.95 a resolution
18	d1fftb2	Alignment		30.7	20	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
19	c2jp3A_	Alignment		30.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles
20	c2c1nA_	Alignment		28.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**14-3-3 protein zeta/delta; **PDBTitle:** molecular basis for the recognition of phosphorylated and2 phosphoacetylated histone h3 by 14-3-3
21	d1tlja_	Alignment	not modelled	26.6	25	**Fold:**SSo0622-like **Superfamily:**SSo0622-like **Family:**SSo0622-like
22	c1tljA_	Alignment	not modelled	26.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0130 protein sso0622; **PDBTitle:** crystal structure of conserved protein of unknown function2 sso0622 from sulfolobus solfataricus
23	d1q1la_	Alignment	not modelled	25.0	15	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
24	d1hywa_	Alignment	not modelled	24.0	21	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
25	c1ztbA_	Alignment	not modelled	22.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**chorismate synthase; **PDBTitle:** crystal structure of chorismate synthase from mycobacterium2 tuberculosis
26	d1xrda1	Alignment	not modelled	22.8	30	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
27	d1wfya_	Alignment	not modelled	22.5	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
28	c2jo1A_	Alignment	not modelled	22.1	33	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
29	c2k1aA_	Alignment	not modelled	21.9	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib;

29	c2k1aA_	Alignment	not modelled	21.9	14	**PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
30	d1ijda_	Alignment	not modelled	21.6	60	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
31	c2x2oA_	Alignment	not modelled	21.1	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
32	d1o9da_	Alignment	not modelled	18.4	7	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
33	d1mx3a2	Alignment	not modelled	17.9	19	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
34	d1nkza_	Alignment	not modelled	17.5	43	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
35	c2mltB_	Alignment	not modelled	17.2	33	**PDB header:**toxin (hemolytic polypeptide) **Chain:** B: **PDB Molecule:**melittin; **PDBTitle:** melittin
36	c2npmB_	Alignment	not modelled	16.9	7	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**14-3-3 domain containing protein; **PDBTitle:** crystal structure of cryptosporidium parvum 14-3-3 protein2 in complex with peptide
37	c2mltA_	Alignment	not modelled	16.9	33	**PDB header:**toxin (hemolytic polypeptide) **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** melittin
38	d1c99a_	Alignment	not modelled	16.0	26	**Fold:**Transmembrane helix hairpin **Superfamily:**F1F0 ATP synthase subunit C **Family:**F1F0 ATP synthase subunit C
39	d1qw1a1	Alignment	not modelled	16.0	16	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
40	d1qxoa_	Alignment	not modelled	15.9	14	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
41	c1qcrD_	Alignment	not modelled	15.1	25	**PDB header:** **PDB COMPND:**
42	c1fftG_	Alignment	not modelled	14.2	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
43	c2kluA_	Alignment	not modelled	14.1	32	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
44	c3u5eL_	Alignment	not modelled	14.0	14	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution
45	c3e6yB_	Alignment	not modelled	13.5	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**14-3-3-like protein c; **PDBTitle:** structure of 14-3-3 in complex with the differentiation-inducing agent2 cotylenin a
46	c2kxhB_	Alignment	not modelled	13.5	50	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**peptide of far upstream element-binding protein 1; **PDBTitle:** solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
47	d2o8pa1	Alignment	not modelled	13.1	17	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
48	c4a1bO_	Alignment	not modelled	12.9	22	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rpl28; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
49	c2k9yA_	Alignment	not modelled	12.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
50	c2k9yB_	Alignment	not modelled	12.8	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
51	c2hg5D_	Alignment	not modelled	12.2	4	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
52	c2zxeG_	Alignment	not modelled	12.2	20	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**phospholemman-like protein; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
53	d1ydla1	Alignment	not modelled	11.9	20	**Fold:**TFB5-like **Superfamily:**TFB5-like **Family:**TFB5-like
54	c3bwwA_	Alignment	not modelled	11.8	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein of unknown function duf692/cog3220; **PDBTitle:** crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution

55	c3cs5B_	Alignment	not modelled	11.6	27	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942
56	c2j7aC_	Alignment	not modelled	11.2	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome c quinol dehydrogenase nrfh; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
57	d2nlya1	Alignment	not modelled	10.7	12	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
58	c3dgpB_	Alignment	not modelled	10.5	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna polymerase ii transcription factor b subunit 5; **PDBTitle:** crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
59	d1ul7a_	Alignment	not modelled	10.5	3	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Kinase associated domain 1, KA1
60	c2pcrA_	Alignment	not modelled	10.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** crystal structure of myo-inositol-1(or 4)-monophosphatase (aq_1983)2 from aquifex aeolicus vf5
61	d1v54i_	Alignment	not modelled	9.0	13	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc **Family:**Mitochondrial cytochrome c oxidase subunit VIc
62	c3mk7F_	Alignment	not modelled	9.0	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
63	d2bkra1	Alignment	not modelled	8.8	6	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
64	d1rlja_	Alignment	not modelled	8.8	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
65	c3n23E_	Alignment	not modelled	8.5	27	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
66	c2latA_	Alignment	not modelled	8.2	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
67	d1xzpa3	Alignment	not modelled	8.1	20	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**TrmE formyl-THF-binding domain
68	c1xzqB_	Alignment	not modelled	8.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
69	c2q74B_	Alignment	not modelled	7.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** mycobacterium tuberculosis suhb
70	c2g2bA_	Alignment	not modelled	7.7	7	**PDB header:**immune system **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** nmr structure of the human allograft inflammatory factor 1
71	c2i7gA_	Alignment	not modelled	7.6	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
72	c3otbB_	Alignment	not modelled	7.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna(his) guanylyltransferase; **PDBTitle:** crystal structure of human trnahis guanylyltransferase (thg1) - dgtp2 complex
73	c2qflA_	Alignment	not modelled	7.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** structure of suhb: inositol monophosphatase and extragenic2 suppressor from e. coli
74	c1s7fA_	Alignment	not modelled	7.3	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyl transferase; **PDBTitle:** riml- ribosomal l7/l12 alpha-n-protein acetyltransferase crystal form2 i (apo)
75	c2l2tA_	Alignment	not modelled	7.2	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
76	c1qleB_	Alignment	not modelled	7.2	16	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
77	c1ar1B_	Alignment	not modelled	7.2	16	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
78	c3ih5A_	Alignment	not modelled	7.2	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
79	d3clsd1	Alignment	not modelled	6.8	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits

80	c3dwcA_	Alignment	not modelled	6.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallocarboxypeptidase; **PDBTitle:** trypanosoma cruzi metallocarboxypeptidase 1
81	d1ap4a_	Alignment	not modelled	6.7	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
82	c2rmzA_	Alignment	not modelled	6.5	35	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-3; **PDBTitle:** bicelle-embedded integrin beta3 transmembrane segment
83	c1bh1A_	Alignment	not modelled	6.2	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**melittin; **PDBTitle:** structural studies of d-pro melittin, nmr, 20 structures
84	c2l16A_	Alignment	not modelled	6.0	38	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
85	d1ueka2	Alignment	not modelled	6.0	31	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
86	c3tcvB_	Alignment	not modelled	5.9	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of a gcn5-related n-acetyltransferase from brucella2 melitensis
87	d1fi5a_	Alignment	not modelled	5.8	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
88	c1fi5A_	Alignment	not modelled	5.8	15	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**protein (troponin c); **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i.
89	d1a0pa1	Alignment	not modelled	5.7	11	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
90	d1lf6a2	Alignment	not modelled	5.6	14	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Bacterial glucoamylase N-terminal domain-like
91	d3ehbb2	Alignment	not modelled	5.5	16	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
92	d1yoba1	Alignment	not modelled	5.4	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
93	d2fcka1	Alignment	not modelled	5.4	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
94	c2b19A_	Alignment	not modelled	5.4	22	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**neuropeptide k; **PDBTitle:** solution structure of mammalian tachykinin peptide,2 neuropeptide k
95	d3dtub2	Alignment	not modelled	5.3	19	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
96	c3kdpH_	Alignment	not modelled	5.3	27	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
97	c3kdpG_	Alignment	not modelled	5.3	27	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
98	c3owcA_	Alignment	not modelled	5.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable acetyltransferase; **PDBTitle:** crystal structure of gnat superfamily protein pa2578 from pseudomonas2 aeruginosa
99	c3fj2A_	Alignment	not modelled	5.2	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**monooxygenase-like protein; **PDBTitle:** crystal structure of a monooxygenase-like protein (lin2316) from2 listeria innocua at 1.85 a resolution