Phyre^2

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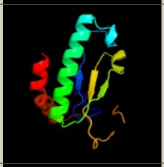
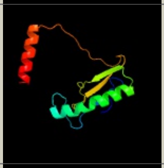
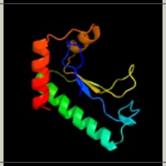
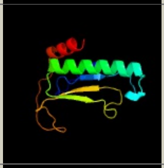
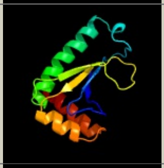
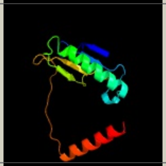
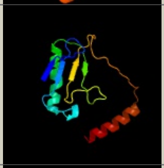
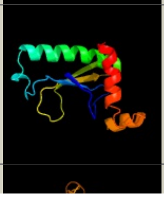
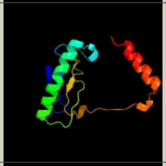
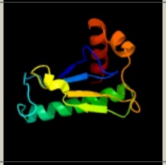
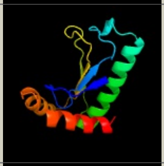
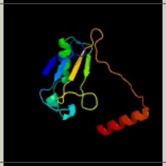
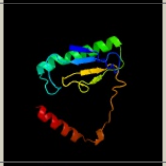
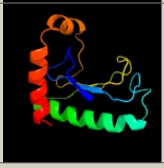
Description	RVBD0759c_(-)_853828_854160
Date	Fri Jul 26 01:50:34 BST 2019
Unique Job ID	32bf619bb8e85a65

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p0tB_	Alignment		100.0	86	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
2	c3i24B_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of a hit family hydrolase protein from vibrio2 fischeri. northeast structural genomics consortium target id vfr176
3	c3oheA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
4	c3l7xA_	Alignment		100.0	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
5	c3nrdB_	Alignment		100.0	19	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
6	c3i4sB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
7	d2oika1	Alignment		100.0	14	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
8	c5cs2A_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of plasmodium falciparum diadenosine triphosphate2 hydrolase in complex with cyclomarin a
9	c3ksvA_	Alignment		100.0	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** hypothetical protein from leishmania major
10	c6iq1A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine 5'-monophosphoramidase; **PDBTitle:** crystal structure of histidine triad nucleotide-binding protein from2 candida albicans
11	d1fita_	Alignment		99.9	24	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins

12	c3anoA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ap-4-a phosphorylase; **PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
13	c3imiB_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
14	c1emsB_	Alignment		99.9	26	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
15	c2eo4A_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**150aa long hypothetical histidine triad nucleotide-binding **PDBTitle:** crystal structure of hypothetical histidine triad nucleotide-binding2 protein st2152 from sulfolobus tokodaii strain7
16	d1emsa1	Alignment		99.9	26	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
17	c3o0mB_	Alignment		99.9	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zn-bound histidine triad family protein from2 mycobacterium smegmatis
18	c3r6fA_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family protein; **PDBTitle:** crystal structure of a zinc-containing hit family protein from2 encephalitozoon cuniculi
19	d1y23a_	Alignment		99.9	26	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
20	c3lb5B_	Alignment		99.9	35	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**hit-like protein involved in cell-cycle regulation; **PDBTitle:** crystal structure of hit-like protein involved in cell-cycle2 regulation from bartonella henselae with unknown ligand
21	c4incA_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad nucleotide-binding protein 2, **PDBTitle:** human histidine triad nucleotide binding protein 2
22	d1rzya_	Alignment	not modelled	99.8	24	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
23	d1kpfa_	Alignment	not modelled	99.8	23	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
24	d1z84a2	Alignment	not modelled	99.8	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
25	c4eguA_	Alignment	not modelled	99.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** 0.95a resolution structure of a histidine triad protein from2 clostridium difficile
26	c6d6jB_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of hit family hydrolase from legionella pneumophila2 philadelphia 1
27	c3n1tE_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**hit-like protein hint; **PDBTitle:** crystal structure of the h101a mutant echint gmp complex
28	d1xqua_	Alignment	not modelled	99.8	19	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
29	c1xquA	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hit family hydrolase;

29	c1xquA_	Alignment	not modelled	99.8	19	**PDBTitle:** hit family hydrolase from clostridium thermocellum cth-393
30	c3oj7A_	Alignment	not modelled	99.8	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative histidine triad family protein; **PDBTitle:** crystal structure of a histidine triad family protein from entamoeba2 histolytica, bound to sulfate
31	c4q61J_	Alignment	not modelled	99.8	26	**PDB header:**cell cycle **Chain:** J: **PDB Molecule:**uncharacterized hit-like protein hp_0404; **PDBTitle:** hit like protein from helicobacter pylori 26695
32	d1guqa2	Alignment	not modelled	99.8	14	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
33	c1zwjA_	Alignment	not modelled	99.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative galactose-1-phosphate uridyl transferase; **PDBTitle:** x-ray structure of galt-like protein from arabidopsis thaliana2 at5g18200
34	c1gupC_	Alignment	not modelled	99.6	15	**PDB header:**nucleotidyltransferase **Chain:** C: **PDB Molecule:**galactose-1-phosphate uridylyltransferase; **PDBTitle:** structure of nucleotidyltransferase complexed with udp-2 galactose
35	c5in3A_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of glucose-1-phosphate bound nucleotidylated human2 galactose-1-phosphate uridylyltransferase
36	c4ndgB_	Alignment	not modelled	99.6	20	**PDB header:**dna binding protein/rna/dna **Chain:** B: **PDB Molecule:**aprataxin; **PDBTitle:** human aprataxin (aptx) bound to rna-dna and zn - adenosine vanadate2 transition state mimic complex
37	c3splC_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**aprataxin-like protein; **PDBTitle:** crystal structure of aprataxin ortholog hnt3 in complex with dna and2 amp
38	c4i5wA_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5',5'''-p-1,p-4-tetraphosphate phosphorylase 2; **PDBTitle:** crystal structure of yeast ap4a phosphorylase apa2 in complex with amp
39	c3jb9c_	Alignment	not modelled	99.2	15	**PDB header:**rna binding protein/rna **Chain:** C: **PDB Molecule:**u5 snrna; **PDBTitle:** cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
40	d1z84a1	Alignment	not modelled	99.1	14	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
41	c4qvuA_	Alignment	not modelled	98.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf4931 family protein (bce0241) from bacillus2 cereus atcc 10987 at 2.65 a resolution
42	c6id1U_	Alignment	not modelled	98.7	14	**PDB header:**splicing **Chain:** U: **PDB Molecule:**cwf19-like protein 2; **PDBTitle:** cryo-em structure of a human intron lariat spliceosome after prp432 loaded (ils2 complex) at 2.9 angstrom resolution
43	d3bl9a1	Alignment	not modelled	98.1	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
44	d1vlra1	Alignment	not modelled	98.0	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**mRNA decapping enzyme DcpS C-terminal domain
45	c3bl9B_	Alignment	not modelled	97.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**scavenger mrna-decapping enzyme dcps; **PDBTitle:** synthetic gene encoded dcps bound to inhibitor dg157493
46	c6gbsB_	Alignment	not modelled	97.5	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative mrna decapping protein; **PDBTitle:** crystal structure of the c. themophilum scavenger decapping enzyme2 dcps apo form
47	c1xmlA_	Alignment	not modelled	97.5	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock-like protein 1; **PDBTitle:** structure of human dcps
48	c5bv3C_	Alignment	not modelled	97.5	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**m7gpppx diphosphatase; **PDBTitle:** yeast scavenger decapping enzyme in complex with m7gdp
49	d1guqa1	Alignment	not modelled	95.4	7	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
50	c4lvjA_	Alignment	not modelled	87.3	11	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**plasmid recombination enzyme; **PDBTitle:** mobm relaxase domain (mobv; mob_pre) bound to plasmid pmv158 orit dna2 (22nt). mn-bound crystal structure at ph 5.5
51	d2pofa1	Alignment	not modelled	83.7	18	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**CDH-like
52	c3csqC_	Alignment	not modelled	44.3	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
53	c3sdsA_	Alignment	not modelled	43.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
54	d1mg4a_	Alignment	not modelled	39.4	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)

55	c4euvA_	Alignment	not modelled	35.1	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**peld; **PDBTitle:** crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
56	d2b7oa1	Alignment	not modelled	32.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
57	d1uf0a_	Alignment	not modelled	31.4	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
58	c5ip4E_	Alignment	not modelled	29.1	3	**PDB header:**transferase **Chain:** E: **PDB Molecule:**neuronal migration protein doublecortin; **PDBTitle:** x-ray structure of the c-terminal domain of human doublecortin
59	c6bmcA_	Alignment	not modelled	26.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
60	c3l6tB_	Alignment	not modelled	25.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mobilization protein trai; **PDBTitle:** crystal structure of an n-terminal mutant of the plasmid pcu1 trai2 relaxase domain
61	c3txxD_	Alignment	not modelled	24.8	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putrescine carbamoyltransferase; **PDBTitle:** crystal structure of putrescine transcarbamylase from enterococcus2 faecalis
62	d1vlva1	Alignment	not modelled	21.9	9	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
63	c4atul_	Alignment	not modelled	21.8	9	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**neuronal migration protein doublecortin; **PDBTitle:** human doublecortin n-dc repeat plus linker, and tubulin (2xrp) docked2 into an 8a cryo-em map of doublecortin-stabilised microtubules3 reconstructed in absence of kinesin
64	d1omha_	Alignment	not modelled	19.9	21	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
65	d1mjda_	Alignment	not modelled	19.8	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Doublecortin (DC) **Family:**Doublecortin (DC)
66	c4dmzB_	Alignment	not modelled	18.8	11	**PDB header:**nucleotide-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein peld; **PDBTitle:** peld 156-455 from pseudomonas aeruginosa pa14, apo form
67	d1p4da_	Alignment	not modelled	18.0	50	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Relaxase domain
68	d1dxha1	Alignment	not modelled	17.7	7	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
69	c5uxmA_	Alignment	not modelled	17.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** type ii dah7ps from pseudomonas aeruginosa with trp bound
70	d1duvg1	Alignment	not modelled	17.0	5	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
71	c3ezuA_	Alignment	not modelled	16.6	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
72	c2dnfA_	Alignment	not modelled	16.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**doublecortin domain-containing protein 2; **PDBTitle:** solution structure of rsgi ruh-062, a dcx domain from human
73	d1ml4a1	Alignment	not modelled	15.6	7	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
74	d1hska2	Alignment	not modelled	14.4	18	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
75	d1pvva1	Alignment	not modelled	13.4	2	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
76	c6cslA_	Alignment	not modelled	13.3	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**histidine triad protein d; **PDBTitle:** pneumococcal phtd protein 269-339 fragment with bound zn(ii)
77	d2cs7a1	Alignment	not modelled	12.8	27	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
78	c5nnqA_	Alignment	not modelled	12.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ctatc; **PDBTitle:** aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
79	d2at2a1	Alignment	not modelled	11.4	4	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
						PDB header:hydrolase

80	c3rcnA_	Alignment	not modelled	11.3	11	**Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
81	c5hudA_	Alignment	not modelled	11.3	16	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) **PDBTitle:** non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
82	c4jayC_	Alignment	not modelled	10.3	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of p. aeruginosa murb in complex with nadp+
83	c2ef0A_	Alignment	not modelled	9.6	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
84	d1uxya2	Alignment	not modelled	9.1	21	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
85	d1ekxa1	Alignment	not modelled	9.1	7	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
86	c1mbbA_	Alignment	not modelled	9.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
87	d1tuga1	Alignment	not modelled	8.9	7	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
88	c5ilqA_	Alignment	not modelled	8.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of truncated unliganded aspartate transcarbamoylase2 from plasmodium falciparum
89	c1ml4A_	Alignment	not modelled	8.6	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
90	c3j4rA_	Alignment	not modelled	8.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**a-kinase anchor protein 18; **PDBTitle:** pseudo-atomic model of the akap18-pka complex in a linear conformation2 derived from electron microscopy
91	c5g1oF_	Alignment	not modelled	8.0	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**cad protein; **PDBTitle:** aspartate transcarbamoylase domain of human cad in apo form
92	c5n6yC_	Alignment	not modelled	7.9	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nitrogenase vanadium-iron protein delta chain; **PDBTitle:** azotobacter vinelandii vanadium nitrogenase
93	c3sluB_	Alignment	not modelled	7.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**m23 peptidase domain protein; **PDBTitle:** crystal structure of nmb0315
94	d1otha1	Alignment	not modelled	7.5	7	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
95	c6b4aB_	Alignment	not modelled	7.2	9	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**doublecortin; **PDBTitle:** crystal structure of the c-terminal domain of doublecortin (tgdcx)2 from toxoplasma gondii me49
96	c1ortD_	Alignment	not modelled	7.1	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
97	d1r3na2	Alignment	not modelled	7.1	16	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
98	c4iv5E_	Alignment	not modelled	7.1	7	**PDB header:**transferase **Chain:** E: **PDB Molecule:**aspartate carbamoyltransferase, putative; **PDBTitle:** x-ray crystal structure of a putative aspartate carbamoyltransferase2 from trypanosoma cruzi
99	d1nc7a_	Alignment	not modelled	7.0	18	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070