Phyre2

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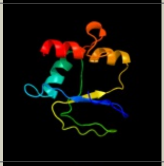
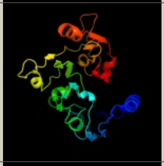
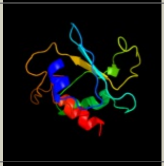
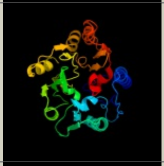
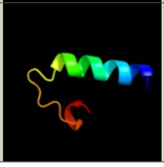
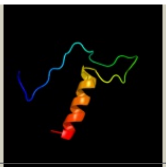
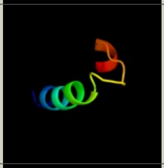
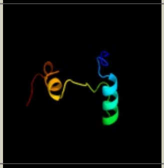
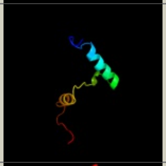
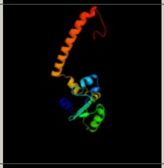
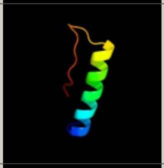
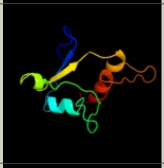
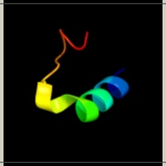
Description	P76216
Date	Thu Jan 5 12:20:40 GMT 2012
Unique Job ID	5d0247ce2fe6dce9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ynha1	Alignment		100.0	100	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Succinylarginine dihydrolase-like
2	d1h70a_	Alignment		97.0	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Dimethylarginine dimethylaminohydrolase DDAH
3	d1bwda_	Alignment		90.3	12	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
4	c3dydB_	Alignment		81.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** human tyrosine aminotransferase
5	d1jdwa_	Alignment		76.1	15	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
6	c1jdwA_	Alignment		76.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-arginine\:glycine amidinotransferase; **PDBTitle:** crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
7	c2ci6A_	Alignment		75.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ng, ng-dimethylarginine dimethylaminohydrolase 1; **PDBTitle:** crystal structure of dimethylarginine2 dimethylaminohydrolase i bound with zinc low ph
8	d1wsta1	Alignment		66.4	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
9	c8jdwA_	Alignment		64.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (l-arginine:glycine amidinotransferase); **PDBTitle:** crystal structure of human l-arginine:glycine2 amidinotransferase in complex with l-alanine
10	c3i4aA_	Alignment		61.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(g),n(g)-dimethylarginine dimethylaminohydrolase **PDBTitle:** crystal structure of dimethylarginine2 dimethylaminohydrolase-1 (ddah-1) in complex with n5-(1-3 iminopropyl)-l-ornithine
11	d1bl0a1	Alignment		53.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator

12	c3pdxA_	Alignment		53.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine aminotransferase; **PDBTitle:** crystal structural of mouse tyrosine aminotransferase
13	d1d5ya1	Alignment		43.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
14	c3fkdC_	Alignment		41.8	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**l-threonine-o-3-phosphate decarboxylase; **PDBTitle:** the crystal structure of l-threonine-o-3-phosphate2 decarboxylase from porphyromonas gingivalis
15	c3p1tB_	Alignment		37.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
16	c3ctzA_	Alignment		36.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro aminopeptidase 1; **PDBTitle:** structure of human cytosolic x-prolyl aminopeptidase
17	d2bo9b1	Alignment		32.8	25	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Latexin-like
18	c3eibB_	Alignment		31.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ll-diaminopimelate aminotransferase; **PDBTitle:** crystal structure of k270n variant of ll-diaminopimelate2 aminotransferase from arabidopsis thaliana
19	c3oouA_	Alignment		30.0	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2118 protein; **PDBTitle:** the structure of a protein with unkown function from listeria innocua
20	c3mklB_	Alignment		28.6	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator gadx; **PDBTitle:** crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
21	d1rxxa_	Alignment	not modelled	28.3	24	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
22	d1fg7a_	Alignment	not modelled	28.0	30	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
23	c1bl0A_	Alignment	not modelled	27.8	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (multiple antibiotic resistance protein); **PDBTitle:** multiple antibiotic resistance protein (mara)/dna complex
24	c3t18D_	Alignment	not modelled	26.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aminotransferase class i and ii; **PDBTitle:** crystal structure of aminotransferase from anaerococcus prevotii dsm2 20548.
25	c3g7qA_	Alignment	not modelled	24.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**valine-pyruvate aminotransferase; **PDBTitle:** crystal structure of valine-pyruvate aminotransferase avta2 (np_462565.1) from salmonella typhimurium lt2 at 1.80 a resolution
26	c2k9sA_	Alignment	not modelled	22.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
27	c2of5K_	Alignment	not modelled	21.7	15	**PDB header:**apoptosis **Chain:** K: **PDB Molecule:**leucine-rich repeat and death domain-containing **PDBTitle:** oligomeric death domain complex
28	c3hdoB_	Alignment	not modelled	21.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a histidinol-phosphate

						aminotransferase from2 geobacter metallireducens
29	c3oioA_	Alignment	not modelled	21.0	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (arac-type dna-binding domain- **PDBTitle:** crystal structure of transcriptional regulator (arac-type dna-binding2 domain-containing proteins) from chromobacterium violaceum
30	d2v7fa1	Alignment	not modelled	19.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rps19E-like
31	d2vnud3	Alignment	not modelled	18.5	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
32	c2bo9B_	Alignment	not modelled	18.4	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**human latexin; **PDBTitle:** human carboxypeptidase a4 in complex with human latexin.
33	d2foka1	Alignment	not modelled	18.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
34	c3e4wB_	Alignment	not modelled	17.6	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a 33kda catalase-related protein from2 mycobacterium avium subsp. paratuberculosis. p2(1)2(1)2(1) crystal3 form.
35	c3nzlA_	Alignment	not modelled	17.4	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding protein satb1; **PDBTitle:** crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
36	c3gbgA_	Alignment	not modelled	17.3	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**tcp pilus virulence regulatory protein; **PDBTitle:** crystal structure of toxt from vibrio cholerae o395
37	c3iz6S_	Alignment	not modelled	16.5	20	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**40s ribosomal protein s19 (s19e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	c2zc0C_	Alignment	not modelled	15.8	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alanine glyoxylate transaminase; **PDBTitle:** crystal structure of an archaeal alanine:glyoxylate aminotransferase
39	d1s9ra_	Alignment	not modelled	15.5	12	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
40	d1lc5a_	Alignment	not modelled	15.5	24	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
41	d1x0ma1	Alignment	not modelled	14.7	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
42	c3jyvT_	Alignment	not modelled	14.6	20	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**s19e protein; **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
43	d1vp4a_	Alignment	not modelled	14.6	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
44	c3mn2B_	Alignment	not modelled	14.5	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**probable arac family transcriptional regulator; **PDBTitle:** the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
45	c3cq6E_	Alignment	not modelled	13.9	17	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** histidinol-phosphate aminotransferase from corynebacterium2 glutamicum holo-form (plp covalently bound)
46	c3ismA_	Alignment	not modelled	13.6	19	**PDB header:**hydrolase inhibitor/hydrolase **Chain:** A: **PDB Molecule:**cg8862; **PDBTitle:** crystal structure of the endog/endogi complex: mechanism of endog2 inhibition
47	c3getA_	Alignment	not modelled	13.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
48	c3ftbA_	Alignment	not modelled	13.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
49	c3aiiA_	Alignment	not modelled	12.7	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
50	c3by0B_	Alignment	not modelled	12.5	18	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**neutrophil gelatinase-associated lipocalin; **PDBTitle:** crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
51	c3lsgD_	Alignment	not modelled	12.4	18	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
						PDB header:transferase **Chain:** C: **PDB Molecule:**putative histidinol-phosphate

52	c3ly1C_	Alignment	not modelled	12.0	16	aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
53	c3ezsB_	Alignment	not modelled	11.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase aspb; **PDBTitle:** crystal structure of aminotransferase aspb (np_207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
54	d1bw0a_	Alignment	not modelled	11.7	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
55	c3s1sA_	Alignment	not modelled	11.4	10	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
56	c2douA_	Alignment	not modelled	10.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n-succinyldiaminopimelate aminotransferase; **PDBTitle:** probable n-succinyldiaminopimelate aminotransferase (ttha0342) from2 thermus thermophilus hb8
57	c2re3A_	Alignment	not modelled	10.6	45	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
58	c2xznT_	Alignment	not modelled	10.5	17	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rps19e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
59	c2yx5A_	Alignment	not modelled	10.1	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
60	d1n26a1	Alignment	not modelled	10.0	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
61	d2nwva1	Alignment	not modelled	9.9	39	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
62	d1v30a_	Alignment	not modelled	9.8	43	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
63	c2e12B_	Alignment	not modelled	9.7	50	**PDB header:**translation **Chain:** B: **PDB Molecule:**hypothetical protein xcc3642; **PDBTitle:** the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
64	d1xhsa_	Alignment	not modelled	9.6	71	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
65	c1d5yD_	Alignment	not modelled	9.5	15	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**rob transcription factor; **PDBTitle:** crystal structure of the e. coli rob transcription factor2 in complex with dna
66	c2wo3B_	Alignment	not modelled	9.4	40	**PDB header:**transferase/signaling protein **Chain:** B: **PDB Molecule:**ephrin-a2; **PDBTitle:** crystal structure of the epha4-ephrina2 complex
67	c3ke2A_	Alignment	not modelled	9.4	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
68	c2k6lA_	Alignment	not modelled	9.0	50	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the solution structure of xacb0070 from xanthonomas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors
69	c3a0hL_	Alignment	not modelled	8.8	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
70	c3a0hl_	Alignment	not modelled	8.8	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
71	d2nlva1	Alignment	not modelled	8.8	28	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
72	c3if2B_	Alignment	not modelled	8.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of putative amino-acid aminotransferase2 (yp_265399.1) from psychrobacter arcticum 273-4 at 2.50 a resolution
73	c3arcL_	Alignment	not modelled	8.6	67	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
74	c1s5lL_	Alignment	not modelled	8.6	67	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
75	c3prrL_	Alignment	not modelled	8.6	67	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
76	c2axtl_	Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from

						thermosynechococcus elongatus
77	c3a0bL_	 Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
78	c3a0bl_	 Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
79	c3bz1L_	 Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
80	d2axtl1	 Alignment	not modelled	8.6	67	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
81	c3bz2L_	 Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
82	c3prqL_	 Alignment	not modelled	8.6	67	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
83	c2axtL_	 Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
84	c3kziL_	 Alignment	not modelled	8.6	67	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
85	c1s5lI_	 Alignment	not modelled	8.6	67	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
86	c2e58D_	 Alignment	not modelled	8.5	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**mnmc2; **PDBTitle:** crystal structure of mnmc2 from aquifex aeolicus
87	d1j32a_	 Alignment	not modelled	8.2	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
88	c2euzA_	 Alignment	not modelled	7.9	29	**PDB header:**cell cycle/dna **Chain:** A: **PDB Molecule:**ndt80 protein; **PDBTitle:** structure of a ndt80-dna complex (mse mutant mc5t)
89	d1mnna_	 Alignment	not modelled	7.6	29	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**DNA-binding domain from NDT80
90	d1dqna_	 Alignment	not modelled	7.5	32	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
91	c1wr1B_	 Alignment	not modelled	7.5	29	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
92	d1xi9a_	 Alignment	not modelled	7.2	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
93	d2p97a1	 Alignment	not modelled	7.0	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
94	d1smye_	 Alignment	not modelled	6.9	41	**Fold:**RPB6/omega subunit-like **Superfamily:**RPB6/omega subunit-like **Family:**RNA polymerase omega subunit
95	c3ol4B_	 Alignment	not modelled	6.7	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
96	c2xstA_	 Alignment	not modelled	6.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 15; **PDBTitle:** crystal structure of the human lipocalin 15
97	d1dxha2	 Alignment	not modelled	6.6	8	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
98	d1lfpa_	 Alignment	not modelled	6.5	16	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
99	d1gg4a3	 Alignment	not modelled	6.4	9	**Fold:**MurF and HprK N-domain-like **Superfamily:**MurE/MurF N-terminal domain **Family:**MurE/MurF N-terminal domain