Phyre^2

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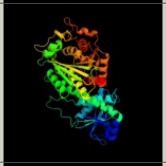
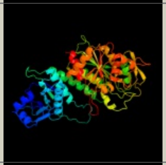
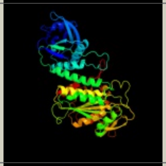
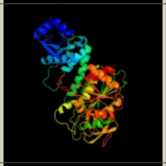
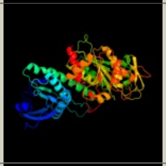
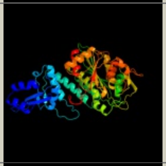
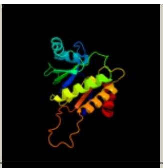
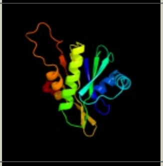
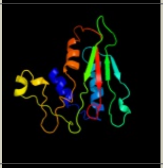
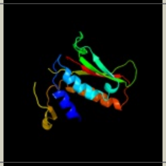
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gytG_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** e. coli aminopeptidase a (pepa)
2	c3h8gC_	Alignment		100.0	54	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
3	c3jruB_	Alignment		100.0	49	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable cytosol aminopeptidase; **PDBTitle:** crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
4	c3kzwD_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from staphylococcus aureus2 col
5	c1lanA_	Alignment		100.0	34	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
6	c3kr5E_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m17 leucyl aminopeptidase; **PDBTitle:** structure of a protease 4
7	c3peiA_	Alignment		100.0	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
8	c3ij3A_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
9	d1gyta2	Alignment		100.0	100	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain
10	c2hc9A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase 1; **PDBTitle:** structure of caenorhabditis elegans leucine aminopeptidase-zinc2 complex (lap1)
11	d1lama1	Alignment		100.0	42	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Leucine aminopeptidase, C-terminal domain

12	d1gyta1	Alignment		99.9	100	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
13	d1lama2	Alignment		99.7	18	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
14	c3rzaA_	Alignment		95.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidase; **PDBTitle:** crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
15	d1vhea2	Alignment		95.6	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
16	c2dx6B_	Alignment		93.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha0132; **PDBTitle:** crystal structure of conserved hypothetical protein, ttha0132 from2 thermus thermophilus hb8
17	c3ct9B_	Alignment		93.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31 a resolution
18	d2grea2	Alignment		92.8	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
19	c3q71A_	Alignment		91.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
20	d1cg2a1	Alignment		91.4	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
21	c3t6mA_	Alignment	not modelled	91.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
22	d1yloa2	Alignment	not modelled	90.1	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
23	d1spva_	Alignment	not modelled	87.8	10	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
24	d1vgya1	Alignment	not modelled	86.5	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
25	d1yd9a1	Alignment	not modelled	85.9	7	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
26	c2q43A_	Alignment	not modelled	85.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**iaa-amino acid hydrolase ilr1-like 2; **PDBTitle:** ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
27	c3kh6A_	Alignment	not modelled	85.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 15; **PDBTitle:** human poly(adp-ribose) polymerase 15, macro domain 2 in2 complex with adenosine-5-diphosphoribose
28	c3gb0A_	Alignment	not modelled	84.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution

29	d1vhoa2	Alignment	not modelled	83.8	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
30	c3pfoB_	Alignment	not modelled	83.5	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
31	c3q6zA_	Alignment	not modelled	80.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 14; **PDBTitle:** human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose
32	d1zr5a1	Alignment	not modelled	78.8	8	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
33	d2fvga2	Alignment	not modelled	78.3	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
34	d2hgaa1	Alignment	not modelled	78.0	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
35	c1q7lA_	Alignment	not modelled	77.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
36	c3ejfA_	Alignment	not modelled	76.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of ibv x-domain at ph 8.5
37	c2x47A_	Alignment	not modelled	73.4	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**macro domain-containing protein 1; **PDBTitle:** crystal structure of human macrod1
38	c2qyvB_	Alignment	not modelled	71.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-his dipeptidase; **PDBTitle:** crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
39	c2xd7B_	Alignment	not modelled	70.9	10	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**core histone macro-h2a.2; **PDBTitle:** crystal structure of the macro domain of human core histone2 h2a
40	c1vgyB_	Alignment	not modelled	70.6	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
41	d1xmba1	Alignment	not modelled	69.7	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
42	c3mruB_	Alignment	not modelled	69.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
43	c1zr5B_	Alignment	not modelled	66.4	7	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**h2afy protein; **PDBTitle:** crystal structure of the macro-domain of human core histone variant2 macroh2a1.2
44	c3i18A_	Alignment	not modelled	63.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
45	c2pokB_	Alignment	not modelled	62.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
46	d1sota1	Alignment	not modelled	62.3	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
47	c1ysjB_	Alignment	not modelled	60.6	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein yxep; **PDBTitle:** crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
48	c2p3wB_	Alignment	not modelled	57.6	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**probable serine protease htra3; **PDBTitle:** crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
49	c1vhoA_	Alignment	not modelled	57.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
50	c2greC_	Alignment	not modelled	56.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
51	d1vhua_	Alignment	not modelled	55.7	11	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
52	c2kl1A_	Alignment	not modelled	55.3	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ylbl protein; **PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
53	d2z9ia1	Alignment	not modelled	54.0	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
54	d1ky9a1	Alignment	not modelled	53.9	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like

						Family: HtrA-like serine proteases
55	d1ky9b2	Alignment	not modelled	50.4	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
56	c2kjpA_	Alignment	not modelled	49.5	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ylbl; **PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
57	c2joaA_	Alignment	not modelled	49.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
58	d1mfga_	Alignment	not modelled	47.5	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
59	d1lcya1	Alignment	not modelled	47.0	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
60	c3tc8A_	Alignment	not modelled	45.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distasonis atcc 8503 at 1.06 a3 resolution
61	c3pv4A_	Alignment	not modelled	45.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
62	c2zplA_	Alignment	not modelled	45.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
63	c2r3yC_	Alignment	not modelled	44.1	13	**PDB header:**hydrolase/hydrolase activator **Chain:** C: **PDB Molecule:**protease degs; **PDBTitle:** crystal structure of the degs protease in complex with the2 ywf activating peptide
64	c1ky9A_	Alignment	not modelled	43.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
65	d2i4sa1	Alignment	not modelled	43.1	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
66	d2h3la1	Alignment	not modelled	42.6	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	c2eguA_	Alignment	not modelled	42.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
68	d2i6va1	Alignment	not modelled	42.0	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
69	d1fnoa4	Alignment	not modelled	41.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
70	c3bpuA_	Alignment	not modelled	40.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant
71	d1ysja1	Alignment	not modelled	40.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
72	c1lcyA_	Alignment	not modelled	39.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
73	d1z2la1	Alignment	not modelled	39.5	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
74	d1ed7a_	Alignment	not modelled	39.3	40	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
75	d2w6ka1	Alignment	not modelled	38.9	8	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
76	c1vheA_	Alignment	not modelled	38.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog; **PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
77	d1fc6a3	Alignment	not modelled	38.0	37	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
78	c2fvgA_	Alignment	not modelled	36.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
79	c3tx8A_	Alignment	not modelled	36.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a succinyl-diaminopimelate desuccinylase (argе)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
						PDB header:ribosome

80	c3d5bD_	Alignment	not modelled	35.3	21	**Chain:** D: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
81	d1sroa_	Alignment	not modelled	34.5	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
82	c3ramC_	Alignment	not modelled	34.3	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
83	c3l4fD_	Alignment	not modelled	32.5	32	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex
84	c3stjC_	Alignment	not modelled	32.2	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
85	d1xfoa2	Alignment	not modelled	31.8	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
86	c3pv5B_	Alignment	not modelled	31.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
87	c3gqhB_	Alignment	not modelled	30.6	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the bacteriophage phi29 gene product2 12 c-terminal fragment
88	c2zpmA_	Alignment	not modelled	30.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
89	c3fj1A_	Alignment	not modelled	30.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
90	c3gdsA_	Alignment	not modelled	30.1	12	**PDB header:**hydrolase/hydrolase activator **Chain:** A: **PDB Molecule:**protease degs; **PDBTitle:** crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with dnrdgnvyyf peptide
91	c3pc3A_	Alignment	not modelled	29.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
92	c2floA_	Alignment	not modelled	29.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
93	c3qo6B_	Alignment	not modelled	28.7	36	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
94	c2z9iB_	Alignment	not modelled	28.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable serine protease pepd; **PDBTitle:** crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
95	c2es4D_	Alignment	not modelled	28.2	30	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lipase chaperone; **PDBTitle:** crystal structure of the burkholderia glumae lipase-2 specific foldase in complex with its cognate lipase
96	d2es4d1	Alignment	not modelled	28.2	30	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Lipase chaperone-like **Family:**Lipase chaperone LifO-like
97	c2hc8A_	Alignment	not modelled	28.1	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
98	d2nn6i1	Alignment	not modelled	27.8	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
99	c3shuB_	Alignment	not modelled	27.0	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
100	c2d90A_	Alignment	not modelled	26.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain containing protein 1; **PDBTitle:** solution structure of the third pdz domain of pdz domain2 containing protein 1
101	c3epmB_	Alignment	not modelled	26.8	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiamine biosynthesis protein thic; **PDBTitle:** crystal structure of caulobacter crescentus thic
102	c2posD_	Alignment	not modelled	26.2	27	**PDB header:**toxin **Chain:** D: **PDB Molecule:**sylvaticin; **PDBTitle:** crystal structure of sylvaticin, a new secreted protein2 from pythium sylvaticum
103	d2plta_	Alignment	not modelled	25.9	33	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
104	d1gmua1	Alignment	not modelled	25.4	40	**Fold:**Urease metallochaperone UreE, N-terminal domain **Superfamily:**Urease metallochaperone UreE, N-terminal domain **Family:**Urease metallochaperone UreE, N-terminal domain
105	c3k50A_	Alignment	not modelled	25.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative s41 protease; **PDBTitle:** crystal structure of putative s41 protease (yp_211611.1) from2 bacteroides fragilis nctc 9343 at 2.00 a resolution

106	d1fcja_	Alignment	not modelled	24.7	15	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
107	c2a3nA_	Alignment	not modelled	24.6	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
108	c1cg2D_	Alignment	not modelled	24.5	14	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
109	d1l1ca_	Alignment	not modelled	24.4	29	**Fold:**GroES-like **Superfamily:**SacY-like RNA-binding domain **Family:**BglG-like antiterminator proteins
110	c3omlA_	Alignment	not modelled	24.1	13	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**peroxisomal multifunctional enzyme type 2, cg3415; **PDBTitle:** structure of full-length peroxisomal multifunctional enzyme type 22 from drosophila melanogaster
111	d2v4jc1	Alignment	not modelled	23.9	36	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
112	c3ixzA_	Alignment	not modelled	23.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
113	d1uepa_	Alignment	not modelled	23.7	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
114	d2ba0a1	Alignment	not modelled	23.5	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
115	c2q3gA_	Alignment	not modelled	22.6	19	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**pdz and lim domain protein 7; **PDBTitle:** structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
116	c3gpqA_	Alignment	not modelled	22.3	9	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of macro domain of chikungunya virus in complex with2 rna
117	d2c4va1	Alignment	not modelled	22.2	23	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
118	c2e6zA_	Alignment	not modelled	22.1	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
119	d1qvpa_	Alignment	not modelled	22.0	33	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
120	c2cauA_	Alignment	not modelled	21.8	21	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean