Phyre^2

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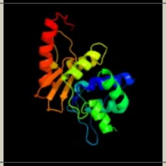
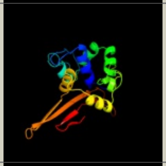
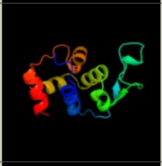
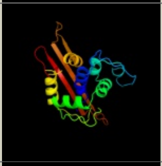
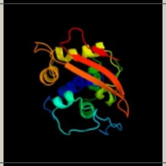
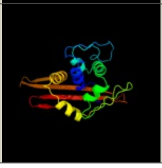
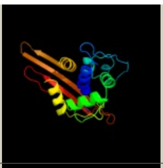
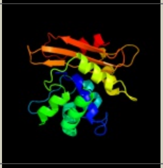
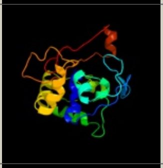
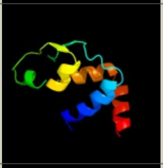
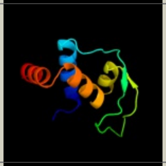
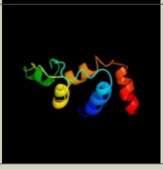
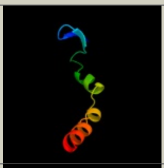
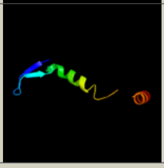
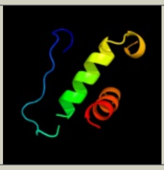
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jc7A_	Alignment		96.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase oxa-24; **PDBTitle:** the crystal structure of the carbapenemase oxa-24 reveals2 new insights into the mechanism of carbapenem-hydrolysis
2	c3oc2A_	Alignment		96.3	17	**PDB header:**penicillin-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa
3	c3if6C_	Alignment		96.1	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**oxa-46 oxacillinase; **PDBTitle:** crystal structure of oxa-46 beta-lactamase from p.2 aeruginosa
4	c3lo7A_	Alignment		96.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein a; **PDBTitle:** crystal structure of pbpa from mycobacterium tuberculosis
5	d1k55a_	Alignment		95.4	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
6	d1nrfa_	Alignment		95.1	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
7	c3hbrD_	Alignment		94.6	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**oxa-48; **PDBTitle:** crystal structure of oxa-48 beta-lactamase
8	d1xa1a_	Alignment		94.5	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
9	c3equB_	Alignment		94.3	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** crystal structure of penicillin-binding protein 2 from neisseria2 gonorrhoeae
10	c3udiA_	Alignment		94.1	19	**PDB header:**penicillin-binding protein/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 1a; **PDBTitle:** crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
11	d1k38a_	Alignment		93.9	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase

12	c2iwdA_	Alignment		93.7	12	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**methicillin resistance mecr1 protein; **PDBTitle:** oxacilloyl-acylated mecr1 extracellular antibiotic-sensor2 domain.
13	c3ue3A_	Alignment		93.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3, **PDBTitle:** crystal structure of acinetobacter baumanni pbp3
14	c3pbqA_	Alignment		92.8	19	**PDB header:**hydrolase/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 3; **PDBTitle:** crystal structure of pbp3 complexed with imipenem
15	d1vqqa3	Alignment		91.9	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
16	c2olvA_	Alignment		89.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
17	d1rp5a4	Alignment		88.8	16	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
18	d1pyya4	Alignment		88.1	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
19	c1qmfA_	Alignment		87.7	16	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**penicillin-binding protein 2x; **PDBTitle:** penicillin-binding protein 2x (pbp-2x) acyl-enzyme complex
20	c1pmdA_	Alignment		86.9	16	**PDB header:**peptidoglycan synthesis **Chain:** A: **PDB Molecule:**peptidoglycan synthesis multifunctional enzyme; **PDBTitle:** penicillin-binding protein 2x (pbp-2x)
21	c2bg1A_	Alignment	not modelled	86.6	17	**PDB header:**peptidoglycan **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** active site restructuring regulates ligand recognition in2 classa penicillin-binding proteins (pbps)
22	d1mr1c_	Alignment	not modelled	84.0	30	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SMAD4-binding domain of oncoprotein Ski
23	c3fwlA_	Alignment	not modelled	82.9	16	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
24	d2c5wb1	Alignment	not modelled	82.6	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
25	c3dwkC_	Alignment	not modelled	81.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**penicillin-binding protein 2; **PDBTitle:** identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
26	d2bg1a1	Alignment	not modelled	79.7	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
27	c2wadB_	Alignment	not modelled	78.0	21	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**penicillin-binding protein 2b; **PDBTitle:** penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
28	c2jciA_	Alignment	not modelled	77.9	19	**PDB header:**drug-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b
						PDB header:biosynthetic protein

29	c1mwuA_	Alignment	not modelled	70.8	16	**Chain:** A: **PDB Molecule:**penicillin-binding protein 2a; **PDBTitle:** structure of methicillin acyl-penicillin binding protein 2a2 from methicillin resistant staphylococcus aureus strain3 27r at 2.60 a resolution.
30	c1t6sB_	Alignment		63.6	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a conserved hypothetical protein from chlorobium2 tepidum
31	c2z99A_	Alignment		63.2	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of scpb from mycobacterium tuberculosis
32	d2olua2	Alignment	not modelled	61.1	18	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
33	c3dtkA_	Alignment		52.0	31	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**irre protein; **PDBTitle:** crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
34	c2xftA_	Alignment	not modelled	41.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**orf12; **PDBTitle:** structural and mechanistic studies on a cephalosporin esterase from2 the clavulanic acid biosynthesis pathway
35	c3gwrA_	Alignment	not modelled	41.1	8	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative calcium/calmodulin-dependent protein kinase type **PDBTitle:** crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
36	d3elga1	Alignment	not modelled	35.4	26	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
37	d1m6ka_	Alignment	not modelled	32.8	14	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
38	d1dy6a_	Alignment	not modelled	31.4	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
39	c2hcbC_	Alignment	not modelled	30.4	35	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
40	c2dafA_	Alignment	not modelled	28.1	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flj35834 protein; **PDBTitle:** solution structure of the novel identified ubiquitin-like2 domain in the human hypothetical protein flj35834
41	c3k7cC_	Alignment	not modelled	27.8	25	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**putative ntf2-like transpeptidase; **PDBTitle:** crystal structure of putative ntf2-like transpeptidase (np_281412.1)2 from campylobacter jejuni at 2.00 a resolution
42	d2pf5a1	Alignment	not modelled	27.6	50	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Link domain
43	c1aduB_	Alignment	not modelled	25.7	28	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**adenovirus single-stranded dna-binding protein; **PDBTitle:** early e2a dna-binding protein
44	c1wg8B_	Alignment	not modelled	25.6	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-dependent **PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
45	c1m6yA_	Alignment	not modelled	23.3	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
46	d3duea1	Alignment	not modelled	23.3	29	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
47	d3cnxa1	Alignment	not modelled	22.5	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SAV4671-like
48	c1zb7A_	Alignment	not modelled	20.2	28	**PDB header:**toxin **Chain:** A: **PDB Molecule:**neurotoxin; **PDBTitle:** crystal structure of botulinum neurotoxin type g light chain
49	d1l8qa2	Alignment	not modelled	18.4	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
50	c3g5jA_	Alignment	not modelled	18.3	18	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630

51	d1adta2	Alignment	not modelled	17.2	24	**Fold:**Zn-binding domains of ADDBP **Superfamily:**Zn-binding domains of ADDBP **Family:**Zn-binding domains of ADDBP
52	c3c0fB_	Alignment	not modelled	14.3	32	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_1514; **PDBTitle:** crystal structure of a novel non-pfam protein af1514 from archeoglobus2 fulgidus dsm 4304 solved by s-sad using a cr x-ray source
53	d1k25a4	Alignment	not modelled	13.7	23	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**beta-Lactamase/D-ala carboxypeptidase
54	c3u1nC_	Alignment	not modelled	13.3	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
55	d1t3ka_	Alignment	not modelled	12.2	33	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
56	c3fkaD_	Alignment	not modelled	12.0	25	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized ntf-2 like protein; **PDBTitle:** crystal structure of a ntf-2 like protein of unknown function2 (spo1084) from silicibacter pomeroyi dss-3 at 1.69 a resolution
57	c2c99A_	Alignment	not modelled	11.7	21	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
58	d1kyfa2	Alignment	not modelled	11.7	26	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Clathrin adaptor appendage, alpha and beta chain-specific domain
59	d1jqna_	Alignment	not modelled	11.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
60	c1xnjB_	Alignment	not modelled	11.4	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
61	d2aq2b1	Alignment	not modelled	11.4	28	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
62	d1mhyd_	Alignment	not modelled	11.0	18	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
63	d1p5dx4	Alignment	not modelled	10.9	18	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
64	c2jx8A_	Alignment	not modelled	10.7	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phosphorylated ctd-interacting factor 1; **PDBTitle:** solution structure of hpcif1 ww domain
65	d1whqa_	Alignment	not modelled	10.4	28	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
66	c1jqoA_	Alignment	not modelled	10.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
67	d1jqoa_	Alignment	not modelled	10.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
68	c2r44A_	Alignment	not modelled	10.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
69	c3nfiB_	Alignment	not modelled	10.0	14	**PDB header:**dna binding protein, transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa49; **PDBTitle:** crystal structure of tandem winged helix domain of rna polymerase i2 subunit a49
70	c2givA_	Alignment	not modelled	10.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable histone acetyltransferase myst1; **PDBTitle:** human myst histone acetyltransferase 1
71	d2giva1	Alignment	not modelled	10.0	26	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
72	c3dukD_	Alignment	not modelled	9.7	25	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
73	d1qvra2	Alignment	not modelled	9.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
74	c3hfkB_	Alignment	not modelled	9.7	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-methylmuconolactone methylisomerase; **PDBTitle:** crystal structure of 4-methylmuconolactone methylisomerase2 (h52a) in complex with 4-methylmuconolactone
75	c3nhvE_	Alignment	not modelled	9.6	21	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**bh2092 protein; **PDBTitle:** crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f

76	c3iukB_	Alignment	not modelled	9.3	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
77	c2jofA_	Alignment	not modelled	9.1	60	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**trp-cage; **PDBTitle:** the trp-cage: optimizing the stability of a globular2 miniprotein
78	d1g8fa3	Alignment	not modelled	9.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
79	c2q14A_	Alignment	not modelled	9.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
80	c3f7sA_	Alignment	not modelled	8.7	5	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
81	d1fw8a_	Alignment	not modelled	8.5	29	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
82	d1k82a2	Alignment	not modelled	8.4	17	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
83	c1wx4B_	Alignment	not modelled	8.3	18	**PDB header:**oxidoreductase/metal transport **Chain:** B: **PDB Molecule:**melc; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
84	c2g7rA_	Alignment	not modelled	8.3	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein 1
85	c2ee7A_	Alignment	not modelled	8.2	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sperm flagellar protein 1; **PDBTitle:** solution structure of the ch domain from human sperm2 flagellar protein 1
86	d1fnua1	Alignment	not modelled	8.1	22	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
87	c1c4gB_	Alignment	not modelled	8.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
88	c2wuqA_	Alignment	not modelled	7.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**beta-lactamase regulatory protein blab; **PDBTitle:** crystal structure of blab protein from streptomyces cacaoi
89	d1yt8a4	Alignment	not modelled	7.8	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
90	d2bgca1	Alignment	not modelled	7.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
91	c2bgcA_	Alignment	not modelled	7.6	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
92	d2cb5a_	Alignment	not modelled	7.5	27	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
93	d1yt8a1	Alignment	not modelled	7.5	36	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
94	d1b24a2	Alignment	not modelled	7.5	26	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
95	d1e32a3	Alignment	not modelled	7.3	19	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
96	d2ux0a1	Alignment	not modelled	7.3	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
97	d2f86b1	Alignment	not modelled	7.3	15	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
98	c3nbxX_	Alignment	not modelled	7.2	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
99	c3emeA_	Alignment	not modelled	7.1	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rhodanese-like domain protein; **PDBTitle:** crystal structure of rhodanese-like domain protein from2 staphylococcus aureus