Phyre^2

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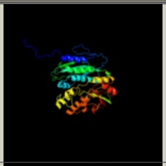
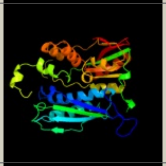
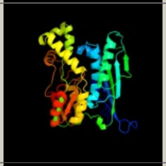
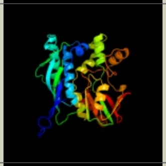
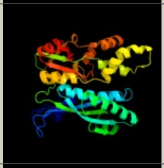
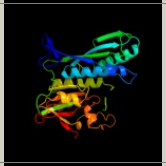
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3m84A_	Alignment		100.0	41	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
2	c1cliD_	Alignment		100.0	100	**PDB header:**ligase **Chain:** D: **PDB Molecule:**protein (phosphoribosyl-aminoimidazole synthetase); **PDBTitle:** x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
3	c2z01A_	Alignment		100.0	48	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus
4	c3mdoB_	Alignment		100.0	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of a putative phosphoribosylformylglycinamidine2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
5	c2btuB_	Alignment		100.0	55	**PDB header:**synthase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole synthetase; **PDBTitle:** crystal structure of phosphoribosylformylglycinamidine2 cyclo-ligase from bacillus anthracis at 2.3a resolution.
6	c3kizA_	Alignment		100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of putative phosphoribosylformylglycinamidine cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
7	c2v9yA_	Alignment		100.0	49	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** human aminoimidazole ribonucleotide synthetase
8	c3fd5B_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp
9	c2zauB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
10	c3mcqA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine-monophosphate kinase; **PDBTitle:** crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution
11	c2z1tA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype

12	c2rb9D_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hype protein; **PDBTitle:** crystal structure of e.coli hype
13	c2zodB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
14	c3c9uB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** aathil complexed with adp and tpp
15	c2z1eA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hype from thermococcus kodakaraensis (outward2 form)
16	c2yxzA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin-monophosphate kinase; **PDBTitle:** crystal structure of tt0281 from thermus thermophilus hb8
17	c1vqvB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus
18	c3ac6A_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
19	c2hs0A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** t. maritima purl complexed with atp
20	c3d54I_	Alignment		100.0	20	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** stucture of purlqs from thermotoga maritima
21	d1clia1	Alignment	not modelled	100.0	100	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
22	d1clib1	Alignment	not modelled	100.0	100	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
23	d1clia2	Alignment	not modelled	100.0	100	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
24	c1t3tA_	Alignment	not modelled	100.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
25	d3c9ua1	Alignment	not modelled	100.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
26	d2zaua1	Alignment	not modelled	100.0	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
27	d2zoda2	Alignment	not modelled	99.9	18	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
28	d2z1ea2	Alignment	not modelled	99.9	18	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
29	d3c9ua2	Alignment	not modelled	99.9	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like

						Family: PurM C-terminal domain-like
30	d2z1ea1	Alignment	not modelled	99.9	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
31	d2zoda1	Alignment	not modelled	99.9	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
32	d1vk3a2	Alignment	not modelled	99.9	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
33	d1vk3a3	Alignment	not modelled	99.9	18	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
34	d1vk3a1	Alignment	not modelled	99.8	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
35	d1t3ta6	Alignment	not modelled	99.8	11	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
36	d1t3ta7	Alignment	not modelled	99.7	22	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
37	d1t3ta4	Alignment	not modelled	99.3	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
38	d1t3ta5	Alignment	not modelled	98.6	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
39	d1to3a_	Alignment	not modelled	84.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
40	d3dhxa1	Alignment	not modelled	71.2	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
41	c3dzvB_	Alignment	not modelled	58.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
42	d1q3oa_	Alignment	not modelled	49.5	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
43	d2qrra1	Alignment	not modelled	49.3	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
44	c1jyeA_	Alignment	not modelled	49.0	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
45	d1jyea_	Alignment	not modelled	49.0	29	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
46	c3o1hB_	Alignment	not modelled	46.7	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
47	c3d8uA_	Alignment	not modelled	42.9	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
48	c3jrkG_	Alignment	not modelled	42.4	21	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
49	c2vk2A_	Alignment	not modelled	41.2	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
50	c3rotA_	Alignment	not modelled	40.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc sugar transporter, periplasmic sugar binding protein; **PDBTitle:** crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
51	c3l4fD_	Alignment	not modelled	40.8	16	**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
52	c3gndC_	Alignment	not modelled	37.0	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
53	c2eg5C_	Alignment	not modelled	36.7	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**xanthosine methyltransferase; **PDBTitle:** the structure of xanthosine methyltransferase
54	c3l49D_	Alignment	not modelled	35.8	9	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc sugar (ribose) transporter, periplasmic **PDBTitle:** crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
						PDB header:replication

55	c3bgwD_	Alignment	not modelled	35.8	8	**Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
56	c2qjhH_	Alignment	not modelled	35.8	24	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
57	c2rjoA_	Alignment	not modelled	35.0	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
58	c2q6tB_	Alignment	not modelled	34.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
59	c3qglD_	Alignment	not modelled	34.4	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3
60	c2xkxB_	Alignment	not modelled	31.7	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
61	d1v8aa_	Alignment	not modelled	31.4	28	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
62	d1m6ex_	Alignment	not modelled	30.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Salicylic acid carboxyl methyltransferase (SAMT)
63	d8abpa_	Alignment	not modelled	30.6	3	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
64	d1iz0a2	Alignment	not modelled	30.1	5	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
65	c3jy6B_	Alignment	not modelled	29.9	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
66	d2csua1	Alignment	not modelled	29.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
67	c3cs3A_	Alignment	not modelled	29.4	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
68	c3qi7A_	Alignment	not modelled	29.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
69	c3ma0A_	Alignment	not modelled	28.9	9	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**d-xylose-binding periplasmic protein; **PDBTitle:** closed liganded crystal structure of xylose binding protein from2 escherichia coli
70	c3l6uA_	Alignment	not modelled	28.6	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system periplasmic **PDBTitle:** crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum
71	c3ksmA_	Alignment	not modelled	28.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
72	c3shwA_	Alignment	not modelled	28.0	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
73	c3e61A_	Alignment	not modelled	27.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional repressor of ribose operon; **PDBTitle:** crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
74	d1guda_	Alignment	not modelled	26.8	17	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
75	c3bblA_	Alignment	not modelled	25.7	3	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**regulatory protein of laci family; **PDBTitle:** crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
76	c3fokH_	Alignment	not modelled	25.5	8	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
77	d2nzug1	Alignment	not modelled	25.1	6	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
78	d2dria_	Alignment	not modelled	24.7	15	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
79	c3jvdA	Alignment	not modelled	24.2	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators;

79	c3jvdA_	Alignment	not modelled	24.2	15	**PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
80	c2jreA_	Alignment	not modelled	24.2	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**c60-1 pdz domain peptide; **PDBTitle:** c60-1, a pdz domain designed using statistical coupling2 analysis
81	c3diwB_	Alignment	not modelled	23.3	19	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
82	d2cz4a1	Alignment	not modelled	23.2	8	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
83	d1o6xa_	Alignment	not modelled	23.0	16	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
84	c3egcF_	Alignment	not modelled	22.8	15	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative ribose operon repressor; **PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
85	d1kkha2	Alignment	not modelled	22.6	19	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
86	c3bilA_	Alignment	not modelled	22.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable laci-family transcriptional regulator; **PDBTitle:** crystal structure of a probable laci family transcriptional2 regulator from corynebacterium glutamicum
87	d1pcaa1	Alignment	not modelled	22.2	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
88	c3d02A_	Alignment	not modelled	22.1	3	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative laci-type transcriptional regulator; **PDBTitle:** crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
89	c3gybB_	Alignment	not modelled	22.1	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulators (laci-family **PDBTitle:** crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
90	c3o74A_	Alignment	not modelled	22.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fructose transport system repressor frur; **PDBTitle:** crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
91	d1tjya_	Alignment	not modelled	22.0	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
92	d1tlfa_	Alignment	not modelled	22.0	30	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
93	c2ioyB_	Alignment	not modelled	21.9	12	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
94	d1pbaa_	Alignment	not modelled	21.8	8	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
95	d2boaa2	Alignment	not modelled	21.7	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
96	c3hs3A_	Alignment	not modelled	21.5	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**ribose operon repressor; **PDBTitle:** crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
97	c3e3mA_	Alignment	not modelled	21.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
98	d1uita_	Alignment	not modelled	21.4	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
99	d1pyta_	Alignment	not modelled	21.4	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
100	c2fn9A_	Alignment	not modelled	21.3	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein; **PDBTitle:** thermotoga maritima ribose binding protein unliganded form
101	c3kkeA_	Alignment	not modelled	21.0	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
102	c3eggC_	Alignment	not modelled	20.8	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**spinophilin; **PDBTitle:** crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin