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Description	P0AGG0
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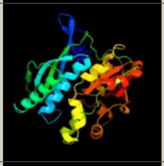
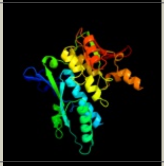
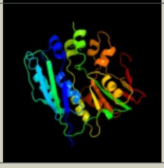
Unique Job ID	32249af2e0229989

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mcqA_	Alignment		100.0	42	**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
2	c3c9uB_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** aathil complexed with adp and tpp
3	c1vqvB_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus
4	c2yxzA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin-monophosphate kinase; **PDBTitle:** crystal structure of tt0281 from thermus thermophilus hb8
5	c2btuB_	Alignment		100.0	16	**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	c1cliD_	Alignment		100.0	17	**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
7	c2rb9D_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hype protein; **PDBTitle:** crystal structure of e.coli hype
8	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
9	c2z01A_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus
10	c3m84A_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
11	c3fd5B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp

12	c2zauB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
13	c2zodB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
14	c3ac6A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
15	c2z1eA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hype from thermococcus kodakaraensis (outward2 form)
16	c2v9yA_	Alignment		100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** human aminoimidazole ribonucleotide synthetase
17	c2hs0A_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** t. maritima purl complexed with atp
18	c3d54I_	Alignment		100.0	16	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** stucture of purlqs from thermotoga maritima
19	c1t3tA_	Alignment		100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
20	c3mdoB_	Alignment		100.0	15	**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
21	c3kizA_	Alignment	not modelled	100.0	13	**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
22	d3c9ua1	Alignment	not modelled	100.0	31	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
23	d1clib1	Alignment	not modelled	100.0	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
24	d1clia1	Alignment	not modelled	100.0	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
25	d3c9ua2	Alignment	not modelled	100.0	36	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
26	d2zaua1	Alignment	not modelled	100.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
27	d1vk3a2	Alignment	not modelled	100.0	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
28	d2zoda2	Alignment	not modelled	99.9	24	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like

29	d2zoda1	Alignment	not modelled	99.9	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
30	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
31	d1clia2	Alignment	not modelled	99.9	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
32	d2z1ea1	Alignment	not modelled	99.9	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
33	d1vk3a3	Alignment	not modelled	99.9	16	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
34	d1t3ta6	Alignment	not modelled	99.9	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
35	d1vk3a1	Alignment	not modelled	99.9	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
36	d1t3ta7	Alignment	not modelled	99.7	20	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
37	d1t3ta4	Alignment	not modelled	99.7	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
38	d1t3ta5	Alignment	not modelled	99.4	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
39	c3qi7A_	Alignment	not modelled	88.4	15	**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
40	d1to3a_	Alignment	not modelled	86.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
41	c3fokH_	Alignment	not modelled	77.1	19	**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
42	c3o1hB_	Alignment	not modelled	71.5	9	**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
43	d3dhxa1	Alignment	not modelled	63.7	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
44	c2vk2A_	Alignment	not modelled	61.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
45	d1jyea_	Alignment	not modelled	59.9	3	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
46	c1jyeA_	Alignment	not modelled	59.9	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
47	c2rjoA_	Alignment	not modelled	57.4	12	**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
48	c3d8uA_	Alignment	not modelled	54.8	29	**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
49	c3l49D_	Alignment	not modelled	52.1	15	**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
50	c3jrkG_	Alignment	not modelled	51.8	8	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
51	c3rotA_	Alignment	not modelled	51.7	9	**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
52	c3ma0A_	Alignment	not modelled	50.1	6	**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
53	d8abpa_	Alignment	not modelled	49.8	15	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
						PDB header:transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator,

54	c3cs3A_	Alignment	not modelled	45.9	15	laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
55	c3jy6B_	Alignment	not modelled	45.6	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
56	d2csua1	Alignment	not modelled	45.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
57	d2dria_	Alignment	not modelled	44.8	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
58	c3ksmA_	Alignment	not modelled	44.5	16	**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
59	c3l6uA_	Alignment	not modelled	44.4	3	**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
60	d1guda_	Alignment	not modelled	44.0	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
61	c3e61A_	Alignment	not modelled	43.2	18	**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
62	c2q6tB_	Alignment	not modelled	42.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
63	d2nzug1	Alignment	not modelled	42.0	18	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
64	d2qrra1	Alignment	not modelled	41.9	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
65	c2ioyB_	Alignment	not modelled	41.3	9	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
66	c3hs3A_	Alignment	not modelled	41.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**ribose operon repressor; **PDBTitle:** crystal structure of periplasmic binding ribose operon2 repressor protein from lactobacillus acidophilus
67	c3jvdA_	Alignment	not modelled	41.0	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
68	c3h5oB_	Alignment	not modelled	39.8	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
69	c3egcF_	Alignment	not modelled	39.5	6	**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
70	c3kkeA_	Alignment	not modelled	38.5	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
71	c3o74A_	Alignment	not modelled	37.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fructose transport system repressor frur; **PDBTitle:** crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
72	c3e3mA_	Alignment	not modelled	37.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
73	c3bilA_	Alignment	not modelled	36.9	9	**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
74	c3c3kA_	Alignment	not modelled	35.4	3	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
75	c3ctpB_	Alignment	not modelled	35.0	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of periplasmic binding protein/laci transcriptional2 regulator from alkaliphilus metalliredigens qymf complexed with d-3 xylulofuranose
76	c3gybB_	Alignment	not modelled	34.6	24	**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
77	c3d02A_	Alignment	not modelled	34.1	6	**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
						PDB header:transcription

78	c2h0aA_	Alignment	not modelled	33.6	18	**Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus
79	c2rgyA_	Alignment	not modelled	32.9	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
80	c3brqA_	Alignment	not modelled	32.1	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
81	c2o20H_	Alignment	not modelled	32.1	18	**PDB header:**transcription **Chain:** H: **PDB Molecule:**catabolite control protein a; **PDBTitle:** crystal structure of transcription regulator ccpa of lactococcus2 lactis
82	c2qvcC_	Alignment	not modelled	31.8	3	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
83	d1dbqa_	Alignment	not modelled	31.7	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
84	d1tlfa_	Alignment	not modelled	31.6	0	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
85	c2iksA_	Alignment	not modelled	31.3	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding transcriptional dual regulator; **PDBTitle:** crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
86	c3dzvB_	Alignment	not modelled	30.7	17	**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
87	d1tjya_	Alignment	not modelled	30.3	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
88	c2qjhH_	Alignment	not modelled	28.8	17	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
89	d1byka_	Alignment	not modelled	28.7	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
90	c2fn9A_	Alignment	not modelled	26.7	6	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein; **PDBTitle:** thermotoga maritima ribose binding protein unliganded form
91	d1o6xa_	Alignment	not modelled	24.5	28	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
92	c3gndC_	Alignment	not modelled	23.3	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
93	d1puca_	Alignment	not modelled	23.1	11	**Fold:**Cell cycle regulatory proteins **Superfamily:**Cell cycle regulatory proteins **Family:**Cell cycle regulatory proteins
94	d1pyta_	Alignment	not modelled	23.0	24	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
95	c3bblA_	Alignment	not modelled	22.6	14	**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
96	d1qd1a2	Alignment	not modelled	22.4	11	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
97	d1pcaa1	Alignment	not modelled	22.2	28	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
98	d2boaa2	Alignment	not modelled	21.8	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
99	c3hulA_	Alignment	not modelled	21.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine kinase; **PDBTitle:** structure of putative homoserine kinase thrb from listeria2 monocytogenes
100	d1ayea2	Alignment	not modelled	20.9	28	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
101	d1kwma2	Alignment	not modelled	20.9	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
102	c2qu7B_	Alignment	not modelled	20.5	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
						Fold: Cell cycle regulatory proteins

103	d1qb3a_	Alignment	not modelled	20.3	22	**Superfamily:**Cell cycle regulatory proteins **Family:**Cell cycle regulatory proteins