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Description	P37028
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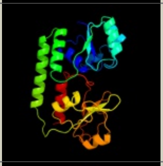
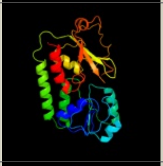
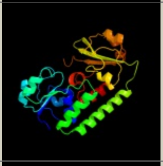
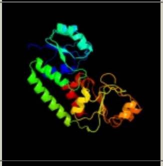
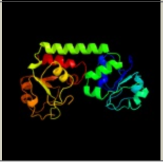
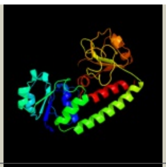
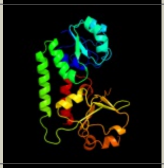
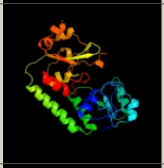
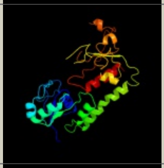
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n2za_	Alignment		100.0	100	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
2	c3md9A_	Alignment		100.0	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hemin-binding periplasmic protein hmut; **PDBTitle:** structure of apo form of a periplasmic heme binding protein
3	c2r7aC_	Alignment		100.0	26	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
4	c2r79A_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein from2 pseudomonas aeruginosa
5	c2q8pA_	Alignment		100.0	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron-regulated surface determinant e; **PDBTitle:** crystal structure of selenomethionine labelled s. aureus isde2 complexed with heme
6	c3pshA_	Alignment		100.0	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein hi_1472; **PDBTitle:** classification of a haemophilus influenzae abc transporter hi1470/712 through its cognate molybdate periplasmic binding protein mola (mola3 bound to molybdate)
7	d2chua1	Alignment		100.0	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
8	c3eiwA_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**htsa protein; **PDBTitle:** crystal structure of staphylococcus aureus lipoprotein, htsa
9	c3gfvA_	Alignment		100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized abc transporter solute-binding **PDBTitle:** crystal structure of petrobactin-binding protein yclq from2 bacillu subtilis
10	d1esza_	Alignment		100.0	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Periplasmic ferric siderophore binding protein FhuD
11	c3be5D_	Alignment		100.0	18	**PDB header:**metal transport **Chain:** D: **PDB Molecule:**putative iron compound-binding protein of abc transporter **PDBTitle:** crystal structure of fite (crystal form 1), a group iii periplasmic2 siderophore binding protein

12	c3g9qA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ferrichrome-binding protein; **PDBTitle:** crystal structure of the fhud fold-family bsu3320, a periplasmic2 binding protein component of a fep/fec-like ferrichrome abc3 transporter from bacillus subtilis. northeast structural genomics4 consortium target sr577a
13	c3mwgA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-regulated abc transporter siderophore-binding protein **PDBTitle:** crystal structure of staphylococcus aureus sira
14	c2phzA_	Alignment		100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron-uptake system-binding protein; **PDBTitle:** crystal structure of iron-uptake system-binding protein2 feua from bacillus subtilis. northeast structural genomics3 target sr580.
15	d2phza1	Alignment		100.0	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
16	d2etva1	Alignment		100.0	16	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TM0189-like
17	c2x4lA_	Alignment		100.0	18	**PDB header:**transport **Chain:** A: **PDB Molecule:**ferric-siderophore receptor protein; **PDBTitle:** crystal structure of dese, a ferric-siderophore receptor2 protein from streptomyces coelicolor
18	d1qh8a_	Alignment		96.4	16	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
19	c3aerC_	Alignment		96.3	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
20	c3pdiG_	Alignment		96.1	11	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
21	c2xdqA_	Alignment	not modelled	96.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
22	d1m1na_	Alignment	not modelled	95.8	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
23	d1mioa_	Alignment	not modelled	95.0	16	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
24	c3pdiB_	Alignment	not modelled	93.9	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
25	d1qh8b_	Alignment	not modelled	93.4	16	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
26	d1miob_	Alignment	not modelled	90.2	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
27	d7reqa2	Alignment	not modelled	81.3	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
28	d1m1nb_	Alignment	not modelled	77.3	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
						Fold: Chelatase-like

29	d1pq4a_	Alignment	not modelled	74.1	13	**Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
30	c1e1cA_	Alignment	not modelled	71.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase alpha chain; **PDBTitle:** methylmalonyl-coa mutase h244a mutant
31	c1toaA_	Alignment	not modelled	70.5	11	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
32	d1toaa_	Alignment	not modelled	70.5	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
33	c2xdqB_	Alignment	not modelled	68.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
34	d1p3da1	Alignment	not modelled	66.5	10	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
35	c3mfqB_	Alignment	not modelled	64.6	16	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
36	c2r8rB_	Alignment	not modelled	64.5	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
37	d1ovma1	Alignment	not modelled	62.6	8	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
38	d1q3qa2	Alignment	not modelled	58.9	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
39	d1psza_	Alignment	not modelled	58.0	9	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
40	c2zkqb_	Alignment	not modelled	57.8	7	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
41	c3bchA_	Alignment	not modelled	57.6	7	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
42	c1s1hB_	Alignment	not modelled	57.5	20	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
43	c2xznB_	Alignment	not modelled	57.5	13	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
44	c2gm2A_	Alignment	not modelled	57.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
45	d1assa_	Alignment	not modelled	57.2	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
46	d1kjqa2	Alignment	not modelled	57.1	26	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
47	d1gmla_	Alignment	not modelled	56.0	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
48	d1x74a1	Alignment	not modelled	55.1	20	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
49	c3izbA_	Alignment	not modelled	52.8	20	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
50	d1j6ua1	Alignment	not modelled	52.5	13	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
51	c3bbnB_	Alignment	not modelled	50.4	24	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
52	d2ioja1	Alignment	not modelled	50.0	15	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
53	d1vi6a_	Alignment	not modelled	49.9	20	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2

54	c3kc2A_	Alignment	not modelled	49.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
55	c3iz6A_	Alignment	not modelled	48.3	17	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
56	d2gy9b1	Alignment	not modelled	47.2	21	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
57	c2dc1A_	Alignment	not modelled	46.7	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
58	d1pjca2	Alignment	not modelled	45.4	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
59	d2q4qa1	Alignment	not modelled	45.3	21	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
60	d2uubb1	Alignment	not modelled	45.1	21	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
61	d1a9xa4	Alignment	not modelled	43.5	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
62	c3hjtB_	Alignment	not modelled	42.9	15	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
63	d1a6db2	Alignment	not modelled	41.3	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
64	c3sg0A_	Alignment	not modelled	38.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
65	d1f06a1	Alignment	not modelled	38.3	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	d1ig3a2	Alignment	not modelled	38.3	10	**Fold:**Thiamin pyrophosphokinase, catalytic domain **Superfamily:**Thiamin pyrophosphokinase, catalytic domain **Family:**Thiamin pyrophosphokinase, catalytic domain
67	c1kjjA_	Alignment	not modelled	37.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
68	d2jfga1	Alignment	not modelled	37.2	20	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
69	d7reqb2	Alignment	not modelled	35.6	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
70	c3cu5B_	Alignment	not modelled	35.5	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family; **PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
71	d1ig0a2	Alignment	not modelled	33.3	8	**Fold:**Thiamin pyrophosphokinase, catalytic domain **Superfamily:**Thiamin pyrophosphokinase, catalytic domain **Family:**Thiamin pyrophosphokinase, catalytic domain
72	c3o3nB_	Alignment	not modelled	32.1	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
73	c2f17A_	Alignment	not modelled	31.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin pyrophosphokinase 1; **PDBTitle:** mouse thiamin pyrophosphokinase in a ternary complex with2 pyrithiamin pyrophosphate and amp at 2.5 angstrom
74	c2ov3A_	Alignment	not modelled	31.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
75	c2ayxA_	Alignment	not modelled	31.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor kinase protein rcsc; **PDBTitle:** solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
76	c1ig0A_	Alignment	not modelled	30.7	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** crystal structure of yeast thiamin pyrophosphokinase
77	d1li4a2	Alignment	not modelled	29.3	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
78	c2hh9A_	Alignment	not modelled	29.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** thiamin pyrophosphokinase from candida albicans

79	d1a9xb2	Alignment	not modelled	28.6	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
80	c3dapB_	Alignment	not modelled	28.5	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
81	c3e18A_	Alignment	not modelled	27.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
82	c2yxbA_	Alignment	not modelled	27.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
83	c2dwcB_	Alignment	not modelled	27.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
84	d1zpda1	Alignment	not modelled	27.0	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
85	d1zcca1	Alignment	not modelled	26.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
86	c1z7eC_	Alignment	not modelled	26.1	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
87	c3cx3A_	Alignment	not modelled	26.0	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
88	d1wraa1	Alignment	not modelled	26.0	23	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
89	d1eo1a_	Alignment	not modelled	25.2	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
90	c2vhyB_	Alignment	not modelled	24.0	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
91	c2bibA_	Alignment	not modelled	22.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
92	c1jdwA_	Alignment	not modelled	22.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-arginine\:glycine amidinotransferase; **PDBTitle:** crystal structure and mechanism of l-arginine: glycine2 amidinotransferase: a mitochondrial enzyme involved in3 creatine biosynthesis
93	d1jdwa_	Alignment	not modelled	22.0	18	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase
94	d1krwa_	Alignment	not modelled	21.6	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
95	d1xvla1	Alignment	not modelled	21.1	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
96	c8jdwA_	Alignment	not modelled	21.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (l-arginine:glycine amidinotransferase); **PDBTitle:** crystal structure of human l-arginine:glycine2 amidinotransferase in complex with l-alanine
97	d1s9ra_	Alignment	not modelled	20.8	27	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
98	c3d64A_	Alignment	not modelled	20.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
99	d1bwda_	Alignment	not modelled	19.4	21	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Amidinotransferase