Phyre2

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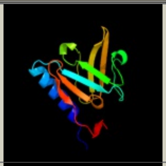
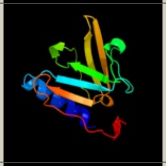
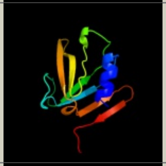
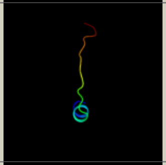
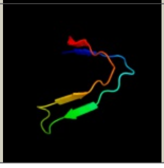
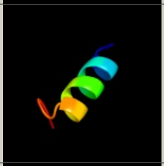
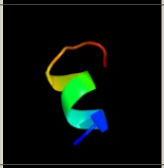
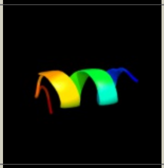
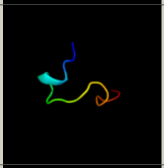
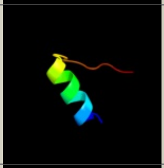
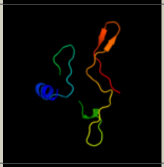
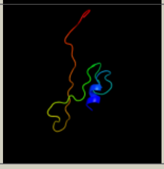
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yfna1	Alignment		100.0	100	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
2	d1ou9a_	Alignment		100.0	57	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
3	d1ou8a_	Alignment		100.0	63	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
4	d1zszc1	Alignment		100.0	61	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB
5	c2qasA_	Alignment		99.8	24	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of caulobacter crescentus sspb ortholog
6	c2nysA_	Alignment		99.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**agr_c_3712p; **PDBTitle:** x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.
7	d2nysa1	Alignment		99.7	16	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**AGR C 3712p-like
8	c2qazC_	Alignment		99.7	24	**PDB header:**hydrolase activator **Chain:** C: **PDB Molecule:**sspb protein; **PDBTitle:** structure of c. crescentus sspb ortholog
9	d1whqa_	Alignment		56.7	18	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
10	c3nrwA_	Alignment		43.4	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**phage integrase/site-specific recombinase; **PDBTitle:** crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
11	d2azea1	Alignment		43.0	18	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**DP dimerization segment

12	d1a0pa1	Alignment		29.2	13	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
13	c2kj5A_	Alignment		25.0	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage2 integrase protein nmul_a0064 from nitrosospira multiformis,3 northeast structural genomics consortium target nmr46c
14	d1xb4a2	Alignment		20.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
15	c3i5pA_	Alignment		18.9	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup170; **PDBTitle:** nup170(aa979-1502), s.cerevisiae
16	c3htuE_	Alignment		18.2	13	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** crystal structure of the human vps25-vps20 subcomplex
17	d6rxna_	Alignment		17.6	11	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
18	d1ro5a_	Alignment		17.2	25	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
19	d1nosa_	Alignment		16.1	26	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
20	c2qdzA_	Alignment		15.6	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**tpsb transporter fhac; **PDBTitle:** structure of the membrane protein fhac: a member of the2 omp85/tpsb transporter family
21	c2h0pA_	Alignment	not modelled	15.4	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** nmr structure of the dengue-4 virus envelope protein domain2 iii
22	c2g0bG_	Alignment	not modelled	15.3	14	**PDB header:**transferase **Chain:** G: **PDB Molecule:**feem; **PDBTitle:** the structure of feem, an n-acyl amino acid synthase from uncultured2 soil microbes
23	d2gena2	Alignment	not modelled	15.1	25	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
24	d1t4na_	Alignment	not modelled	15.0	13	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
25	c3nglA_	Alignment	not modelled	14.3	24	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
26	c3c5pF_	Alignment	not modelled	13.8	28	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**protein bas0735 of unknown function; **PDBTitle:** crystal structure of bas0735, a protein of unknown function from2 bacillus anthracis str. sterne
27	c2khvA_	Alignment	not modelled	13.7	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
28	c2kdrX_	Alignment	not modelled	13.7	44	**PDB header:**viral protein, membrane protein **Chain:** X: **PDB Molecule:**non-structural protein 4b; **PDBTitle:** solution structure of hcv ns4b(227-254)

29	d1a4ia1	Alignment	not modelled	13.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
30	c3kb4D_	Alignment	not modelled	13.3	36	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**alr8543 protein; **PDBTitle:** crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
31	d1qw9a2	Alignment	not modelled	13.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
32	c2kkpA_	Alignment	not modelled	12.4	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
33	c3qxyA_	Alignment	not modelled	11.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-lysine methyltransferase setd6; **PDBTitle:** human setd6 in complex with rela lys310
34	d1d5va_	Alignment	not modelled	11.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
35	d1b0aa1	Alignment	not modelled	11.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
36	c2kd1A_	Alignment	not modelled	11.7	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dna integration/recombination/invertion protein; **PDBTitle:** solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
37	d1h3ga1	Alignment	not modelled	11.6	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
38	c2kiwA_	Alignment	not modelled	11.5	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**int protein; **PDBTitle:** solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
39	c3rnvA_	Alignment	not modelled	11.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
40	d1jhfa1	Alignment	not modelled	10.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
41	c2kobA_	Alignment	not modelled	10.7	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of clolep_01837 (fragment 61-160)2 from clostridium leptum. northeast structural genomics3 consortium target qlr8a
42	c1e17A_	Alignment	not modelled	10.7	28	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
43	d1kzfa_	Alignment	not modelled	10.6	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
44	d1hl9a2	Alignment	not modelled	10.6	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
45	d1t4lb_	Alignment	not modelled	10.5	14	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
46	d2basa2	Alignment	not modelled	10.4	8	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
47	d1t4oa_	Alignment	not modelled	10.4	13	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
48	c1t4oA_	Alignment	not modelled	10.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease iii; **PDBTitle:** crystal structure of rnt1p dsrbd
49	d3bpya1	Alignment	not modelled	10.2	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
50	c1kq8A_	Alignment	not modelled	10.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
51	d1kq8a_	Alignment	not modelled	10.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
52	d1uhra_	Alignment	not modelled	10.0	22	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
53	c3msqC_	Alignment	not modelled	10.0	0	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**putative ubiquinone biosynthesis protein; **PDBTitle:** crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution

54	d1ok8a1	Alignment	not modelled	9.9	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
55	c3g73A_	Alignment	not modelled	9.8	33	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
56	d2c7fa2	Alignment	not modelled	9.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
57	c2c2xB_	Alignment	not modelled	9.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
58	c3htrB_	Alignment	not modelled	9.3	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized prc-barrel domain protein; **PDBTitle:** crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
59	c1asyA_	Alignment	not modelled	9.1	22	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
60	d2cxha1	Alignment	not modelled	9.0	14	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Brix domain
61	c2cxhA_	Alignment	not modelled	9.0	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable brix-domain ribosomal biogenesis protein; **PDBTitle:** crystal structure of probable ribosomal biogenesis protein from2 aeropyrum pernix k1
62	c2keyA_	Alignment	not modelled	8.9	0	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative phage integrase; **PDBTitle:** solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
63	c4a5oB_	Alignment	not modelled	8.6	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
64	d2hfha_	Alignment	not modelled	8.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
65	c3da4B_	Alignment	not modelled	8.5	20	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m; **PDBTitle:** crystal structure of colicin m, a novel phosphatase2 specifically imported by escherichia coli
66	d2gpia1	Alignment	not modelled	8.2	12	**Fold:**Shew3726-like **Superfamily:**Shew3726-like **Family:**Shew3726-like
67	d1v31a_	Alignment	not modelled	8.2	22	**Fold:**SWIB/MDM2 domain **Superfamily:**SWIB/MDM2 domain **Family:**SWIB/MDM2 domain
68	d2a07f1	Alignment	not modelled	8.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
69	d2c6ya1	Alignment	not modelled	8.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
70	c2kcuA_	Alignment	not modelled	8.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ctr107; **PDBTitle:** nmr solution structure of an uncharacterized protein from2 chlorobium tepidum. northeast structural genomics target3 ctr107
71	c3co7C_	Alignment	not modelled	7.8	22	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
72	c3b49A_	Alignment	not modelled	7.8	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2189 protein; **PDBTitle:** crystal structure of an uncharacterized conserved protein from2 listeria innocua
73	c1a4iB_	Alignment	not modelled	7.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
74	c2y9zB_	Alignment	not modelled	7.2	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**iswi one complex protein 3; **PDBTitle:** chromatin remodeling factor isw1a(del_atpase) in dna complex
75	c1eqrC_	Alignment	not modelled	6.9	21	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
76	c1r7gA_	Alignment	not modelled	6.9	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** nmr structure of the membrane anchor domain (1-31) of the2 nonstructural protein 5a (ns5a) of hepatitis c virus3 (minimized average structure, sample in 100mm dpc)
77	d1ib8a1	Alignment	not modelled	6.7	21	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
78	c1edzA_	Alignment	not modelled	6.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate dehydrogenase;

78	c1edzA_	Alignment	not modelled	6.7	24	**PDBTitle:** structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
79	c1b8aB_	Alignment	not modelled	6.5	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
80	d1f44a1	Alignment	not modelled	6.5	20	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
81	c1b0aA_	Alignment	not modelled	6.0	18	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
82	d2i7na2	Alignment	not modelled	5.9	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
83	d1dgwa_	Alignment	not modelled	5.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
84	c2oxoA_	Alignment	not modelled	5.8	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**integrase; **PDBTitle:** crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
85	c2gjmA_	Alignment	not modelled	5.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactoperoxidase; **PDBTitle:** crystal structure of buffalo lactoperoxidase at 2.75a resolution
86	c3p2oB_	Alignment	not modelled	5.8	12	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
87	d1z66a1	Alignment	not modelled	5.8	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
88	d1epwa3	Alignment	not modelled	5.8	32	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
89	c4a26B_	Alignment	not modelled	5.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
90	c1p0yA_	Alignment	not modelled	5.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulose-1,5 bisphosphate carboxylase/oxygenase **PDBTitle:** crystal structure of the set domain of lsmt bound to2 melysine and adohcy
91	d1phpa_	Alignment	not modelled	5.6	28	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
92	d1uika1	Alignment	not modelled	5.5	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
93	d1wlna1	Alignment	not modelled	5.5	11	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
94	d2g1la1	Alignment	not modelled	5.4	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
95	d1m0da_	Alignment	not modelled	5.3	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
96	d1wmha_	Alignment	not modelled	5.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
97	c2w27A_	Alignment	not modelled	5.3	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ykui protein; **PDBTitle:** crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium
98	d1uija1	Alignment	not modelled	5.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
99	c1vloA_	Alignment	not modelled	5.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution