Phyre^2

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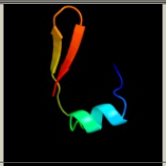
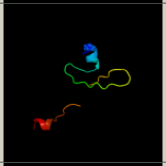
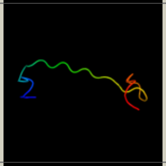
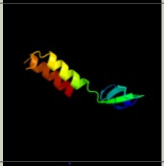
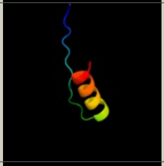
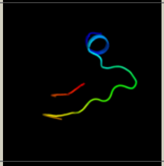
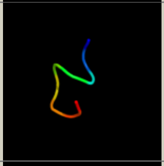
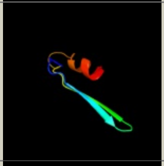
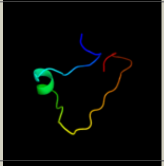
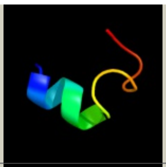
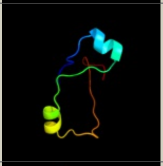
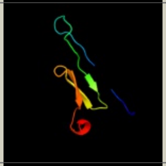
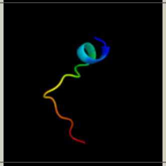
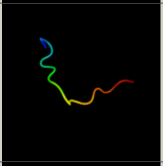
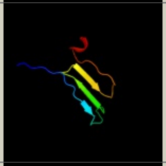
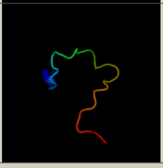
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mvfd_	Alignment		95.1	12	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
2	d1ub4c_	Alignment		89.1	16	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
3	c2hdeA_	Alignment		59.1	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap18; **PDBTitle:** solution structure of human sap18
4	d2j0na1	Alignment		46.2	20	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
5	d1w44a_	Alignment		37.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
6	c3mhxB_	Alignment		37.4	18	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**putative ferrous iron transport protein a; **PDBTitle:** crystal structure of stenotrophomonas maltophilia feoa complexed with2 zinc: a unique procaryotic sh3 domain protein possibly acting as a3 bacterial ferrous iron transport activating factor
7	d2dkya1	Alignment		29.7	56	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
8	c2jpiA_	Alignment		28.6	9	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
9	d1hn0a3	Alignment		27.5	27	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
10	c2l66B_	Alignment		27.1	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
11	d2h80a1	Alignment		26.7	75	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain

12	c1rijA_	Alignment		26.1	44	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apn1 peptide; **PDBTitle:** e6-bind trp-cage (e6apn1)
13	d1rqpa1	Alignment		25.7	14	**Fold:**Bacterial fluorinating enzyme, C-terminal domain **Superfamily:**Bacterial fluorinating enzyme, C-terminal domain **Family:**Bacterial fluorinating enzyme, C-terminal domain
14	d1je6a2	Alignment		24.9	15	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
15	d2h3ja1	Alignment		21.8	38	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
16	d1y8xb1	Alignment		20.2	27	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
17	c1o4zA_	Alignment		20.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-agarase b; **PDBTitle:** the three-dimensional structure of beta-agarase b from2 zobellia galactanivorans
18	d1o4za_	Alignment		20.0	25	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
19	d3frua2	Alignment		19.4	13	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
20	d2qdya1	Alignment		18.7	22	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
21	c3d33B_	Alignment	not modelled	17.0	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
22	c2k5lA_	Alignment	not modelled	16.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**feoa; **PDBTitle:** solution nmr structure of protein feoa from clostridium2 thermocellum, northeast structural genomics consortium3 target cmr17
23	d1qvpa_	Alignment	not modelled	16.5	26	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
24	c1x1aA_	Alignment	not modelled	16.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**crtf-related protein; **PDBTitle:** crystal structure of bchu complexed with s-adenosyl-l-methionine
25	c2im5C_	Alignment	not modelled	16.3	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
26	d1vlfm1	Alignment	not modelled	16.0	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
27	c3os4A_	Alignment	not modelled	16.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate phosphoribosyltransferase; **PDBTitle:** the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
						PDB header:metal transport

28	c2k5fA_	Alignment	not modelled	15.3	18	**Chain:** A: **PDB Molecule:**ferrous iron transport protein a; **PDBTitle:** solution nmr structure of feoa protein from chlorobium2 tepidum. northeast structural genomics consortium target3 ctr121
29	d1yira2	Alignment	not modelled	15.3	17	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
30	c2k4yA_	Alignment	not modelled	15.1	23	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**feoa-like protein; **PDBTitle:** nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178
31	d1fp2a2	Alignment	not modelled	15.0	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
32	c3mczB_	Alignment	not modelled	14.8	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
33	d1h0ha1	Alignment	not modelled	14.6	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
34	d1udxa3	Alignment	not modelled	14.5	36	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
35	d1dmra1	Alignment	not modelled	14.2	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
36	d1yfba1	Alignment	not modelled	14.0	26	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
37	d1s6la2	Alignment	not modelled	13.6	38	**Fold:**NosL/MerB-like **Superfamily:**NosL/MerB-like **Family:**MerB-like
38	c2rf4A_	Alignment	not modelled	13.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa4; **PDBTitle:** crystal structure of the rna polymerase i subcomplex a14/43
39	c3nrlB_	Alignment	not modelled	13.2	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rumgna_01417; **PDBTitle:** crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
40	d2jioa1	Alignment	not modelled	12.8	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
41	c3pcsB_	Alignment	not modelled	12.6	22	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
42	d1ok3a2	Alignment	not modelled	12.6	27	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
43	c2klrA_	Alignment	not modelled	12.5	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
44	c1qw1A_	Alignment	not modelled	12.1	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** solution structure of the c-terminal domain of dtxr2 residues 110-226
45	d2fzva1	Alignment	not modelled	12.0	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
46	d2fy9a1	Alignment	not modelled	11.5	21	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
47	c2e5qA_	Alignment	not modelled	11.5	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 19; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
48	c2dxbR_	Alignment	not modelled	11.5	22	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
49	d1kqfa1	Alignment	not modelled	11.5	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
50	c3lstB_	Alignment	not modelled	11.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calo1 methyltransferase; **PDBTitle:** crystal structure of calo1, methyltransferase in calicheamicin2 biosynthesis, sah bound form
51	c3ocjA_	Alignment	not modelled	11.2	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** the crystal structure of a possilbe exported protein from bordetella2 parapertussis
52	d1g8ka1	Alignment	not modelled	11.2	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
53	c3qyhG	Alignment	not modelled	11.0	22	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit;

53	c3qyhG_	Alignment	not modelled	11.0	22	**PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
54	c1fp2A_	Alignment	not modelled	11.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoflavone o-methyltransferase; **PDBTitle:** crystal structure analysis of isoflavone o-methyltransferase
55	d1im8a_	Alignment	not modelled	10.9	33	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein HI0319 (YecO)
56	d1v29a_	Alignment	not modelled	10.7	25	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
57	d1tmoa1	Alignment	not modelled	10.7	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
58	d2qdyb1	Alignment	not modelled	10.7	33	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
59	c2dxcG_	Alignment	not modelled	10.6	40	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
60	d2nn6h1	Alignment	not modelled	10.5	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
61	d1eu1a1	Alignment	not modelled	10.5	24	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
62	d1qw1a1	Alignment	not modelled	10.4	24	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
63	c3pjyB_	Alignment	not modelled	10.4	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
64	d2d9ra1	Alignment	not modelled	10.4	23	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
65	d1y5ia1	Alignment	not modelled	10.2	21	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
66	d2gcxa1	Alignment	not modelled	10.1	29	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
67	d1kyza2	Alignment	not modelled	10.1	30	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
68	c2pjhB_	Alignment	not modelled	9.9	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
69	d1o4ya_	Alignment	not modelled	9.9	15	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
70	d1qzza2	Alignment	not modelled	9.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
71	d2iv2x1	Alignment	not modelled	9.8	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
72	c2yqsA_	Alignment	not modelled	9.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
73	d1b35b_	Alignment	not modelled	9.3	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
74	c2wy3C_	Alignment	not modelled	9.2	15	**PDB header:**immune system/viral protein **Chain:** C: **PDB Molecule:**mhc class i polypeptide-related sequence b; **PDBTitle:** structure of the hcmv ul16-micb complex elucidates select2 binding of a viral immunoevasin to diverse nkg2d ligands
75	d2pbza2	Alignment	not modelled	9.2	42	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
76	d2ffsa1	Alignment	not modelled	9.1	10	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**PA1206-like
77	c2zbvC_	Alignment	not modelled	9.0	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermotoga2 maritima
78	d1vqoq1	Alignment	not modelled	8.8	29	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
						PDB header:transferase

79	c3dh0B_	Alignment	not modelled	8.4	44	**Chain:** B: **PDB Molecule:**sam dependent methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
80	d3bzka4	Alignment	not modelled	8.3	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
81	c1ezaA_	Alignment	not modelled	8.2	8	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
82	c2zkrq_	Alignment	not modelled	8.2	38	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
83	c3q9qB_	Alignment	not modelled	8.2	24	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
84	c2kieA_	Alignment	not modelled	8.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1; **PDBTitle:** a ph domain within ocrl bridges clathrin mediated membrane2 trafficking to phosphoinositide metabolis
85	c2r7mA_	Alignment	not modelled	8.0	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formaminoimidazole-4-carboxamide-1-(beta)-d- **PDBTitle:** crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp
86	c3nnqA_	Alignment	not modelled	7.8	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**n-terminal domain of moloney murine leukemia virus **PDBTitle:** crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
87	c3p9kD_	Alignment	not modelled	7.7	30	**PDB header:**transferase **Chain:** D: **PDB Molecule:**caffeic acid o-methyltransferase; **PDBTitle:** crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
88	d2jb0b1	Alignment	not modelled	7.6	35	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
89	c2vkcA_	Alignment	not modelled	7.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
90	d2pwwa1	Alignment	not modelled	7.6	18	**Fold:**TBP-like **Superfamily:**YugN-like **Family:**YugN-like
91	c3ilfA_	Alignment	not modelled	7.4	23	**PDB header:**hydrolase/carbohydrate **Chain:** A: **PDB Molecule:**porphyranase a; **PDBTitle:** crystal structure of porphyranase a (pora) in complex with2 neo-porphyrotetraose
92	d1zt1a2	Alignment	not modelled	7.4	23	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
93	c3tixB_	Alignment	not modelled	7.3	24	**PDB header:**gene regulation/protein binding **Chain:** B: **PDB Molecule:**chromo domain-containing protein 1; **PDBTitle:** crystal structure of the chp1-tas3 complex core
94	c2zxeB_	Alignment	not modelled	7.3	42	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**na+,k+-atpase beta subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
95	c3k7cC_	Alignment	not modelled	7.2	19	**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
96	d1cz5a1	Alignment	not modelled	7.2	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
97	c2r5xA_	Alignment	not modelled	7.1	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein yugn from2 geobacillus kaustophilus hta426
98	c3u02C_	Alignment	not modelled	7.0	4	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative transcription-associated protein tfiis; **PDBTitle:** crystal structure of the trna modifier tias from pyrococcus furiosus,2 northeast structural genomics consortium target pfr225
99	c2c45F_	Alignment	not modelled	6.9	19	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase