Phyre^2

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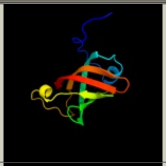
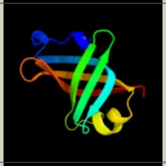
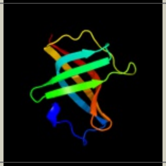
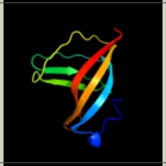
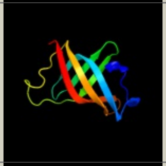
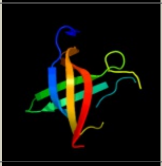
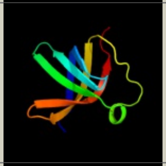
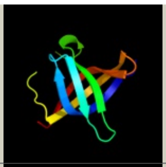
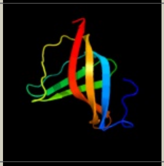
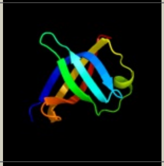
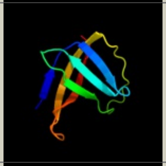
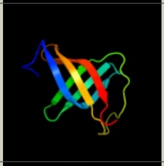
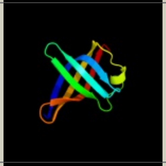
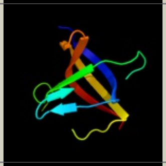
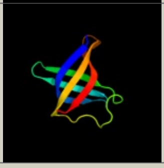
Description	P0ADU5
Date	Thu Jan 5 11:21:52 GMT 2012
Unique Job ID	3d8a265d58a59ce0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nnxa_	Alignment		100.0	97	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
2	d1l0wa1	Alignment		97.4	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
3	d1b8aa1	Alignment		97.4	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
4	c1wydB_	Alignment		97.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
5	c1b8aB_	Alignment		97.2	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
6	d1c0aa1	Alignment		97.1	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
7	d1n9wa1	Alignment		97.0	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
8	c3bjuB_	Alignment		96.8	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
9	c1eqrC_	Alignment		96.8	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
10	c3e9hB_	Alignment		96.8	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
11	c3m4qA_	Alignment		96.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)

12	d1e1oa1	Alignment		96.6	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
13	c3i7fA_	Alignment		96.6	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
14	d1bbua1	Alignment		96.5	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
15	c3kf6A_	Alignment		96.5	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
16	c1n9wA_	Alignment		96.4	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
17	d1eova1	Alignment		96.2	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
18	c1x55A_	Alignment		96.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
19	c1e22A_	Alignment		96.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
20	d2pi2a1	Alignment		96.0	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
21	c1efwA_	Alignment	not modelled	95.7	17	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
22	c2pi2A_	Alignment	not modelled	95.6	21	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
23	c2xgtB_	Alignment	not modelled	95.2	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
24	c3mxnB_	Alignment	not modelled	95.0	17	**PDB header:**replication **Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2; **PDBTitle:** crystal structure of the rmi core complex
25	c3e0eA_	Alignment	not modelled	94.9	23	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
26	c1asyA_	Alignment	not modelled	94.6	17	**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
27	d1krta_	Alignment	not modelled	93.0	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
						PDB header:replication

28	c3dm3A_	Alignment	not modelled	92.5	18	**Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
29	d1gm5a2	Alignment	not modelled	91.8	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
30	d2oq0a1	Alignment	not modelled	91.1	16	**Fold:**OB-fold **Superfamily:**HIN-2000 domain-like **Family:**HIN-200/IF120x domain
31	c3kf8C_	Alignment	not modelled	90.2	29	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
32	c2oq0D_	Alignment	not modelled	86.0	16	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
33	c3b6yB_	Alignment	not modelled	85.4	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the second hin-200 domain of interferon-inducible2 protein 16
34	c2k50A_	Alignment	not modelled	81.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
35	c3e0jG_	Alignment	not modelled	79.5	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
36	c2k75A_	Alignment	not modelled	74.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
37	c1gm5A_	Alignment	not modelled	71.5	14	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
38	d2pi2e1	Alignment	not modelled	54.5	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
39	c3hbcA_	Alignment	not modelled	51.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**choloylglycine hydrolase; **PDBTitle:** crystal structure of choloylglycine hydrolase from bacteroides2 thetaiotaomicron vpi
40	c2pqaB_	Alignment	not modelled	49.9	14	**PDB header:**replication **Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit; **PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer
41	c2kenA_	Alignment	not modelled	46.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
42	d1t9ha1	Alignment	not modelled	44.7	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
43	c2hezB_	Alignment	not modelled	38.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bile salt hydrolase; **PDBTitle:** bifidobacterium longum bile salt hydrolase
44	c3cp0A_	Alignment	not modelled	37.7	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
45	d1cz5a1	Alignment	not modelled	37.0	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
46	c2k14A_	Alignment	not modelled	36.9	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**yuaf protein; **PDBTitle:** solution structure of the soluble domain of the nfed2 protein yuaf from bacillus subtilis
47	d1jt8a_	Alignment	not modelled	36.6	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
48	c3h43F_	Alignment	not modelled	32.2	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
49	c3ka5A_	Alignment	not modelled	31.1	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
50	c2wg6L_	Alignment	not modelled	27.7	19	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
51	c3obyB_	Alignment	not modelled	27.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
52	d2pvaa	Alignment	not modelled	25.1	44	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn

52	d2pvaa_	Alignment	not modelled	25.1	44	hydrolases) **Family:**Penicillin V acylase
53	d2do3a1	Alignment	not modelled	25.0	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
54	d2cs7a1	Alignment	not modelled	24.6	16	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
55	d2exda1	Alignment	not modelled	24.1	18	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
56	c2oqkA_	Alignment	not modelled	24.0	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
57	c2bx6A_	Alignment	not modelled	23.8	10	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
58	d1qcsa1	Alignment	not modelled	23.4	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
59	c2bjgB_	Alignment	not modelled	23.3	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**choloylglycine hydrolase; **PDBTitle:** crystal structure of conjugated bile acid hydrolase from2 clostridium perfringens in complex with reaction products3 taurine and deoxycholate
60	d1qkia2	Alignment	not modelled	22.9	27	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
61	c2jqoA_	Alignment	not modelled	22.0	15	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein yoba; **PDBTitle:** nmr solution structure of bacillus subtilis yoba 21-120:2 northeast structural genomics consortium target sr547
62	c3k2tA_	Alignment	not modelled	21.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
63	c1cz5A_	Alignment	not modelled	21.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
64	d1h9aa2	Alignment	not modelled	21.2	33	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
65	c1ltlE_	Alignment	not modelled	20.0	23	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
66	d1vr3a1	Alignment	not modelled	19.9	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
67	c3f6hA_	Alignment	not modelled	19.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
68	d2vgna1	Alignment	not modelled	19.0	17	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
69	d1g4ma2	Alignment	not modelled	18.8	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
70	c3e0dA_	Alignment	not modelled	18.7	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
71	d1sr3a_	Alignment	not modelled	18.3	19	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
72	c3lgjA_	Alignment	not modelled	18.3	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
73	c1h9aA_	Alignment	not modelled	18.3	33	**PDB header:**oxidoreductase (choh(d) - nad(p)) **Chain:** A: **PDB Molecule:**glucose 6-phosphate 1-dehydrogenase; **PDBTitle:** complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
74	c2k5hA_	Alignment	not modelled	18.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
75	d1ltla_	Alignment	not modelled	18.0	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
76	d1v1qa_	Alignment	not modelled	17.8	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
77	c2vgmA_	Alignment	not modelled	17.5	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34;

77	c2vghA_	Alignment	not modelled	17.5	15	**PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
78	c2bhlB_	Alignment	not modelled	17.5	27	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
79	d2cu3a1	Alignment	not modelled	17.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
80	d1u0la1	Alignment	not modelled	17.1	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
81	d1o7ia_	Alignment	not modelled	17.1	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
82	c2kl0A_	Alignment	not modelled	16.5	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
83	d1cf1a2	Alignment	not modelled	16.2	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
84	c3cl5A_	Alignment	not modelled	16.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hemagglutinin-esterase; **PDBTitle:** structure of coronavirus hemagglutinin-esterase in complex with 4,9-o-2 diacetyl sialic acid
85	c1qkiE_	Alignment	not modelled	15.9	27	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
86	d1j6qa_	Alignment	not modelled	15.9	21	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
87	c1j6qA_	Alignment	not modelled	15.9	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
88	c1tygG_	Alignment	not modelled	15.9	32	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
89	d1tygb_	Alignment	not modelled	15.5	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
90	c2oqcB_	Alignment	not modelled	15.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin v acylase; **PDBTitle:** crystal structure of penicillin v acylase from bacillus subtilis
91	d1hr0w_	Alignment	not modelled	14.7	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	d1y9qa2	Alignment	not modelled	14.7	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
93	c2pjhB_	Alignment	not modelled	14.2	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
94	c3cwiA_	Alignment	not modelled	14.1	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
95	c3i4oA_	Alignment	not modelled	13.9	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
96	c2gu9B_	Alignment	not modelled	13.8	10	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
97	c2yk5A_	Alignment	not modelled	13.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cmp-n-acetylneuraminate-beta-galactosamide-alpha-2,3- **PDBTitle:** structure of neisseria los-specific sialyltransferase (nst),2 in complex with cmp.
98	d1t44g_	Alignment	not modelled	13.4	24	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
99	d1ah9a_	Alignment	not modelled	13.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like