Phyre^2

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Description	RVBD0613c_(-)_706951_709518
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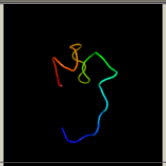
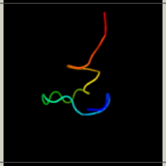
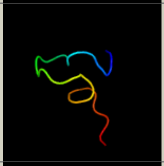
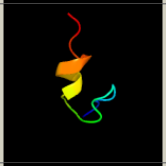
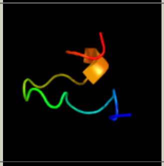
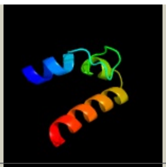
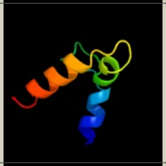
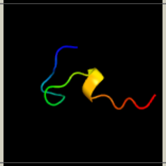
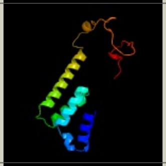
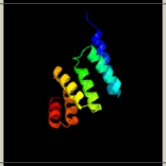
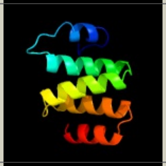
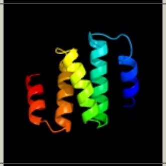
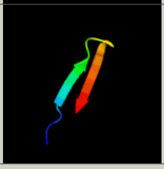
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2i9wA_	Alignment		99.5	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
2	c1ozbI_	Alignment		99.3	67	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of secb complexed with seca c-terminus
3	d1ozbi_	Alignment		99.3	67	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
4	c1ozbJ_	Alignment		99.3	67	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of secb complexed with seca c-terminus
5	d1tm6a_	Alignment		99.2	59	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
6	c1tm6A_	Alignment		99.2	59	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** nmr structure of the free zinc binding c-terminal domain of2 seca
7	c1sx1A_	Alignment		99.1	59	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**seca; **PDBTitle:** solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
8	c1sx0A_	Alignment		99.1	59	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**seca; **PDBTitle:** solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
9	c2jq5A_	Alignment		97.5	22	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**sec-c motif; **PDBTitle:** solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097
10	d2i9wa3	Alignment		97.2	40	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
11	c6d0hB_	Alignment		97.2	33	**PDB header:**toxin **Chain:** B: **PDB Molecule:**pars: cog5642 (duf2384) antitoxin; **PDBTitle:** part: prs adp-ribosylating toxin bound to cognate antitoxin pars

12	c6gw6B_	Alignment		96.9	21	**PDB header:**toxin **Chain:** B: **PDB Molecule:**xre antitoxin; **PDBTitle:** structure of the pseudomonas putida res-xre toxin-antitoxin complex
13	c6fkgC_	Alignment		94.9	24	**PDB header:**toxin **Chain:** C: **PDB Molecule:**rv1990c (mbca); **PDBTitle:** crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
14	c3iddA_	Alignment		93.2	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
15	d1hxia_	Alignment		90.1	18	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
16	c4abnA_	Alignment		86.3	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**tetratricopeptide repeat protein 5; **PDBTitle:** crystal structure of full length mouse strap (ttc5)
17	c5djsA_	Alignment		75.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetratricopeptide tpr_2 repeat protein; **PDBTitle:** thermobaculum terrenum o-glcnac transferase mutant - k341m
18	c2vsnB_	Alignment		73.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
19	c3k9iA_	Alignment		68.9	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bh0479 protein; **PDBTitle:** crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution
20	d1tpna_	Alignment		67.3	67	**Fold:**FnI-like domain **Superfamily:**FnI-like domain **Family:**Fibronectin type I module
21	c5aioA_	Alignment	not modelled	66.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor tau 131 kda subunit; **PDBTitle:** crystal structure of t131 n-terminal tpr array
22	c5xw7B_	Alignment	not modelled	66.7	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cellulose synthase subunit c; **PDBTitle:** crystal structure of the flexible tandem repeat domain of bacterial2 cellulose synthase subunit c
23	c3zn3A_	Alignment	not modelled	64.5	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit 8; **PDBTitle:** n-terminal domain of s. pombe cdc23 apc subunit
24	d2baaa_	Alignment	not modelled	64.4	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Family 19 glycosidase
25	c5fjaA_	Alignment	not modelled	64.2	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc1; **PDBTitle:** cryo-em structure of yeast rna polymerase iii at 4.7 a
26	c2katA_	Alignment	not modelled	64.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206
27	d1o9ga_	Alignment	not modelled	63.1	71	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase AviRa
28	c5dseC_	Alignment	not modelled	61.9	15	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**tetratricopeptide repeat protein 7b; **PDBTitle:** crystal structure of the ttc7b/hyccin complex

29	c5jj6A_	Alignment	not modelled	61.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine monophosphate-protein transferase ficd homolog; **PDBTitle:** fic-1 (aa134 - 508) from c. elegans
30	c4u0zH_	Alignment	not modelled	61.8	22	**PDB header:**transferase **Chain:** H: **PDB Molecule:**adenosine monophosphate-protein transferase ficd; **PDBTitle:** eukaryotic fic domain containing protein with bound apcpp
31	c2avpA_	Alignment	not modelled	60.1	17	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synthetic consensus tpr protein; **PDBTitle:** crystal structure of an 8 repeat consensus tpr superhelix
32	d1bcoa2	Alignment	not modelled	59.3	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**mu transposase, core domain
33	c3pe3D_	Alignment	not modelled	57.8	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
34	c2kcvA_	Alignment	not modelled	57.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tetratricopeptide repeat domain protein; **PDBTitle:** solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c
35	c2mrnB_	Alignment	not modelled	56.2	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**antitoxin maze; **PDBTitle:** structure of truncated ecmaze
36	c4mckA_	Alignment	not modelled	54.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of family gh19, class iv chitinase from zea mays
37	c5xi8A_	Alignment	not modelled	48.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-barrel assembly-enhancing protease; **PDBTitle:** structure and function of the tpr domain
38	c5dseA_	Alignment	not modelled	47.0	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tetratricopeptide repeat protein 7b; **PDBTitle:** crystal structure of the ttc7b/hyccin complex
39	c3hbhA_	Alignment	not modelled	46.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class iv chitinase chia4-pa2; **PDBTitle:** class iv chitinase structure from picea abies at 2.25a
40	c1nuiA_	Alignment	not modelled	45.8	29	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
41	c4ifdI_	Alignment	not modelled	45.8	28	**PDB header:**hydrolase/rna **Chain:** I: **PDB Molecule:**exosome complex component csl4; **PDBTitle:** crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
42	c3beeB_	Alignment	not modelled	44.8	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative yfre protein; **PDBTitle:** crystal structure of putative yfre protein from vibrio2 parahaemolyticus
43	d1ub4c_	Alignment	not modelled	44.3	13	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
44	c2zktB_	Alignment	not modelled	43.8	45	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
45	c2gw1A_	Alignment	not modelled	42.0	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial precursor proteins import receptor; **PDBTitle:** crystal structure of the yeast tom70
46	d1z6ra1	Alignment	not modelled	40.3	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
47	c1nnjA_	Alignment	not modelled	40.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
48	c3khkA_	Alignment	not modelled	39.9	43	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**type i restriction-modification system methylation subunit; **PDBTitle:** crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarcina mazei.
49	d1mvfd_	Alignment	not modelled	38.0	18	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
50	c2dkvA_	Alignment	not modelled	37.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of class i chitinase from oryza sativa l.2 japonica
51	d1zbpa1	Alignment	not modelled	37.1	15	**Fold:**ImpE-like **Superfamily:**ImpE-like **Family:**ImpE-like
52	d1wgea1	Alignment	not modelled	37.0	43	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
53	c3ufbA_	Alignment	not modelled	36.2	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type i restriction-modification system methyltransferase **PDBTitle:** crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus yj016
54	c5m3fA_	Alignment	not modelled	36.1	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit

		Alignment	not modelled			rpa190; **PDBTitle:** yeast rna polymerase i elongation complex at 3.8a
55	d1a0ca_	Alignment	not modelled	35.5	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
56	c1na3A_	Alignment	not modelled	35.2	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein ctpr2; **PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif
57	d1nuia2	Alignment	not modelled	35.2	44	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
58	d1ywsa1	Alignment	not modelled	35.1	43	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
59	c3ly8A_	Alignment	not modelled	34.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**transcriptional activator cadc; **PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc
60	c2z39A_	Alignment	not modelled	33.5	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of brassica juncea chitinase catalytic2 module glu234ala mutant (bjchi3-e234a)
61	c4e82B_	Alignment	not modelled	33.1	55	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**defensin-5; **PDBTitle:** crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)
62	c4e82A_	Alignment	not modelled	33.1	55	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin-5; **PDBTitle:** crystal structure of monomeric variant of human alpha-defensin 5, hd52 (glu21eme mutant)
63	d1lr7a1	Alignment	not modelled	32.3	58	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**Follistatin (FS) module N-terminal domain, FS-N
64	c3gyzB_	Alignment	not modelled	30.9	8	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone protein ipgc; **PDBTitle:** crystal structure of ipgc from shigella flexneri
65	c5ybbA_	Alignment	not modelled	30.3	29	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**type i restriction-modification system methyltransferase **PDBTitle:** structural basis underlying complex assembly andconformational2 transition of the type i r-m system
66	c1dvbA_	Alignment	not modelled	29.4	27	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
67	c5lmxA_	Alignment	not modelled	28.5	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa190; **PDBTitle:** monomeric rna polymerase i at 4.9 a resolution
68	c5nnrD_	Alignment	not modelled	28.4	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**n-terminal acetyltransferase-like protein; **PDBTitle:** structure of naa15/naa10 bound to hypk-thb
69	c5jqyA_	Alignment	not modelled	27.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartyl/asparaginyl beta-hydroxylase; **PDBTitle:** aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
70	c3mkrA_	Alignment	not modelled	27.7	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer subunit epsilon; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
71	c3s1sA_	Alignment	not modelled	26.6	43	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**restriction endonuclease bpusi; **PDBTitle:** characterization and crystal structure of the type iig restriction2 endonuclease bpusi
72	d2ef1a1	Alignment	not modelled	26.4	38	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
73	c4i2wA_	Alignment	not modelled	26.2	23	**PDB header:**chaperone/protein binding **Chain:** A: **PDB Molecule:**protein unc-45; **PDBTitle:** crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
74	c4uzyA_	Alignment	not modelled	26.2	17	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar associated protein; **PDBTitle:** crystal structure of the chlamydomonas ift70 and ift52 complex
75	c5d5hA_	Alignment	not modelled	26.0	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** crystal structure of mycobacterium tuberculosis topoisomerase i
76	d1j0ha2	Alignment	not modelled	25.8	11	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
77	c2kckA_	Alignment	not modelled	25.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tpr repeat; **PDBTitle:** nmr solution structure of the northeast structural genomics consortium2 (nesg) target mrr121a
78	c3cvpA_	Alignment	not modelled	25.5	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**peroxisome targeting signal 1 receptor pex5; **PDBTitle:** structure of peroxisomal targeting signal 1 (pts1) binding domain of2 trypanosoma brucei peroxin 5 (tbpex5)complexed to pts1 peptide (10-3 skl)
79	c1k82D_	Alignment	not modelled	25.4	60	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna

80	c4limA_	Alignment	not modelled	25.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase small subunit; **PDBTitle:** crystal structure of the catalytic subunit of yeast primase
81	c3ssbI_	Alignment	not modelled	24.9	44	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**inducible metalloproteinase inhibitor protein; **PDBTitle:** structure of insect metalloproteinase inhibitor in complex with2 thermolysin
82	d1wzla2	Alignment	not modelled	24.7	22	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
83	c4c3iA_	Alignment	not modelled	24.6	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase i subunit rpa190; **PDBTitle:** structure of 14-subunit rna polymerase i at 3.0 a resolution, crystal2 form c2-100
84	c2ns5A_	Alignment	not modelled	24.4	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
85	c5of4A_	Alignment	not modelled	24.0	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex helicase xpb **PDBTitle:** the cryo-em structure of human tfiih
86	c5e72A_	Alignment	not modelled	24.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n2, n2-dimethylguanosine trna methyltransferase; **PDBTitle:** crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis
87	c5ic8A_	Alignment	not modelled	23.9	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of utp6
88	c2jr7A_	Alignment	not modelled	23.5	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
89	c2y4tA_	Alignment	not modelled	23.4	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
90	c2pjhB_	Alignment	not modelled	23.2	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
91	c4houB_	Alignment	not modelled	23.0	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**interferon-induced protein with tetratricopeptide repeats **PDBTitle:** crystal structure of n-terminal human ifit1
92	c2mxmA_	Alignment	not modelled	22.9	56	**PDB header:**toxin **Chain:** A: **PDB Molecule:**entity; **PDBTitle:** nmr solution structure of trtx-tp1a from the tarantula thrixopelma2 pruriens
93	c6g70A_	Alignment	not modelled	22.7	8	**PDB header:**splicing **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 39; **PDBTitle:** structure of murine prpf39
94	c5zv6A_	Alignment	not modelled	22.4	63	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cq2; **PDBTitle:** solution structure of peptide cq2 from chenopodium quinoa
95	c5fzqB_	Alignment	not modelled	22.4	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**designed tpr protein; **PDBTitle:** designed tpr protein m4n
96	c4bujF_	Alignment	not modelled	22.3	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**superkiller protein 3; **PDBTitle:** crystal structure of the s. cerevisiae ski2-3-8 complex
97	c5j9hA_	Alignment	not modelled	22.1	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelopment polyprotein; **PDBTitle:** crystal structure of glycoprotein c from puumala virus in the post-2 fusion conformation (ph 8.0)
98	c1rjuV_	Alignment	not modelled	22.0	42	**PDB header:**metal binding protein **Chain:** V: **PDB Molecule:**metallothionein; **PDBTitle:** crystal structure of a truncated form of yeast copper2 thionein
99	d1isia_	Alignment	not modelled	21.6	30	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**ADP ribosyl cyclase-like
100	c5aftd_	Alignment	not modelled	21.4	27	**PDB header:**motor protein **Chain:** D: **PDB Molecule:**actin related protein 1; **PDBTitle:** cryoem structure of dynactin complex at 4.0 angstrom2 resolution
101	c5aftc_	Alignment	not modelled	21.4	27	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**actin related protein 1; **PDBTitle:** cryoem structure of dynactin complex at 4.0 angstrom2 resolution
102	c5adxc_	Alignment	not modelled	21.4	27	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**actin related protein 1; **PDBTitle:** cryoem structure of dynactin complex at 4.0 angstrom resolution
103	d1a1va1	Alignment	not modelled	21.4	50	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
104	c5jjtA_	Alignment	not modelled	20.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine-protein phosphatase 5; **PDBTitle:** crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
						PDB header:isomerase

105	c2gajA_	Alignment	not modelled	20.9	29	**Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
106	c2e2eA_	Alignment	not modelled	20.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**formate-dependent nitrite reductase complex nrfg subunit; **PDBTitle:** tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7
107	c4v19W_	Alignment	not modelled	20.8	22	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**mitoribosomal protein ul22m, mrpl22; **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 12 of 2
108	d1hh8a_	Alignment	not modelled	20.6	8	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**Tetratricopeptide repeat (TPR)
109	c6nmiA_	Alignment	not modelled	20.5	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription and dna repair factor iih helicase **PDBTitle:** cryo-em structure of the human tfiih core complex
110	c4kvmA_	Alignment	not modelled	20.5	13	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**n-terminal acetyltransferase a complex subunit nat1; **PDBTitle:** the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
111	c3bjwE_	Alignment	not modelled	20.4	35	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**phospholipase a2; **PDBTitle:** crystal structure of ecarpholin s complexed with suramin
112	c2ftcM_	Alignment	not modelled	20.4	20	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**mitochondrial ribosomal protein l22 isoform a; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
113	c2if4A_	Alignment	not modelled	20.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana