Phyre^2

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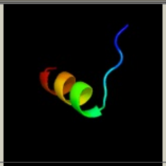
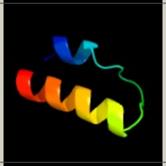
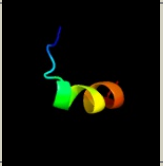
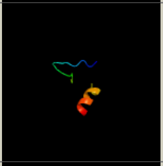
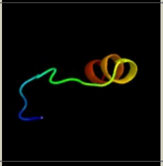
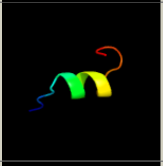
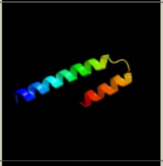
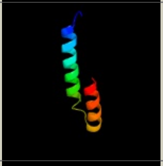
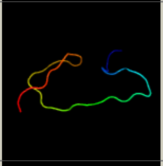
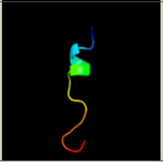
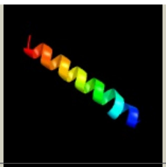
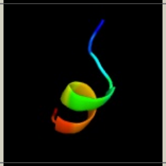
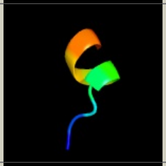
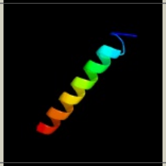
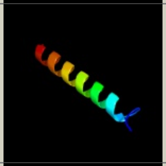
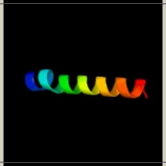
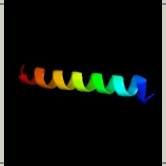
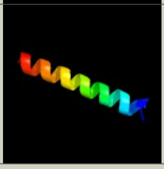
Description	RVBD2312_(-)_2584496_2584765
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	fb393218d48bfae9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pcfa_	Alignment		31.5	19	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
2	c1xdtT_	Alignment		27.7	31	**PDB header:**complex (toxin/growth factor) **Chain:** T: **PDB Molecule:**diphtheria toxin; **PDBTitle:** complex of diphtheria toxin and heparin-binding epidermal growth2 factor
3	c4aghA_	Alignment		27.5	56	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mosub1, transcription cofactor; **PDBTitle:** structural features of ssdna binding protein mosub1 from magnaporthe2 oryzae
4	c5a4nB_	Alignment		24.3	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**bpsl1147; **PDBTitle:** crystal structure of bpsl1147, a pc4 homolog from burkholderia2 pseudomallei k96243 (tetragonal crystal form)
5	d1ej5a_	Alignment		23.7	28	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
6	c1ceeB_	Alignment		21.6	23	**PDB header:**structural protein regulation **Chain:** B: **PDB Molecule:**wiskott-aldrich syndrome protein wasp; **PDBTitle:** solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
7	c3trkA_	Alignment		21.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nonstructural polyprotein; **PDBTitle:** structure of the chikungunya virus nsp2 protease
8	c3i9yA_	Alignment		20.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the v. parahaemolyticus histidine kinase sensor2 tors sensor domain
9	c3i9wA_	Alignment		19.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein tors; **PDBTitle:** crystal structure of the e. coli histidine kinase sensor tors sensor2 domain
10	c5wk1L_	Alignment		19.3	36	**PDB header:**virus **Chain:** L: **PDB Molecule:**capsid stabilizing protein; **PDBTitle:** structure of the major capsid protein and the capsid stabilizing2 protein of the marine siphovirus tw1
11	d1yuaa2	Alignment		19.1	50	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment

12	c6eikE_	Alignment		18.0	40	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
13	d2it9a1	Alignment		16.9	19	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
14	c6b4fD_	Alignment		16.8	40	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**nucleoporin like 2; **PDBTitle:** crystal structure of human gle1 ctd-nup42 gbm complex
15	c6b4jC_	Alignment		16.6	40	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**nucleoporin like 2; **PDBTitle:** crystal structure of human gle1 ctd-nup42 gbm-ddx19b(amppnp) complex
16	c6eikF_	Alignment		16.5	40	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
17	c6eikB_	Alignment		16.5	40	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
18	c6eikA_	Alignment		16.5	40	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
19	c6eikD_	Alignment		16.5	40	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
20	c6eikC_	Alignment		16.5	40	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
21	c6eikG_	Alignment	not modelled	16.5	40	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cc-hept-i24e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i24e
22	c2k42A_	Alignment	not modelled	15.7	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
23	d2nvna1	Alignment	not modelled	15.4	25	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**PMN2A0962/syc2379c-like
24	c4e18B_	Alignment	not modelled	15.3	28	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**catenin alpha-1; **PDBTitle:** alpha-e-catenin is an autoinhibited molecule that co-activates2 vinculin
25	c2lnhA_	Alignment	not modelled	13.7	23	**PDB header:**signaling protein/protein binding **Chain:** A: **PDB Molecule:**neural wiskott-aldrich syndrome protein; **PDBTitle:** enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
26	c5ez9C_	Alignment	not modelled	13.6	59	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
27	c5ez9D_	Alignment	not modelled	13.6	59	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
28	c5ez9A_	Alignment	not modelled	13.6	59	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
						PDB header:de novo protein

29	c5ez9E_	Alignment	not modelled	13.6	59	**Chain:** E: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
30	c5ez9G_	Alignment	not modelled	13.6	59	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
31	c5ez9B_	Alignment	not modelled	13.1	59	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
32	c5ez9F_	Alignment	not modelled	13.1	59	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cc-hept-l22h; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i-h-i
33	c3obhA_	Alignment	not modelled	12.4	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
34	c5ezeD_	Alignment	not modelled	11.7	63	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
35	c5f2yD_	Alignment	not modelled	11.5	63	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
36	c5ezeB_	Alignment	not modelled	11.5	63	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
37	c3bolB_	Alignment	not modelled	11.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
38	c5ezcA_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
39	c5ezcE_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
40	c5ezcD_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
41	c5ezcC_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
42	c5f2yC_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
43	c5f2yF_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
44	c5f2yB_	Alignment	not modelled	10.9	63	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
45	c2i7aA_	Alignment	not modelled	10.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calpain 13; **PDBTitle:** domain iv of human calpain 13
46	d1gzsb_	Alignment	not modelled	10.5	18	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
47	c5ezcB_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
48	c5ezcF_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
49	c5ezcG_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cc-hept-c-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h-i25e
50	c5ezaB_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
51	c5ezaD_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
52	c5ezaC_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
53	c5ezaG_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
54	c5ezaE_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
						PDB header:de novo protein

55	c5ezaA_	Alignment	not modelled	10.5	63	**Chain:** A: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
56	c5ezaF_	Alignment	not modelled	10.5	63	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cc-hept-c-h-i; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18c-l22h
57	c5ezeC_	Alignment	not modelled	10.4	63	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
58	c5ezeE_	Alignment	not modelled	10.4	63	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
59	c5f2yE_	Alignment	not modelled	10.4	63	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
60	c5f2yA_	Alignment	not modelled	10.1	63	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
61	c5ezeA_	Alignment	not modelled	10.1	63	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
62	c5f2yG_	Alignment	not modelled	10.1	63	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cc-hept-hcys-h-e; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-homocys-h-e
63	c5ezeF_	Alignment	not modelled	10.1	63	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
64	c6b4iD_	Alignment	not modelled	10.0	40	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**nucleoporin like 2; **PDBTitle:** crystal structure of human gle1 ctd-nup42 gbm-ddx19b(adp) complex
65	c5ezeG_	Alignment	not modelled	9.9	63	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cc-hept-bmecys-his-glu; **PDBTitle:** a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
66	c6b4jD_	Alignment	not modelled	9.9	40	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**nucleoporin like 2; **PDBTitle:** crystal structure of human gle1 ctd-nup42 gbm-ddx19b(amppnp) complex
67	c3pm7A_	Alignment	not modelled	9.4	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
68	c2azqA_	Alignment	not modelled	9.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
69	d2qi2a2	Alignment	not modelled	9.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
70	c1yuaA_	Alignment	not modelled	8.4	50	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**topoisomerase i; **PDBTitle:** c-terminal domain of escherichia coli topoisomerase i
71	c2m4hA_	Alignment	not modelled	8.1	30	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**feline calicivirus vpg protein; **PDBTitle:** solution structure of the core domain (10-76) of the feline2 calicivirus vpg protein
72	c2ltdA_	Alignment	not modelled	8.1	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ydbc; **PDBTitle:** solution nmr structure of apo ydbc from lactococcus lactis, northeast2 structural genomics consortium (nesg) target kr150
73	c1tmxA_	Alignment	not modelled	8.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from nocardioides2 simplex 3e
74	c6gtsC_	Alignment	not modelled	7.8	13	**PDB header:**transcription **Chain:** C: **PDB Molecule:**duf1778 domain-containing protein; **PDBTitle:** structure of the atat-atar complex bound dna
75	d1dmha_	Alignment	not modelled	7.7	20	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
76	c2cooA_	Alignment	not modelled	7.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
77	c2ma2A_	Alignment	not modelled	7.5	14	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**ras guanyl-releasing protein 2; **PDBTitle:** solution structure of rasgrp2 ef hands bound to calcium
78	c1mgtA_	Alignment	not modelled	7.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (o6-methylguanine-dna methyltransferase); **PDBTitle:** crystal structure of o6-methylguanine-dna methyltransferase from2 hyperthermophilic archaeon pyrococcus kodakaraensis strain kod1
79	d1w4ha1	Alignment	not modelled	7.0	7	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex

						Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
80	c3iynO_	Alignment	not modelled	6.7	63	**PDB header:**virus **Chain:** O: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
81	c2l95A_	Alignment	not modelled	6.5	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crammer; **PDBTitle:** solution structure of cytotoxic t-lymphocyte antigent-2(ctla protein),2 crammer at ph 6.0
82	c4qoyE_	Alignment	not modelled	6.4	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase (dihydrolipoyltransacetylase **PDBTitle:** novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
83	c2eq9C_	Alignment	not modelled	6.3	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
84	c4guaB_	Alignment	not modelled	6.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**non-structural polyprotein; **PDBTitle:** alphavirus p23pro-zbd
85	c2l3aA_	Alignment	not modelled	6.2	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
86	c2a5wC_	Alignment	not modelled	6.1	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
87	c5z4gA_	Alignment	not modelled	6.1	47	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sahs4; **PDBTitle:** crystal structure of secretory abundant heat soluble protein 4 from2 ramazzottius varieornatus
88	c6mrrA_	Alignment	not modelled	5.9	57	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**foldit1; **PDBTitle:** de novo designed protein foldit1
89	d1uoua1	Alignment	not modelled	5.9	24	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
90	c3f75P_	Alignment	not modelled	5.8	18	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**cathepsin l propeptide; **PDBTitle:** activated toxoplasma gondii cathepsin l (tgcpl) in complex with its2 propeptide
91	c2eq7C_	Alignment	not modelled	5.7	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
92	c2hwkA_	Alignment	not modelled	5.5	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helicase nsp2; **PDBTitle:** crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
93	c3zifR_	Alignment	not modelled	5.5	50	**PDB header:**virus **Chain:** R: **PDB Molecule:**pviii; **PDBTitle:** cryo-em structures of two intermediates provide insight into2 adenovirus assembly and disassembly
94	c2kkrA_	Alignment	not modelled	5.4	36	**PDB header:**transcription, protein binding **Chain:** A: **PDB Molecule:**ataxin-7; **PDBTitle:** solution structure of sca7 zinc finger domain from human ataxin-72 protein
95	d2cyua1	Alignment	not modelled	5.3	9	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
96	d1ctda_	Alignment	not modelled	5.3	34	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
97	c6eyyB_	Alignment	not modelled	5.2	50	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**acriia6; **PDBTitle:** anti-crispr acriia6 cubic form
98	c1yx3A_	Alignment	not modelled	5.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
99	c1smzA_	Alignment	not modelled	5.1	53	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transportan in bicellar solution with **PDBTitle:** structure of transportan in phospholipid bicellar solution