Phyre^2

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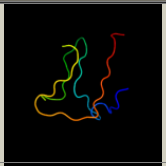
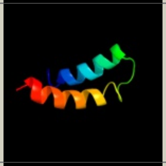
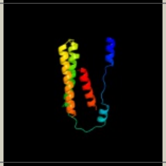
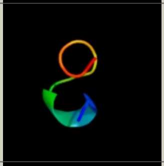
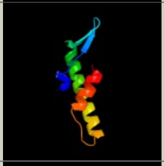
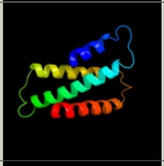
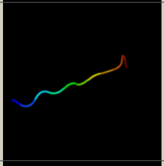
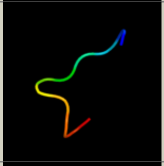
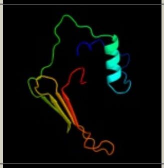
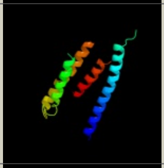
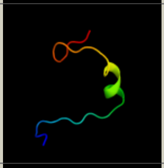
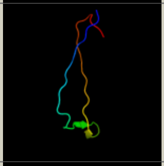
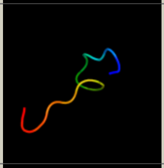
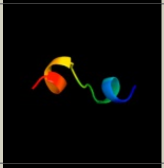
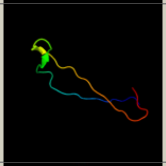
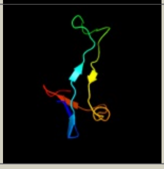
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hnga1	Alignment		46.1	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
2	c2kr6A_	Alignment		45.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit
3	d1v54c_	Alignment		36.6	27	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
4	c1q8hA_	Alignment		32.5	45	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**osteocalcin; **PDBTitle:** crystal structure of porcine osteocalcin
5	d1q8ha_	Alignment		32.5	45	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
6	d1ikpa1	Alignment		30.5	18	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Exotoxin A, N-terminal domain
7	c3k3gA_	Alignment		29.9	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
8	c3kp9A_	Alignment		26.5	10	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
9	d1hnfa1	Alignment		26.3	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
10	d1q3ma_	Alignment		25.3	45	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
11	c2vesA_	Alignment		21.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** crystal structure of lpxc from pseudomonas aeruginosa2 complexed with the potent bb-78485 inhibitor

12	d1oria_	Alignment		21.2	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arginine methyltransferase
13	c3nzkB_	Alignment		20.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine **PDBTitle:** structure of lpxc from yersinia enterocolitica complexed with chir0902 inhibitor
14	d1qlec_	Alignment		20.0	23	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
15	c2yboA_	Alignment		19.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah
16	d1e2wa1	Alignment		19.4	12	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
17	d1g47a1	Alignment		18.3	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
18	d1yvra1	Alignment		17.0	33	**Fold:**alpha-alpha superhelix **Superfamily:**TROVE domain-like **Family:**TROVE domain-like
19	d1vf5c1	Alignment		16.9	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
20	d1k0ha_	Alignment		16.7	9	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
21	c3o44G_	Alignment	not modelled	15.9	18	**PDB header:**toxin **Chain:** G: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya) heptameric2 pore
22	c1xezA_	Alignment	not modelled	15.6	18	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya)2 pro-toxin with octylglucoside bound
23	c1e2vB_	Alignment	not modelled	15.3	12	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
24	c3c5oD_	Alignment	not modelled	15.2	9	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**upf0311 protein rpa1785; **PDBTitle:** crystal structure of the conserved protein of unknown function rpa17852 from rhodopseudomonas palustris
25	c2v1lA_	Alignment	not modelled	14.8	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
26	c2p8zS_	Alignment	not modelled	14.7	63	**PDB header:**translation **Chain:** S: **PDB Molecule:**elongation factor tu-b; **PDBTitle:** fitted structure of adpr-eef2 in the 80s:adpr-2 eef2:gdpnp:sordarin cryo-em reconstruction
27	c1q90A_	Alignment	not modelled	14.4	12	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
28	c2rddB	Alignment	not modelled	13.7	6	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc;

28	c2rddB_	Alignment	not modelled	13.7	6	**PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
29	c1ikqA_	Alignment	not modelled	13.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**exotoxin a; **PDBTitle:** pseudomonas aeruginosa exotoxin a, wild type
30	d1ci3m1	Alignment	not modelled	13.6	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
31	c3g7gG_	Alignment	not modelled	13.4	17	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**upf0311 protein ca_c3321; **PDBTitle:** crystal structure of the protein with unknown function from2 clostridium acetobutylicum atcc 824
32	d1tu2b1	Alignment	not modelled	12.6	15	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
33	c2w56B_	Alignment	not modelled	12.6	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**vc0508; **PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
34	d1hcza1	Alignment	not modelled	11.9	12	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
35	c3dwuA_	Alignment	not modelled	11.8	63	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**elongation factor tu-b; **PDBTitle:** transition-state model conformation of the switch i region2 fitted into the cryo-em map of the eef2.80s.alf4.gdp3 complex
36	c3demB_	Alignment	not modelled	11.6	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**complement factor masp-3; **PDBTitle:** cub1-egf-cub2 domain of human masp-1/3
37	c2e75C_	Alignment	not modelled	11.6	15	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**apocytochrome f; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
38	d1iwga8	Alignment	not modelled	11.5	13	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
39	c2k9pA_	Alignment	not modelled	11.5	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles
40	d3c8ya2	Alignment	not modelled	11.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
41	d1v97a1	Alignment	not modelled	10.5	46	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
42	d1jb0l_	Alignment	not modelled	10.5	27	**Fold:**Photosystem I reaction center subunit XI, PsaL **Superfamily:**Photosystem I reaction center subunit XI, PsaL **Family:**Photosystem I reaction center subunit XI, PsaL
43	c1ctmA_	Alignment	not modelled	10.5	14	**PDB header:**electron transport(cytochrome) **Chain:** A: **PDB Molecule:**cytochrome f; **PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
44	d1mtyg_	Alignment	not modelled	10.3	27	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Methane monooxygenase hydrolase, gamma subunit **Family:**Methane monooxygenase hydrolase, gamma subunit
45	d3cx5e2	Alignment	not modelled	9.8	24	**Fold:**Single transmembrane helix **Superfamily:**ISP transmembrane anchor **Family:**ISP transmembrane anchor
46	c2k6zA_	Alignment	not modelled	9.8	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
47	d1m56c_	Alignment	not modelled	9.6	15	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
48	d1mhyg_	Alignment	not modelled	9.5	33	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Methane monooxygenase hydrolase, gamma subunit **Family:**Methane monooxygenase hydrolase, gamma subunit
49	c2nvoA_	Alignment	not modelled	9.4	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ro sixty-related protein, rsr; **PDBTitle:** crystal structure of deinococcus radiodurans ro (rsr) protein
50	c2gutA_	Alignment	not modelled	9.1	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arc/mediator, positive cofactor 2 glutamine/q- **PDBTitle:** solution structure of the trans-activation domain of the2 human co-activator arc105
51	c3lrcC_	Alignment	not modelled	8.9	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
52	c1dnuB_	Alignment	not modelled	8.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myeloperoxidase; **PDBTitle:** structural analyses of human myeloperoxidase-thiocyanate complex
53	c2oarA_	Alignment	not modelled	8.7	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
						Fold: Argininosuccinate synthetase, C-terminal domain

54	d1k92a2	Alignment	not modelled	8.6	30	**Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
55	c2iv1J_	Alignment	not modelled	8.4	36	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
56	c1orhA_	Alignment	not modelled	8.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 1; **PDBTitle:** structure of the predominant protein arginine methyltransferase prmt1
57	c2jxmB_	Alignment	not modelled	8.2	12	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
58	d1x9la_	Alignment	not modelled	8.1	25	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
59	c1tu2B_	Alignment	not modelled	7.8	15	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
60	d1vava_	Alignment	not modelled	7.7	25	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Alginate lyase
61	d2i5nl1	Alignment	not modelled	7.7	14	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
62	c3c25A_	Alignment	not modelled	7.6	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**noti restriction endonuclease; **PDBTitle:** crystal structure of noti restriction endonuclease bound to cognate2 dna
63	c2l4wA_	Alignment	not modelled	7.4	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the xanthomonas virb7
64	d1k8ba_	Alignment	not modelled	7.4	18	**Fold:**Ribosome binding domain-like **Superfamily:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain **Family:**Translation initiation factor 2 beta, aIF2beta, N-terminal domain
65	d2f41a1	Alignment	not modelled	7.3	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
66	d1t3qa1	Alignment	not modelled	7.1	20	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
67	c2kqtD_	Alignment	not modelled	7.1	26	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
68	c2kqtA_	Alignment	not modelled	7.1	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
69	c2kqtB_	Alignment	not modelled	7.1	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
70	c2kqtC_	Alignment	not modelled	7.1	26	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**m2 protein; **PDBTitle:** solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
71	d1mv8a1	Alignment	not modelled	7.1	36	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
72	d1nt0a2	Alignment	not modelled	7.1	13	**Fold:**CUB-like **Superfamily:**Spermadhesin, CUB domain **Family:**Spermadhesin, CUB domain
73	c2lhuA_	Alignment	not modelled	7.0	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mybpc3 protein; **PDBTitle:** structural insight into the unique cardiac myosin binding protein-c2 motif: a partially folded domain
74	c2yvxD_	Alignment	not modelled	7.0	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
75	d2axth1	Alignment	not modelled	6.9	28	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II 10 kDa phosphoprotein PsbH **Family:**PsbH-like
76	d2oiea1	Alignment	not modelled	6.9	58	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
77	c3o0rB_	Alignment	not modelled	6.8	6	**PDB header:**immune system/oxidoreductase **Chain:** B: **PDB Molecule:**nitric oxide reductase subunit b; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
78	d1zxia1	Alignment	not modelled	6.8	25	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like

79	c1nyjC_	Alignment	not modelled	6.8	28	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
80	c1mp6A_	Alignment	not modelled	6.8	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
81	c1nyjB_	Alignment	not modelled	6.8	28	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
82	c1nyjA_	Alignment	not modelled	6.8	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
83	c1nyjD_	Alignment	not modelled	6.8	28	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**matrix protein m2; **PDBTitle:** the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
84	c3pojA_	Alignment	not modelled	6.7	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan-binding lectin serine protease 1; **PDBTitle:** crystal structure of masp-1 cub2 domain bound to ethylamine
85	d2c5ra1	Alignment	not modelled	6.7	25	**Fold:**Phage replication organizer domain **Superfamily:**Phage replication organizer domain **Family:**Phage replication organizer domain
86	d1jroa1	Alignment	not modelled	6.6	50	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
87	c1ds5F_	Alignment	not modelled	6.6	45	**PDB header:**transferase **Chain:** F: **PDB Molecule:**casein kinase, beta chain; **PDBTitle:** dimeric crystal structure of the alpha subunit in complex2 with two beta peptides mimicking the architecture of the3 tetrameric protein kinase ck2 holoenzyme.
88	c2q4pA_	Alignment	not modelled	6.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
89	d2a3qa1	Alignment	not modelled	6.6	32	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
90	c2q9lA_	Alignment	not modelled	6.4	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
91	c2jttD_	Alignment	not modelled	6.3	13	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
92	d2axti1	Alignment	not modelled	6.3	23	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
93	c3nfgG_	Alignment	not modelled	6.3	34	**PDB header:**transcription **Chain:** G: **PDB Molecule:**dna-directed rna polymerase i subunit rpa49; **PDBTitle:** crystal structure of dimerization module of rna polymerase i2 subcomplex a49/a34.5
94	c3s88J_	Alignment	not modelled	6.3	20	**PDB header:**immune system/viral protein **Chain:** J: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6
95	c3dh4A_	Alignment	not modelled	6.3	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
96	c2f3xA_	Alignment	not modelled	6.2	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**transcription factor fapr; **PDBTitle:** crystal structure of fapr (in complex with effector)- a2 global regulator of fatty acid biosynthesis in b. subtilis
97	c2qmaB_	Alignment	not modelled	6.1	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**diaminobutyrate-pyruvate transaminase and l-2,4- **PDBTitle:** crystal structure of glutamate decarboxylase domain of2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
98	c3rceA_	Alignment	not modelled	6.1	14	**PDB header:**transferase/peptide **Chain:** A: **PDB Molecule:**oligosaccharide transferase to n-glycosylate proteins; **PDBTitle:** bacterial oligosaccharyltransferase pglb
99	c1yvrA_	Alignment	not modelled	6.1	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**60-kda ss-a/ro ribonucleoprotein; **PDBTitle:** ro autoantigen