Phyre2

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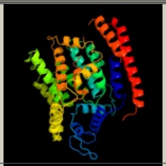
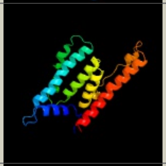
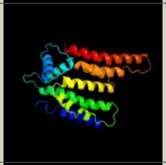
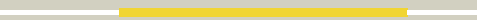
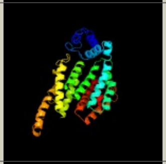
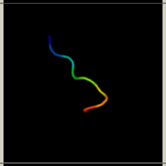
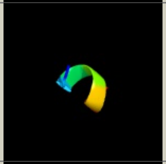
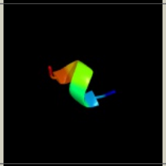
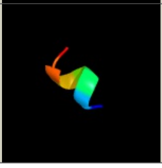
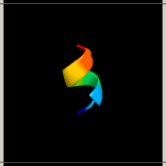
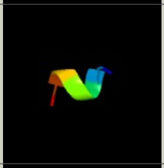
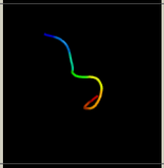
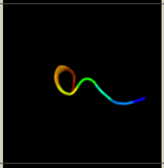
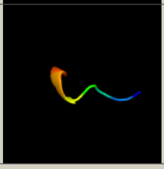
Description	RVBD2174_(-)_2435917_2437467
Date	Mon Aug 5 13:25:29 BST 2019
Unique Job ID	5b5194491295f6b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5f15A_	 Alignment		99.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; **PDBTitle:** crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
2	c6p25A_	 Alignment		98.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-phosphate-mannose--protein mannosyltransferase 1; **PDBTitle:** structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
3	c6p2rB_	 Alignment		98.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dolichyl-phosphate-mannose--protein mannosyltransferase 2; **PDBTitle:** structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
4	c3wajA_	 Alignment		98.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transmembrane oligosaccharyl transferase; **PDBTitle:** crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
5	c3rceA_	 Alignment		95.8	10	**PDB header:**transferase/peptide **Chain:** A: **PDB Molecule:**oligosaccharide transferase to n-glycosylate proteins; **PDBTitle:** bacterial oligosaccharyltransferase pglb
6	c6eznF_	 Alignment		77.4	8	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
7	d1ynjd1	 Alignment		20.2	44	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
8	d1zxoa1	 Alignment		16.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
9	c3e1kD_	 Alignment		15.7	27	**PDB header:**transcription **Chain:** D: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
10	c3e1kF_	 Alignment		15.7	27	**PDB header:**transcription **Chain:** F: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
11	c3e1kP_	 Alignment		15.7	27	**PDB header:**transcription **Chain:** P: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p

12	c3e1kB_	Alignment		15.7	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
13	c3e1kL_	Alignment		15.7	27	**PDB header:**transcription **Chain:** L: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
14	c3e1kJ_	Alignment		15.7	27	**PDB header:**transcription **Chain:** J: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
15	c3e1kH_	Alignment		15.7	27	**PDB header:**transcription **Chain:** H: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
16	c3e1kN_	Alignment		15.7	27	**PDB header:**transcription **Chain:** N: **PDB Molecule:**lactose regulatory protein lac9; **PDBTitle:** crystal structure of kluyveromyces lactis gal80p in complex with the2 acidic activation domain of gal4p
17	c4g7oN_	Alignment		15.2	50	**PDB header:**transcription, transferase/dna **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit beta'; **PDBTitle:** crystal structure of thermus thermophilus transcription initiation2 complex containing 2 nt of rna
18	c5xj0D_	Alignment		15.1	50	**PDB header:**transferase/transcription **Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta'; **PDBTitle:** t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76
19	c3fmtF_	Alignment		13.9	44	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna
20	c5x22D_	Alignment		13.5	50	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta'; **PDBTitle:** crystal structure of thermus thermophilus transcription initiation2 complex with gpa and cmpcpp
21	d1zbsa2	Alignment	not modelled	13.3	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
22	d2r6gf1	Alignment	not modelled	12.9	14	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
23	d1xrxa1	Alignment	not modelled	12.6	50	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
24	c1xrxD_	Alignment	not modelled	12.6	50	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
25	c5z3dA_	Alignment	not modelled	12.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase 15-related protein; **PDBTitle:** glycosidase f290y
26	c4y0lA_	Alignment	not modelled	12.2	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane protein mmpl11; **PDBTitle:** mycobacterial membrane protein mmpl11d2
27	c4rymA_	Alignment	not modelled	12.2	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**integral membrane protein; **PDBTitle:** crystal structure of bctspo iodo type1 monomer
28	d2hu7a1	Alignment	not modelled	11.6	57	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Acylamino-acid-releasing enzyme, N-terminal donain
29	c2lzqA_	Alignment	not modelled	11.6	50	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**ns2 peptide;

						PDBTitle: structure of ns2(32-57) gbvb protein
30	c5l75F_	Alignment	not modelled	11.4	13	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**fig000988: predicted permease; **PDBTitle:** a protein structure
31	c1zzaA_	Alignment	not modelled	11.3	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
32	c6ig4B_	Alignment	not modelled	11.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidate cytidylyltransferase, mitochondrial; **PDBTitle:** structure of mitochondrial cdp-dag synthase tam41, delta 74
33	c3hf1B_	Alignment	not modelled	10.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ribonucleoside-diphosphate reductase subunit m2 b; **PDBTitle:** crystal structure of human p53r2
34	c2npmB_	Alignment	not modelled	10.7	22	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**14-3-3 domain containing protein; **PDBTitle:** crystal structure of cryptosporidium parvum 14-3-3 protein in complex2 with peptide
35	c3efzA_	Alignment	not modelled	10.7	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**14-3-3 protein; **PDBTitle:** crystal structure of a 14-3-3 protein from cryptosporidium parvum2 (cgd1_2980)
36	d3efza1	Alignment	not modelled	10.7	33	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
37	c5x3hA_	Alignment	not modelled	10.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** the y81g mutant of the ung crystal structure from nitratifractor2 salsuginis
38	d1t33a2	Alignment	not modelled	10.5	18	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
39	c5yi8B_	Alignment	not modelled	10.4	50	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**pon peptide from partner of numb; **PDBTitle:** crystal structure of drosophila numb ptb domain and pon peptide2 complex
40	c2lioA_	Alignment	not modelled	10.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322
41	d1q90d_	Alignment	not modelled	10.4	8	**Fold:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
42	c3qqcA_	Alignment	not modelled	10.0	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit b, dna-directed rna **PDBTitle:** crystal structure of archaeal spt4/5 bound to the rnap clamp domain
43	d1o9da_	Alignment	not modelled	10.0	44	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
44	c3dwbA_	Alignment	not modelled	10.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endothelin-converting enzyme 1; **PDBTitle:** structure of human ece-1 complexed with phosphoramidon
45	c2xsbA_	Alignment	not modelled	9.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** ogoga pugnac complex
46	c2c1nA_	Alignment	not modelled	9.7	56	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**14-3-3 protein zeta/delta; **PDBTitle:** molecular basis for the recognition of phosphorylated and2 phosphoacetylated histone h3 by 14-3-3
47	c5un8B_	Alignment	not modelled	9.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein o-glcnacase; **PDBTitle:** crystal structure of human o-glcnacase in complex with glycopeptide2 p53
48	c3tr7A_	Alignment	not modelled	9.6	80	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** structure of a uracil-dna glycosylase (ung) from coxiella burnetii
49	c4iuwA_	Alignment	not modelled	9.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neutral endopeptidase; **PDBTitle:** crystal structure of pepo from lactobacillus rhamnosis hn001 (dr20)
50	c2k8jX_	Alignment	not modelled	9.4	31	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**p7tm2; **PDBTitle:** solution structure of hcv p7 tm2
51	c2yf3F_	Alignment	not modelled	9.3	43	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase; **PDBTitle:** crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese
52	d2o02a1	Alignment	not modelled	9.2	56	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
53	c2rfpA_	Alignment	not modelled	9.2	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
54	c3zf7m	Alignment	not modelled	9.2	33	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l12, putative;

						PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
55	c4uc2B_	Alignment	not modelled	9.1	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**translocator protein tspo; **PDBTitle:** crystal structure of translocator protein 18kda (tspo) from2 rhodobacter sphaeroides (a139t mutant) in p212121 space group
56	c4a19Q_	Alignment	not modelled	9.1	50	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l36; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
57	d2vbua1	Alignment	not modelled	9.1	39	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
58	c6g90J_	Alignment	not modelled	9.1	18	**PDB header:**splicing **Chain:** J: **PDB Molecule:**u1 small nuclear ribonucleoprotein component snu71; **PDBTitle:** prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
59	c2vuxB_	Alignment	not modelled	9.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ribonucleoside-diphosphate reductase subunit m2 b; **PDBTitle:** human ribonucleotide reductase, subunit m2 b
60	c6edjD_	Alignment	not modelled	8.9	60	**PDB header:**virus like particle **Chain:** D: **PDB Molecule:**external core antigen; **PDBTitle:** cryo-em structure of woodchuck hepatitis virus capsid
61	c5t6oA_	Alignment	not modelled	8.9	28	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**poly-beta-hydroxybuterate polymerase; **PDBTitle:** structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
62	d2o8pa1	Alignment	not modelled	8.9	25	**Fold:**alpha-alpha superhelix **Superfamily:**14-3-3 protein **Family:**14-3-3 protein
63	c2owrD_	Alignment	not modelled	8.8	80	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of vaccinia virus uracil-dna glycosylase
64	c3j3bi_	Alignment	not modelled	8.8	50	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10-like; **PDBTitle:** structure of the human 60s ribosomal proteins
65	c6n7xH_	Alignment	not modelled	8.8	18	**PDB header:**rna binding protein/rna **Chain:** H: **PDB Molecule:**u1 small nuclear ribonucleoprotein component snu71; **PDBTitle:** s. cerevisiae u1 snrnp
66	c5ireD_	Alignment	not modelled	8.8	22	**PDB header:**virus **Chain:** D: **PDB Molecule:**m protein; **PDBTitle:** the cryo-em structure of zika virus
67	c3eyiB_	Alignment	not modelled	8.7	46	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
68	c5lc5c_	Alignment	not modelled	8.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, **PDBTitle:** structure of mammalian respiratory complex i, class2
69	c5ldwc_	Alignment	not modelled	8.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, **PDBTitle:** structure of mammalian respiratory complex i, class1
70	d1dmta_	Alignment	not modelled	8.7	24	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Neutral endopeptidase (neprilysin)
71	c5diyB_	Alignment	not modelled	8.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hyaluronidase; **PDBTitle:** thermobaculum terrenum o-glcnac hydrolase mutant - d120n
72	c4b6ai_	Alignment	not modelled	8.5	67	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10; **PDBTitle:** cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
73	c2l4mA_	Alignment	not modelled	8.5	46	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the zbeta domain of human dai and its binding2 modes to b- and z-dna
74	c4dtfA_	Alignment	not modelled	8.5	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vgrg protein; **PDBTitle:** structure of a vgrg vibrio cholerae toxin acd domain in complex with2 amp-pnp and mg++
75	c2m67A_	Alignment	not modelled	8.5	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** full-length mercury transporter protein merf in lipid bilayer2 membranes
76	c3e6yB_	Alignment	not modelled	8.5	50	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**14-3-3-like protein c; **PDBTitle:** structure of 14-3-3 in complex with the differentiation-inducing agent2 cotylenin a
77	c4w8kB_	Alignment	not modelled	8.4	21	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cas1 protein; **PDBTitle:** crystal structure of a putative cas1 enzyme from vibrio phage icp1
78	d1tlha_	Alignment	not modelled	8.4	43	**Fold:**Anti-sigma factor AsiA **Superfamily:**Anti-sigma factor AsiA **Family:**Anti-sigma factor AsiA
79	c3aoiN_	Alignment	not modelled	8.3	50	**PDB header:**transcription, transferase/dna/rna **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit beta'; **PDBTitle:** rna polymerase-gfh1 complex (crystal type 2)

80	c1ckwA_	Alignment	not modelled	8.3	57	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (cystic fibrosis transmembrane **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
81	c5x55A_	Alignment	not modelled	8.2	80	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable uracil-dna glycosylase; **PDBTitle:** crystal structure of mimivirus uracil-dna glycosylase
82	c5zjiH_	Alignment	not modelled	8.2	21	**PDB header:**membrane protein **Chain:** H: **PDB Molecule:**photosystem i reaction center subunit vi, chloroplastic; **PDBTitle:** structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
83	c5nn7A_	Alignment	not modelled	8.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** kshv uracil-dna glycosylase, apo form
84	c2cukC_	Alignment	not modelled	8.2	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
85	c5oypD_	Alignment	not modelled	8.1	39	**PDB header:**virus **Chain:** D: **PDB Molecule:**minor capsid protein micp; **PDBTitle:** sacbrood virus of honeybee
86	c5lsfD_	Alignment	not modelled	8.1	39	**PDB header:**virus **Chain:** D: **PDB Molecule:**vp4; **PDBTitle:** sacbrood honeybee virus
87	c6egvD_	Alignment	not modelled	8.1	39	**PDB header:**virus **Chain:** D: **PDB Molecule:**minor capsid protein micp; **PDBTitle:** sacbrood virus of honeybee
88	c6eh1D_	Alignment	not modelled	8.1	39	**PDB header:**virus **Chain:** D: **PDB Molecule:**minor capsid protein micp; **PDBTitle:** sacbrood virus of honeybee - expansion state ii
89	c6egxD_	Alignment	not modelled	8.1	39	**PDB header:**virus **Chain:** D: **PDB Molecule:**minor capsid protein micp; **PDBTitle:** sacbrood virus of honeybee - expansion state i
90	c1qfqB_	Alignment	not modelled	8.1	25	**PDB header:**transcription/rna **Chain:** B: **PDB Molecule:**36-mer n-terminal peptide of the n protein; **PDBTitle:** bacteriophage lambda n-protein-nutboxb-rna complex
91	c6e6aB_	Alignment	not modelled	8.1	63	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**inclusion membrane protein a; **PDBTitle:** triclinic crystal form of inca g144a point mutant
92	d2cbia2	Alignment	not modelled	8.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
93	c4lzxB_	Alignment	not modelled	8.0	15	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**iq domain-containing protein g; **PDBTitle:** complex of iqcg and ca2+-free cam
94	c3pv9D_	Alignment	not modelled	8.0	11	**PDB header:**immune system **Chain:** D: **PDB Molecule:**putative uncharacterized protein ph1245; **PDBTitle:** structure of ph1245, a cas1 from pyrococcus horikoshii
95	c2vy8A_	Alignment	not modelled	8.0	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
96	c5nv8A_	Alignment	not modelled	7.9	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ef-p arginine 32 rhamnosyl-transferase; **PDBTitle:** structural basis for earp-mediated arginine glycosylation of2 translation elongation factor ef-p
97	c2f5zK_	Alignment	not modelled	7.8	18	**PDB header:**oxidoreductase/protein binding **Chain:** K: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
98	c3j39i_	Alignment	not modelled	7.8	50	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10; **PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins
99	c6hq8B_	Alignment	not modelled	7.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-1,3-oligosaccharide phosphorylase; **PDBTitle:** bacterial beta-1,3-oligosaccharide phosphorylase from gh149 with2 laminarihexaose bound at a surface site