Phyre2

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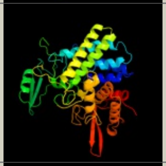
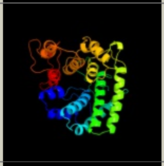
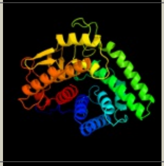
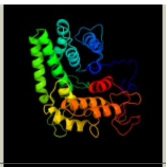
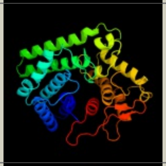
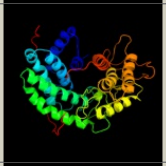
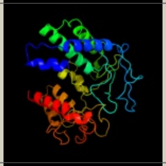
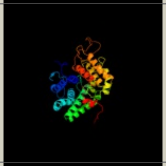
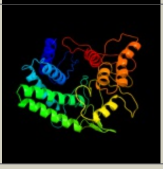
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jg0A_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
2	d2jg0a1	Alignment		100.0	99	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like
3	c3c67B_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ygjk; **PDBTitle:** escherichia coli k12 ygjk in a complexed with glucose
4	c2z07A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0978; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 thermus thermophilus hb8
5	c2okxB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rhamnosidase b; **PDBTitle:** crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
6	c1v7wA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
7	d1v7wa1	Alignment		99.9	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
8	c3cihA_	Alignment		99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
9	c2cqtA_	Alignment		99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
10	d1lf6a1	Alignment		99.8	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
11	c1lf6A_	Alignment		99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase

12	d1ulva1	Alignment		99.3	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
13	d2fbaa1	Alignment		98.5	18	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
14	c2vn4A_	Alignment		98.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** glycoside hydrolase family 15 glucoamylase from hypocrea2 jecorina
15	d1gaia_	Alignment		98.0	20	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
16	c3qspB_	Alignment		97.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
17	c2ww1B_	Alignment		97.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
18	c1ug9A_	Alignment		97.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
19	c2eacB_	Alignment		97.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-fucosidase; **PDBTitle:** crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
20	d2p0va1	Alignment		97.6	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
21	c2p0vA_	Alignment	not modelled	97.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
22	c2rdyB_	Alignment	not modelled	97.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh0842 protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
23	d2nvpa1	Alignment	not modelled	97.5	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
24	d1h54a1	Alignment	not modelled	97.4	12	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
25	c2wvyA_	Alignment	not modelled	97.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
26	c1h54B_	Alignment	not modelled	94.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**maltose phosphorylase; **PDBTitle:** maltose phosphorylase from lactobacillus brevis
27	c3gt5A_	Alignment	not modelled	89.0	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylglucosamine 2-epimerase; **PDBTitle:** crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
28	c2zzrA_	Alignment	not modelled	77.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**unsaturated glucuronyl hydrolase; **PDBTitle:** crystal structure of unsaturated glucuronyl hydrolase from2 streptcoccus agalactiae
						Fold:alpha/alpha toroid

29	d2afaa1	Alignment	not modelled	76.4	11	**Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
30	c3k7xA_	Alignment	not modelled	72.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0763 protein; **PDBTitle:** crystal structure of the lin0763 protein from listeria2 innocua. northeast structural genomics consortium target3 lkr23.
31	c2gz6B_	Alignment	not modelled	68.5	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetyl-d-glucosamine 2-epimerase; **PDBTitle:** crystal structure of anabaena sp. ch1 n-acetyl-d-glucosamine 2-2 epimerase at 2.0 a
32	c3bhwA_	Alignment	not modelled	66.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from magnetospirillum2 magneticum
33	c3ax1A_	Alignment	not modelled	53.7	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**serrate rna effector molecule; **PDBTitle:** molecular insights into mirna processing by arabidopsis serrate
34	c3racA_	Alignment	not modelled	52.7	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidine-trna ligase; **PDBTitle:** crystal strucutre of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
35	c2idxA_	Alignment	not modelled	51.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cob(i)yrinic acid a,c-diamide **PDBTitle:** structure of human atp:cobalamin adenosyltransferase bound2 to atp.
36	c3pg8B_	Alignment	not modelled	44.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
37	d1iwpa_	Alignment	not modelled	40.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit
38	d1nzpa_	Alignment	not modelled	37.7	24	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
39	c2q07A_	Alignment	not modelled	36.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af0587; **PDBTitle:** crystal structure of af0587, a protein of unknown function
40	d1q79a3	Alignment	not modelled	33.3	10	**Fold:**Ferredoxin-like **Superfamily:**PAP/Archaeal CCA-adding enzyme, C-terminal domain **Family:**Poly(A) polymerase, PAP, C-terminal domain
41	d1wu7a2	Alignment	not modelled	31.2	35	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
42	d1dq3a2	Alignment	not modelled	30.6	19	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**PI-Pfui intein middle domain
43	c1wy1B_	Alignment	not modelled	29.7	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein ph0671; **PDBTitle:** crystal structure of the ph0671 protein from pyrococcus horikoshii ot3
44	d1usya_	Alignment	not modelled	28.3	28	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
45	d1uj8a1	Alignment	not modelled	25.9	4	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
46	c2cseW_	Alignment	not modelled	25.4	21	**PDB header:**virus **Chain:** W: **PDB Molecule:**major core protein lambda 1; **PDBTitle:** features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
47	c3k1qB_	Alignment	not modelled	25.2	29	**PDB header:**virus **Chain:** B: **PDB Molecule:**vp3a, the building block protein of inner shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
48	d1z7ma1	Alignment	not modelled	24.9	26	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
49	c3k1qC_	Alignment	not modelled	24.2	29	**PDB header:**virus **Chain:** C: **PDB Molecule:**vp3b, the building block protein of inner shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
50	c1wvtA_	Alignment	not modelled	24.1	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st2180; **PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
51	d1vr6a1	Alignment	not modelled	23.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
52	d2hfha_	Alignment	not modelled	22.9	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
53	d3bpya1	Alignment	not modelled	20.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
54	c3lhrA_	Alignment	not modelled	20.3	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**zinc finger protein 24; **PDBTitle:** crystal structure of the scan domain from human znf24

55	c1z7nB_	Alignment	not modelled	20.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate
56	d1xg7a_	Alignment	not modelled	19.8	8	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
57	d1jmsa1	Alignment	not modelled	18.9	14	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
58	d2bcqa1	Alignment	not modelled	18.6	29	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
59	c3t4cD_	Alignment	not modelled	18.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
60	d2fmpa1	Alignment	not modelled	17.4	27	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
61	c3od1A_	Alignment	not modelled	16.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
62	d1nc5a_	Alignment	not modelled	16.2	10	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Hypothetical protein YteR
63	d1z3xa1	Alignment	not modelled	15.2	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
64	c2q17C_	Alignment	not modelled	15.0	42	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**formylglycine generating enzyme; **PDBTitle:** formylglycine generating enzyme from streptomyces coelicolor
65	d1aina_	Alignment	not modelled	14.9	9	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
66	d1rutx4	Alignment	not modelled	14.8	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
67	c2lmdA_	Alignment	not modelled	14.4	83	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prospero homeobox protein 1; **PDBTitle:** minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b
68	c3c1lB_	Alignment	not modelled	14.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative antioxidant defense protein mlr4105; **PDBTitle:** crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
69	c2ah6B_	Alignment	not modelled	14.1	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
70	c1wozA_	Alignment	not modelled	13.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long conserved hypothetical protein (st1454); **PDBTitle:** crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii
71	d1rtyb_	Alignment	not modelled	13.8	33	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
72	c2yukA_	Alignment	not modelled	13.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
73	c2c1lA_	Alignment	not modelled	13.3	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
74	c2nt8A_	Alignment	not modelled	13.3	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase; **PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
75	c3llbA_	Alignment	not modelled	12.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
76	c3co7C_	Alignment	not modelled	12.8	26	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
77	c2r2vB_	Alignment	not modelled	12.6	27	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** sequence determinants of the topology of the lac repressor2 tetrameric coiled coil
78	d2a21a1	Alignment	not modelled	12.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase

79	d1rtya_	Alignment	not modelled	12.4	33	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
80	c3ha4C_	Alignment	not modelled	12.3	19	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**mix1; **PDBTitle:** crystal structure of the type one membrane protein mix1 from2 leishmania
81	d1noga_	Alignment	not modelled	12.3	50	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
82	c1nogA_	Alignment	not modelled	12.3	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein ta0546; **PDBTitle:** crystal structure of conserved protein 0546 from thermoplasma2 acidophilum
83	c3lzzB_	Alignment	not modelled	12.0	78	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structures of cupin superfamily bbduf985 from branchiostoma2 belcheri tsingtauense in apo and gdp-bound forms
84	d2zdra2	Alignment	not modelled	11.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
85	d1fp3a_	Alignment	not modelled	11.9	13	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
86	c3ke4B_	Alignment	not modelled	11.8	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus
87	c3sz8D_	Alignment	not modelled	11.7	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
88	c2zhzC_	Alignment	not modelled	11.3	43	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
89	c3ci1A_	Alignment	not modelled	11.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase pduo-like protein; **PDBTitle:** structure of the pduo-type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri complexed3 with four-coordinate cob(ii)alamin and atp
90	c1xrsB_	Alignment	not modelled	10.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
91	c2g2dA_	Alignment	not modelled	10.6	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:cobalamin adenosyltransferase; **PDBTitle:** crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
92	d2itka1	Alignment	not modelled	10.5	25	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
93	c2xtdB_	Alignment	not modelled	10.4	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tbl1 f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
94	c3iqtA_	Alignment	not modelled	10.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**signal transduction histidine-protein kinase bara; **PDBTitle:** structure of the hpt domain of sensor protein bara from escherichia2 coli cft073.
95	d1fs1b1	Alignment	not modelled	10.2	22	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
96	c1xuzA_	Alignment	not modelled	10.2	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
97	c2bcuA_	Alignment	not modelled	10.0	28	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
98	d1o65a_	Alignment	not modelled	10.0	6	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**MOSC (MOCO sulphurase C-terminal) domain
99	c2xteH_	Alignment	not modelled	9.8	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain