Phyre2

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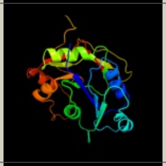
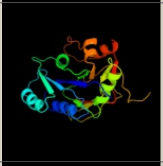
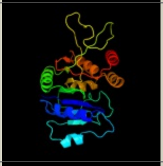
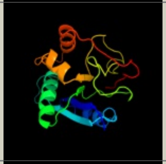
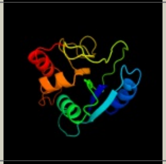
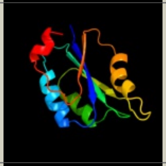
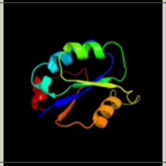
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z86D_	Alignment		100.0	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glcua3 and udp
2	d1xhba2	Alignment		100.0	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
3	c2ffuA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
4	c2d7iA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
5	c1xhbA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
6	d1qg8a_	Alignment		100.0	19	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
7	c3bcvA_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
8	c3f1yC_	Alignment		99.9	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
9	c1omxB_	Alignment		99.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**alpha-1,4-n-acetylhexosaminyltransferase extl2; **PDBTitle:** crystal structure of mouse alpha-1,4-n-2 acetylhexosaminyltransferase (extl2)
10	d1omza_	Alignment		99.9	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
11	c3ckvA_	Alignment		99.9	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein

12	c2qgiA_	Alignment		99.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp synthase subunits region orf 6; **PDBTitle:** the udp complex structure of the sixth gene product of the f1-atpase2 operon of rhodobacter blasticus
13	d1pzta_	Alignment		98.8	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
14	d2bo4a1	Alignment		98.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
15	d1fo8a_	Alignment		98.5	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
16	c3lw6A_	Alignment		98.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
17	c2d0jD_	Alignment		96.4	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
18	d1v82a_	Alignment		95.9	22	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
19	d3cu0a1	Alignment		95.6	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
20	c2wvmA_	Alignment		94.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
21	c2zu8A_	Alignment	not modelled	92.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
22	d1fxoa_	Alignment	not modelled	92.3	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
23	c2wawA_	Alignment	not modelled	91.5	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
24	d1iina_	Alignment	not modelled	90.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
25	d1h5ra_	Alignment	not modelled	90.5	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
26	d1lvwa_	Alignment	not modelled	90.5	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
27	d1w77a1	Alignment	not modelled	87.8	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
28	d1mc3a_	Alignment	not modelled	86.6	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
29	c2px7A_	Alignment	not modelled	83.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate

29	c2px7A_	Alignment	not modelled	83.0	9	**PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from thermus thermophilus hb8
30	d1h7ea_	Alignment	not modelled	81.9	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
31	c3oamD_	Alignment	not modelled	81.8	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** crystal structure of cytidylyltransferase from vibrio cholerae
32	c3hl3A_	Alignment	not modelled	78.4	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucose-1-phosphate thymidylyltransferase; **PDBTitle:** 2.76 angstrom crystal structure of a putative glucose-1-phosphate2 thymidylyltransferase from bacillus anthracis in complex with a3 sucrose.
33	c2we9A_	Alignment	not modelled	76.7	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba-related protein; **PDBTitle:** crystal structure of rv0371c from mycobacterium2 tuberculosis h37rv
34	c3ngwA_	Alignment	not modelled	71.7	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis protein a **PDBTitle:** crystal structure of molybdopterin-guanine dinucleotide biosynthesis2 protein a from archaeoglobus fulgidus, northeast structural genomics3 consortium target gr189
35	c3f1cB_	Alignment	not modelled	71.2	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative 2-c-methyl-d-erythritol 4-phosphate **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 4-phosphate2 cytidylyltransferase from listeria monocytogenes
36	d1vh3a_	Alignment	not modelled	70.4	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
37	d1qwja_	Alignment	not modelled	68.0	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
38	c3tztB_	Alignment	not modelled	67.3	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 8; **PDBTitle:** the structure of a protein in glycosyl transferase family 8 from2 anaerococcus prevotii.
39	d1vpaa_	Alignment	not modelled	67.3	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
40	c3okrA_	Alignment	not modelled	65.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
41	c3polA_	Alignment	not modelled	64.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** 2.3 angstrom crystal structure of 3-deoxy-manno-octulosonate2 cytidylyltransferase (kdsb) from acinetobacter baumannii.
42	d1vkpa_	Alignment	not modelled	63.6	17	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
43	c2xmhB_	Alignment	not modelled	58.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ctp-inositol-1-phosphate cytidylyltransferase; **PDBTitle:** the x-ray structure of ctp:inositol-1-phosphate2 cytidylyltransferase from archaeoglobus fulgidus
44	c2y6pC_	Alignment	not modelled	57.3	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** evidence for a two-metal-ion-mechanism in the2 kdo-cytidylyltransferase kdsb
45	d1i52a_	Alignment	not modelled	56.9	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
46	c1zcyA_	Alignment	not modelled	53.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogenin-1; **PDBTitle:** apo form of a mutant of glycogenin in which asp159 is replaced by ser
47	c3okrC_	Alignment	not modelled	52.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
48	c2vshB_	Alignment	not modelled	52.2	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate **PDBTitle:** synthesis of cdp-activated ribitol for teichoic acid2 precursors in streptococcus pneumoniae
49	d1ll2a_	Alignment	not modelled	49.8	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycogenin
50	c2xwlB_	Alignment	not modelled	49.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ispd from mycobacterium smegmatis in complex2 with ctp and mg
51	d1vgwa_	Alignment	not modelled	48.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
52	d1vica_	Alignment	not modelled	47.2	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases

						Family: Cytidylyltransferase
53	c2jerG_	Alignment	not modelled	46.9	9	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
54	c3tqdA_	Alignment	not modelled	45.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-deoxy-manno-octulosonate cytidylyltransferase; **PDBTitle:** structure of the 3-deoxy-d-manno-octulosonate cytidylyltransferase2 (kdsb) from coxiella burnetii
55	c3ssoE_	Alignment	not modelled	41.4	22	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methyltransferase; **PDBTitle:** myce methyltransferase from the mycinamycin biosynthetic pathway in2 complex with mg and sah, crystal form 2
56	c2pa4B_	Alignment	not modelled	41.3	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp-glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
57	c2gamA_	Alignment	not modelled	40.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-1,6-n-acetylglucosaminyltransferase; **PDBTitle:** x-ray crystal structure of murine leukocyte-type core 2 b1,2 6-n-acetylglucosaminyltransferase (c2gnt-l) in complex3 with galb1,3galnac
58	d1xkna_	Alignment	not modelled	39.4	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
59	c2f59B_	Alignment	not modelled	39.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
60	d2ewoa1	Alignment	not modelled	38.9	13	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
61	d2oi6a2	Alignment	not modelled	35.7	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
62	d1zbra1	Alignment	not modelled	35.5	25	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
63	c2o7qA_	Alignment	not modelled	32.7	20	**PDB header:**oxidoreductase,transferase **Chain:** A: **PDB Molecule:**bifunctional 3-dehydroquinate dehydratase/shikimate **PDBTitle:** crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
64	c3sirD_	Alignment	not modelled	30.5	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice
65	d1w55a1	Alignment	not modelled	30.1	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
66	c3d5nB_	Alignment	not modelled	29.2	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**q97w15_sulso; **PDBTitle:** crystal structure of the q97w15_sulso protein from2 sulfolobus solfataricus. nesg target ssr125.
67	c1zctB_	Alignment	not modelled	27.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogenin-1; **PDBTitle:** structure of glycogenin truncated at residue 270 in a2 complex with udp
68	c1i51A_	Alignment	not modelled	26.7	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7 subunit p20; **PDBTitle:** crystal structure of caspase-7 complexed with xiap
69	d1ga8a_	Alignment	not modelled	25.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Galactosyltransferase LgtC
70	c1ga8A_	Alignment	not modelled	25.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactosyl transferase lgtc; **PDBTitle:** crystal structure of galacosyltransferase lgtc in complex2 with donor and acceptor sugar analogs.
71	c1ez4B_	Alignment	not modelled	25.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
72	d1g97a2	Alignment	not modelled	24.2	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
73	d1ez4a1	Alignment	not modelled	23.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
74	c3h11A_	Alignment	not modelled	22.0	23	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**casp8 and fadd-like apoptosis regulator; **PDBTitle:** zymogen caspase-8:c-flipl protease domain complex
75	d1llca1	Alignment	not modelled	20.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
76	c2e3dB_	Alignment	not modelled	19.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of e. coli glucose-1-phosphate2

						uridylyltransferase
77	d1vh1a_	Alignment	not modelled	19.1	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
78	d1zbsa2	Alignment	not modelled	18.6	44	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
79	d3b48a1	Alignment	not modelled	18.1	14	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
80	c1nmqB_	Alignment	not modelled	18.1	11	**PDB header:**apoptosis, hydrolase **Chain:** B: **PDB Molecule:**caspase-3; **PDBTitle:** extendend tethering: in situ assembly of inhibitors
81	d1ejba_	Alignment	not modelled	16.5	24	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
82	c3pnnA_	Alignment	not modelled	16.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
83	d1uasa2	Alignment	not modelled	15.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	d1nqua_	Alignment	not modelled	14.9	18	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
85	d1szna2	Alignment	not modelled	14.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
86	d1ldna1	Alignment	not modelled	14.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
87	c1t0oA_	Alignment	not modelled	14.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
88	c3sipC_	Alignment	not modelled	14.1	14	**PDB header:**hydrolase/ligase/hydrolase **Chain:** C: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice and diap1-bir1 complex
89	d1c41a_	Alignment	not modelled	14.1	16	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
90	c1uasA_	Alignment	not modelled	13.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
91	c3a5vA_	Alignment	not modelled	13.4	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea
92	c2v65A_	Alignment	not modelled	12.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase a chain; **PDBTitle:** apo ldh from the psychrophile c. gunnari
93	c2ql5A_	Alignment	not modelled	12.3	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of caspase-7 with inhibitor ac-dmqd-cho
94	c3zq4C_	Alignment	not modelled	11.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ribonuclease j 1; **PDBTitle:** unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
95	c3brkX_	Alignment	not modelled	11.7	8	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
96	d1ffki_	Alignment	not modelled	11.6	45	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L15e
97	c2funB_	Alignment	not modelled	11.4	19	**PDB header:**apoptosis/hydrolase **Chain:** B: **PDB Molecule:**caspase-8; **PDBTitle:** alternative p35-caspase-8 complex
98	c3edqC_	Alignment	not modelled	11.1	13	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**caspase-3; **PDBTitle:** crystal structure of caspase-3 with inhibitor ac-ldesd-cho
99	c1pyoA_	Alignment	not modelled	11.0	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-2; **PDBTitle:** crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho