Phyre2

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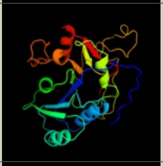
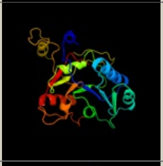
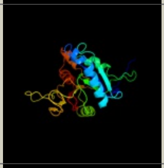
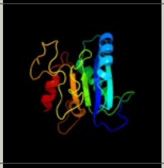
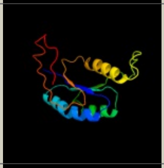
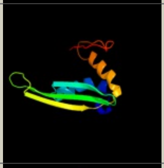
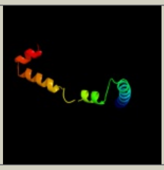
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2d28c1	Alignment		100.0	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**EspE N-terminal domain-like **Family:**GSPII protein E N-terminal domain-like
2	c3f1yC_	Alignment		100.0	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** mannosyl-3-phosphoglycerate synthase from rubrobacter xylanophilus
3	c1xhbA_	Alignment		99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 1; **PDBTitle:** the crystal structure of udp-galnac: polypeptide alpha-n-2 acetylgalactosaminyltransferase-t1
4	d1xhba2	Alignment		99.9	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Polypeptide N-acetylgalactosaminyltransferase 1, N-terminal domain
5	c2z86D_	Alignment		99.9	20	**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
6	c2d7iA_	Alignment		99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 10; **PDBTitle:** crsytal structure of pp-galnac-t10 with udp, galnac and mn2+
7	c2ffuA_	Alignment		99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polypeptide n-acetylgalactosaminyltransferase 2; **PDBTitle:** crystal structure of human ppgalnact-2 complexed with udp2 and ea2
8	c3ckvA_	Alignment		99.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a mycobacterial protein
9	c3bcvA_	Alignment		99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase protein; **PDBTitle:** crystal structure of a putative glycosyltransferase from bacteroides2 fragilis
10	d1qg8a_	Alignment		99.9	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Spore coat polysaccharide biosynthesis protein SpsA
11	c1omxB_	Alignment		99.8	11	**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)

12	d1omza_	Alignment		99.8	12	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Exostosin
13	c2qgiA_	Alignment		99.6	11	**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
14	d2bo4a1	Alignment		99.3	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
15	d1pzta_	Alignment		98.6	18	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
16	c3lw6A_	Alignment		98.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
17	d1fo8a_	Alignment		97.8	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**N-acetylglucosaminyltransferase I
18	d1p9ra_	Alignment		97.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
19	c2wvmA_	Alignment		95.1	21	**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)
20	c2zu8A_	Alignment		94.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** crystal structure of mannosyl-3-phosphoglycerate synthase2 from pyrococcus horikoshii
21	c2bh1Y_	Alignment	not modelled	94.0	15	**PDB header:**transport protein **Chain:** Y: **PDB Molecule:**general secretion pathway protein e,; **PDBTitle:** x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
22	d2bh1x1	Alignment	not modelled	94.0	15	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**EspE N-terminal domain-like **Family:**GSPII protein E N-terminal domain-like
23	c2ch4A_	Alignment		89.1	10	**PDB header:**transferase/chemotaxis **Chain:** A: **PDB Molecule:**chemotaxis protein chea; **PDBTitle:** complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
24	c2oaq1_	Alignment	not modelled	83.3	7	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**type ii secretion system protein; **PDBTitle:** crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
25	d1ugpa_	Alignment		68.3	18	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
26	c1jylC_	Alignment	not modelled	65.6	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ctp:phosphocholine cytidylytransferase; **PDBTitle:** catalytic mechanism of ctp:phosphocholine2 cytidylytransferase from streptococcus pneumoniae (licc)

27	c3qyhG_	Alignment	not modelled	63.9	19	**PDB header:**lyase **Chain:** G: **PDB Molecule:**co-type nitrile hydratase alpha subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-h71l from2 pseudomonas putida.
28	c2dd4H_	Alignment	not modelled	58.1	14	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**thiocyanate hydrolase beta subunit; **PDBTitle:** thiocyanate hydrolase (scnase) from thiobacillus thioparus2 recombinant apo-enzyme
29	d1ugpb_	Alignment	not modelled	56.3	11	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
30	c2gamA_	Alignment	not modelled	56.2	12	**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
31	c2qh5B_	Alignment	not modelled	46.6	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose-6-phosphate isomerase from helicobacter2 pylori
32	c2j0bA_	Alignment	not modelled	44.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-1,3-n-acetylglucosaminyltransferase manic fringe; **PDBTitle:** structure of the catalytic domain of mouse manic fringe in2 complex with udp and manganese
33	d1v29b_	Alignment	not modelled	43.6	10	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
34	d1v29a_	Alignment	not modelled	42.2	14	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
35	c2dxbR_	Alignment	not modelled	39.3	8	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma; **PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers
36	c2xmhB_	Alignment	not modelled	39.0	14	**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
37	c2xzmD_	Alignment	not modelled	37.0	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein s4 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
38	d2qdyb1	Alignment	not modelled	36.3	14	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
39	d1fxoa_	Alignment	not modelled	35.6	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
40	d1jyka_	Alignment	not modelled	34.8	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
41	c3kvhA_	Alignment	not modelled	30.9	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
42	d1fuoa_	Alignment	not modelled	30.0	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
43	c1w57A_	Alignment	not modelled	30.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
44	c3jvvA_	Alignment	not modelled	28.7	9	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
45	d1vh3a_	Alignment	not modelled	28.4	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase
46	d1v82a_	Alignment	not modelled	27.1	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
47	d1kyqa2	Alignment	not modelled	26.6	18	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
48	c3brkX_	Alignment	not modelled	26.1	13	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
49	d1lm5a_	Alignment	not modelled	25.4	10	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Plakin repeat **Family:**Plakin repeat
50	d2p12a1	Alignment	not modelled	25.0	14	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
51	c3fesB_	Alignment	not modelled	24.1	10	**PDB header:**atp binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp endopeptidase; **PDBTitle:** crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
						PDB header:transferase

52	c2x5sB_	Alignment	not modelled	23.6	11	**Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
53	d1lvwa_	Alignment	not modelled	23.2	16	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
54	d1jswa_	Alignment	not modelled	23.2	24	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
55	d1j3ua_	Alignment	not modelled	21.7	23	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
56	d2qdya1	Alignment	not modelled	21.6	11	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
57	d2oqoa1	Alignment	not modelled	21.3	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**PBP transglycosylase domain-like
58	c2d0jD_	Alignment	not modelled	20.7	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
59	c3mwmA_	Alignment	not modelled	19.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
60	c1chmA_	Alignment	not modelled	19.0	21	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
61	d1zq1c3	Alignment	not modelled	16.8	15	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
62	d1dgna_	Alignment	not modelled	15.8	22	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
63	c2nz7A_	Alignment	not modelled	15.7	15	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**caspase recruitment domain-containing protein 4; **PDBTitle:** crystal structure analysis of caspase-recruitment domain2 (card) of nod1
64	d2jera1	Alignment	not modelled	15.7	16	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
65	c2jerG_	Alignment	not modelled	15.3	16	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
66	c3bjrA_	Alignment	not modelled	15.2	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxylesterase; **PDBTitle:** crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
67	d1yp2a2	Alignment	not modelled	15.0	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
68	c1hsjA_	Alignment	not modelled	15.0	13	**PDB header:**transcription/sugar binding protein **Chain:** A: **PDB Molecule:**fusion protein consisting of staphylococcus **PDBTitle:** sarr mbp fusion structure
69	d1z05a1	Alignment	not modelled	14.8	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
70	c1yfmA_	Alignment	not modelled	14.7	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarase; **PDBTitle:** recombinant yeast fumarase
71	d1yfma_	Alignment	not modelled	14.7	28	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
72	c3qz9D_	Alignment	not modelled	14.4	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**co-type nitrile hydratase beta subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
73	d1u20a1	Alignment	not modelled	14.0	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
74	c1egpA_	Alignment	not modelled	13.8	24	**PDB header:**proteinase inhibitor **Chain:** A: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
75	d2ewoa1	Alignment	not modelled	13.7	9	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
76	c3hzsA_	Alignment	not modelled	13.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monofunctional glycosyltransferase; **PDBTitle:** s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
77	d1xkna_	Alignment	not modelled	13.3	9	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
78	c1ex1A_	Alignment	not modelled	13.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (beta-d-glucan exohydrolase isoenzyme exo1);

						PDBTitle: beta-d-glucan exohydrolase from barley
79	d3crda_	Alignment	not modelled	12.8	15	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
80	d2f2ab2	Alignment	not modelled	12.4	19	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
81	c2jciA_	Alignment	not modelled	12.4	9	**PDB header:**drug-binding protein **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b
82	d1zbra1	Alignment	not modelled	12.1	16	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
83	c2wawA_	Alignment	not modelled	11.9	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
84	d2h80a1	Alignment	not modelled	11.6	29	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Variant SAM domain
85	c1s1hO_	Alignment	not modelled	11.5	18	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
86	d2oi6a2	Alignment	not modelled	11.0	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
87	d1iina_	Alignment	not modelled	10.9	11	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
88	c2xnsC_	Alignment	not modelled	10.8	21	**PDB header:**hydrolase/peptide **Chain:** C: **PDB Molecule:**regulator of g-protein signaling 14; **PDBTitle:** crystal structure of human g alpha i1 bound to a designed helical2 peptide derived from the goloco motif of rgs14
89	c2d7cD_	Alignment	not modelled	10.0	25	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of human rab11 in complex with fip3 rab-2 binding domain
90	d2pnwa1	Alignment	not modelled	9.7	24	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
91	c2gszE_	Alignment	not modelled	9.2	13	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
92	d1mc3a_	Alignment	not modelled	9.0	10	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
93	c2o03A_	Alignment	not modelled	8.7	28	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
94	d1mzba_	Alignment	not modelled	8.7	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
95	d1g5ta_	Alignment	not modelled	8.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
96	c3udiA_	Alignment	not modelled	8.5	17	**PDB header:**penicillin-binding protein/antibiotic **Chain:** A: **PDB Molecule:**penicillin-binding protein 1a; **PDBTitle:** crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
97	d1vkpa_	Alignment	not modelled	8.5	6	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
98	c3hxkB_	Alignment	not modelled	8.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sugar hydrolase; **PDBTitle:** crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108
99	c1yshE_	Alignment	not modelled	8.4	18	**PDB header:**structural protein/rna **Chain:** E: **PDB Molecule:**40s ribosomal protein s13; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e