Phyre^2

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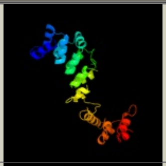
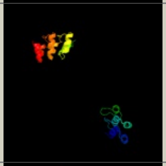
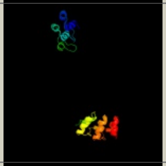
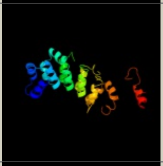
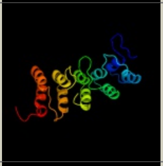
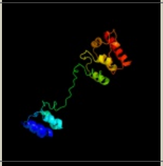
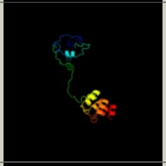
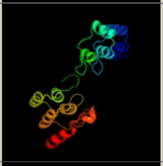
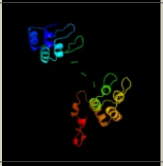
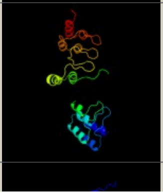
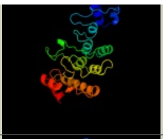
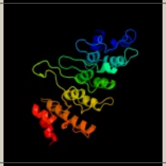
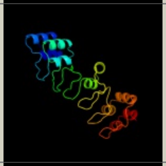
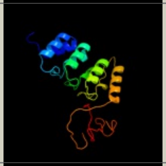
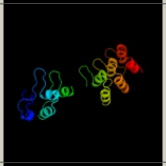
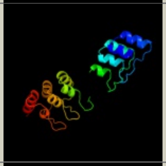
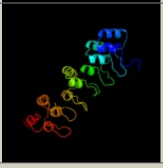
Description	P76205
Date	Thu Jan 5 12:20:31 GMT 2012
Unique Job ID	aced4d7fdb55803c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ajaa1	Alignment		100.0	16	**Fold:**alpha-alpha superhelix **Superfamily:**Pseudo ankyrin repeat-like **Family:**Pseudo ankyrin repeat
2	d1n11a_	Alignment		100.0	35	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
3	c1n11A_	Alignment		100.0	35	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin; **PDBTitle:** d34 region of human ankyrin-r and linker
4	c2ajaA_	Alignment		100.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin repeat family protein; **PDBTitle:** x-ray structure of an ankyrin repeat family protein q5zsv02 from legionella pneumophila. northeast structural genomics3 consortium target lgr21.
5	c3keaB_	Alignment		100.0	19	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**k1l; **PDBTitle:** structure function studies of vaccinia virus host-range protein k12 reveal a novel ankyrin repeat interaction surface for k1s function
6	c3ljnA_	Alignment		100.0	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** ankyrin repeat protein from leishmania major
7	c2fo1E_	Alignment		100.0	25	**PDB header:**gene regulation/signalling protein/dna **Chain:** E: **PDB Molecule:**lin-12 protein; **PDBTitle:** crystal structure of the csl-notch-mastermind ternary2 complex bound to dna
8	d1s70b_	Alignment		100.0	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
9	d2fo1e1	Alignment		100.0	25	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
10	c2xaiD_	Alignment		100.0	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**ankyrin repeat and socs box protein 9; **PDBTitle:** crystal structure of ankyrin repeat and socs box-containing2 protein 9 (asb9) in complex with elonginb and elonginc
11	d1wdya_	Alignment		99.9	21	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat

12	c2f37B_	Alignment		99.9	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transient receptor potential cation channel **PDBTitle:** crystal structure of the ankyrin repeat domain of human2 trpv2
13	d1uoha_	Alignment		99.9	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
14	c3jxiA_	Alignment		99.9	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**vanilloid receptor-related osmotically activated channel **PDBTitle:** crystal structure of the chicken trpv4 ankyrin repeat domain
15	c3eu9B_	Alignment		99.9	15	**PDB header:**protein binding, methyl-lysine-binding p **Chain:** B: **PDB Molecule:**huntingtin-interacting protein 14; **PDBTitle:** the ankyrin repeat domain of huntingtin interacting protein 14
16	c2vgeA_	Alignment		99.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rela-associated inhibitor; **PDBTitle:** crystal structure of the c-terminal region of human iaspp
17	d1k1aa_	Alignment		99.9	26	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
18	c2f8xK_	Alignment		99.9	19	**PDB header:**transcription/dna **Chain:** K: **PDB Molecule:**neurogenic locus notch homolog protein 1; **PDBTitle:** crystal structure of activated notch, csl and maml on hes-12 promoter dna sequence
19	c3b7bB_	Alignment		99.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**euchromatic histone-lysine n-methyltransferase 1; **PDBTitle:** euhmt1 (glp) ankyrin repeat domain (structure 1)
20	c3d9hA_	Alignment		99.9	15	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**cdna flj77766, highly similar to homo sapiens **PDBTitle:** crystal structure of the splice variant of human asb92 (hasb9-2), an ankyrin repeat protein
21	d1sw6a_	Alignment	not modelled	99.9	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
22	c1sw6A_	Alignment	not modelled	99.9	16	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**regulatory protein swi6; **PDBTitle:** s. cerevisiae swi6 ankyrin-repeat fragment
23	c1ycsB_	Alignment	not modelled	99.9	17	**PDB header:**complex (anti-oncogene/ankyrin repeats) **Chain:** B: **PDB Molecule:**53bp2; **PDBTitle:** p53-53bp2 complex
24	c3ui2A_	Alignment	not modelled	99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein, chloroplastic; **PDBTitle:** crystal structure of the cpsrp54 tail bound to cpsrp43
25	d1iknd_	Alignment	not modelled	99.9	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
26	c2nyjA_	Alignment	not modelled	99.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transient receptor potential cation channel **PDBTitle:** crystal structure of the ankyrin repeat domain of trpv1
27	d1oy3d_	Alignment	not modelled	99.9	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
28	c1oy3D_	Alignment	not modelled	99.9	15	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcription factor inhibitor i-kappa-b-beta; **PDBTitle:** crystal structure of an ikbbeta/nf-kb p65 homodimer complex
29	c3ehrB_	Alignment	not modelled	99.9	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**osteoclast-stimulating factor 1;

						PDBTitle: crystal structure of human osteoclast stimulating factor
30	c3t8kB_	Alignment	not modelled	99.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein lebu_0176 from2 leptotrichia buccalis c-1013-b
31	d1ot8a_	Alignment	not modelled	99.9	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
32	d1ixva_	Alignment	not modelled	99.9	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
33	d1dcqa1	Alignment	not modelled	99.9	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
34	c3jueA_	Alignment	not modelled	99.9	15	**PDB header:**protein transport/endocytosis **Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1
35	c2rfaA_	Alignment	not modelled	99.9	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**transient receptor potential cation channel subfamily v **PDBTitle:** crystal structure of the mouse trpv6 ankyrin repeat domain
36	c3deoA_	Alignment	not modelled	99.9	13	**PDB header:**protein transport, membrane protein **Chain:** A: **PDB Molecule:**signal recognition particle 43 kda protein; **PDBTitle:** structural basis for specific substrate recognition by the2 chloroplast signal recognition particle protein cpsrp43
37	c3hraA_	Alignment	not modelled	99.9	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ankyrin repeat family protein; **PDBTitle:** crystal structure of ef0377 an ankyrin repeat protein
38	c2rfmB_	Alignment	not modelled	99.9	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**putative ankyrin repeat protein tv1425; **PDBTitle:** structure of a thermophilic ankyrin repeat protein
39	c2b0oF_	Alignment	not modelled	99.8	16	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
40	c1dcqA_	Alignment	not modelled	99.8	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pyk2-associated protein beta; **PDBTitle:** crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
41	c3twtD_	Alignment	not modelled	99.8	19	**PDB header:**signaling protein/peptide **Chain:** D: **PDB Molecule:**tankyrase-2; **PDBTitle:** crystal structure of arc4 from human tankyrase 2 in complex with2 peptide from human mcl1 (chimeric peptide)
42	c2kbxA_	Alignment	not modelled	99.8	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin-linked protein kinase; **PDBTitle:** solution structure of ilk-pinch complex
43	c3lvrE_	Alignment	not modelled	99.8	16	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain- **PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
44	d1ycsb1	Alignment	not modelled	99.8	16	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
45	d2a5ea_	Alignment	not modelled	99.8	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
46	c3c5rB_	Alignment	not modelled	99.8	20	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**brca1-associated ring domain protein 1; **PDBTitle:** crystal structure of the bard1 ankyrin repeat domain and its2 functional consequences
47	c2zgdA_	Alignment	not modelled	99.8	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**3 repeat synthetic ankyrin; **PDBTitle:** asn-hydroxylation stabilises the ankyrin repeat domain fold
48	d1awcb_	Alignment	not modelled	99.8	20	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
49	c1ympB_	Alignment	not modelled	99.8	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**notch 1 protein; **PDBTitle:** the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
50	c1ympA_	Alignment	not modelled	99.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**notch 1 protein; **PDBTitle:** the crystal structure of a partial mouse notch-1 ankyrin2 domain: repeats 4 through 7 preserve an ankyrin fold
51	c2jabC_	Alignment	not modelled	99.8	20	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**h10-2-g3; **PDBTitle:** a designed ankyrin repeat protein evolved to picomolar2 affinity to her2
52	d1bi7b_	Alignment	not modelled	99.8	19	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
53	d1ihba_	Alignment	not modelled	99.7	18	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
54	d1myoa_	Alignment	not modelled	99.7	15	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
						Fold:beta-hairpin-alpha-hairpin repeat

55	d1bd8a_	Alignment	not modelled	99.7	13	**Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
56	d1blxb_	Alignment	not modelled	99.7	17	**Fold:**beta-hairpin-alpha-hairpin repeat **Superfamily:**Ankyrin repeat **Family:**Ankyrin repeat
57	c2v5qC_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**design ankyrin repeat protein; **PDBTitle:** crystal structure of wild-type plk-1 kinase domain in2 complex with a selective darpin
58	c2xenA_	Alignment	not modelled	99.7	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ni1c mut4; **PDBTitle:** structural determinants for improved thermal stability of2 designed ankyrin repeat proteins with a redesigned c-3 capping module.
59	c2l6bA_	Alignment	not modelled	99.6	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**nr1c; **PDBTitle:** nrc consensus ankyrin repeat protein solution structure
60	c1n0qB_	Alignment	not modelled	99.6	25	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**3 ankyrin repeats; **PDBTitle:** 3ank: a designed ankyrin repeat protein with three identical consensus2 repeats
61	c1n0rA_	Alignment	not modelled	99.5	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**4 ankyrin repeats; **PDBTitle:** 4ank: a designed ankyrin repeat protein with four identical2 consensus repeats
62	c2xumS_	Alignment	not modelled	63.6	22	**PDB header:**oxidoreductase/peptide **Chain:** S: **PDB Molecule:**asp-substrate peptide 2; **PDBTitle:** factor inhibiting hif (fih) q239h mutant in complex with zn(ii), nog2 and asp-substrate peptide (20-mer)
63	c3zrhA_	Alignment	not modelled	49.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin thioesterase zranb1; **PDBTitle:** crystal structure of the lys29, lys33-linkage-specific trabid otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
64	d1d1da1	Alignment	not modelled	41.0	35	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
65	d2qamc2	Alignment	not modelled	39.2	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
66	c1rl2A_	Alignment	not modelled	35.7	33	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**protein (ribosomal protein l2); **PDBTitle:** ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
67	d1rl2a2	Alignment	not modelled	34.5	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	d1ukfa_	Alignment	not modelled	31.3	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Avirulence protein Avrpph3
69	c2y0iS_	Alignment	not modelled	28.1	8	**PDB header:**oxidoreductase/peptide **Chain:** S: **PDB Molecule:**tankyrase-2; **PDBTitle:** factor inhibiting hif-1 alpha in complex with tankyrase-2 (tnks2)2 fragment peptide (21-mer)
70	d1nepa_	Alignment	not modelled	27.2	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**ML domain
71	c2zkrn_	Alignment	not modelled	26.9	13	**PDB header:**ribosomal protein/rna **Chain:** N: **PDB Molecule:**rna expansion segment es27; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
72	c3cixA_	Alignment	not modelled	26.6	17	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
73	d1vqoa2	Alignment	not modelled	26.5	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
74	c2ftcB_	Alignment	not modelled	25.2	43	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**mitochondrial ribosomal protein l2; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
75	d2zjra2	Alignment	not modelled	24.6	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
76	c3go5A_	Alignment	not modelled	22.5	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**multidomain protein with s1 rna-binding domains; **PDBTitle:** crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
77	d1hnga1	Alignment	not modelled	19.8	38	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
78	c1af7A_	Alignment	not modelled	17.9	29	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**chemotaxis receptor methyltransferase cher; **PDBTitle:** cher from salmonella typhimurium
79	d2j01d2	Alignment	not modelled	15.2	57	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
80	d1bvua1	Alignment	not modelled	14.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain

81	c1kqsA_	Alignment	not modelled	14.4	25	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**ribosomal protein l2; **PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
82	d7reqb1	Alignment	not modelled	13.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
83	d2fd5a1	Alignment	not modelled	12.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
84	d1wo8a1	Alignment	not modelled	12.1	26	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
85	d2gsta2	Alignment	not modelled	12.0	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
86	d2c4ja2	Alignment	not modelled	11.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
87	c2k0mA_	Alignment	not modelled	11.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
88	c2zkra_	Alignment	not modelled	11.2	25	**PDB header:**ribosomal protein/rna **Chain:** A: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
89	d2vy4a1	Alignment	not modelled	11.1	40	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**CHHC finger
90	c2b66D_	Alignment	not modelled	11.0	57	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**50s ribosomal protein l2; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
91	c3rrrB_	Alignment	not modelled	9.4	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
92	d1czda1	Alignment	not modelled	9.3	31	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
93	c1d0rA_	Alignment	not modelled	9.1	50	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
94	c1n7qA_	Alignment	not modelled	8.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hyaluronidase; **PDBTitle:** streptococcus pneumoniae hyaluronate lyase w291a/w292a double mutant2 complex with hyaluronan hexasacchride
95	c3ac0B_	Alignment	not modelled	8.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase i; **PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
96	d1fhea2	Alignment	not modelled	8.2	5	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
97	d1eg3a1	Alignment	not modelled	8.1	48	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
98	c3rkiB_	Alignment	not modelled	8.1	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structural basis for immunization with post-fusion rsv f to elicit2 high neutralizing antibody titers
99	d1v5ma_	Alignment	not modelled	7.9	25	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)