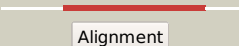



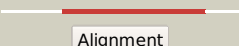


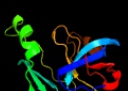


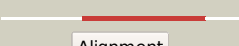


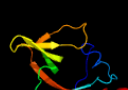








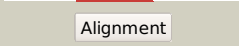




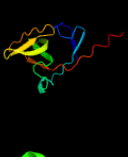


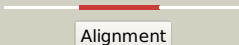

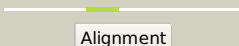
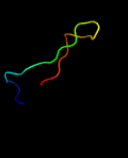
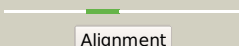
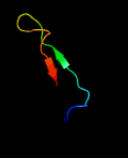
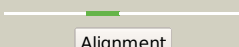
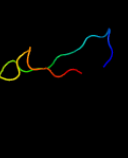
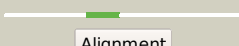


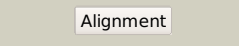



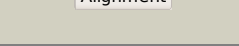




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2903c_(lepB)_3212980_3213864
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	7c8dae9c1b64f885

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4wviA_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,signal peptidase ib; <b>PDBTitle:</b> crystal structure of the type-i signal peptidase from staphylococcus2 aureus (spsb) in complex with a substrate peptide (pep2).
2	<a href="#">d1b12a_</a>	 Alignment		100.0	36	<b>Fold:</b> LexA/Signal peptidase <b>Superfamily:</b> LexA/Signal peptidase <b>Family:</b> Type 1 signal peptidase
3	<a href="#">c4n31A_</a>	 Alignment		100.0	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> sipa; <b>PDBTitle:</b> structure and activity of streptococcus pyogenes sipa: a signal2 peptidase homologue essential for pilus polymerisation
4	<a href="#">c4me8A_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> signal peptidase i; <b>PDBTitle:</b> crystal structure of a signal peptidase i (ef3073) from enterococcus2 faecalis v583 at 2.27 a resolution
5	<a href="#">c4nv4A_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> signal peptidase i; <b>PDBTitle:</b> 1.8 angstrom crystal structure of signal peptidase i from bacillus2 anthracis.
6	<a href="#">c4k8wA_</a>	 Alignment		100.0	28	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> lepa; <b>PDBTitle:</b> an arm-swapped dimer of the s. pyogenes pilin specific assembly factor2 sipa
7	<a href="#">d1f39a_</a>	 Alignment		97.7	30	<b>Fold:</b> LexA/Signal peptidase <b>Superfamily:</b> LexA/Signal peptidase <b>Family:</b> LexA-related
8	<a href="#">c6a2rD_</a>	 Alignment		97.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> mycobacterium tuberculosis lexa c-domain ii
9	<a href="#">c3k2zA_</a>	 Alignment		97.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
10	<a href="#">d1lumua_</a>	 Alignment		96.9	28	<b>Fold:</b> LexA/Signal peptidase <b>Superfamily:</b> LexA/Signal peptidase <b>Family:</b> LexA-related
11	<a href="#">d1jhfa2</a>	 Alignment		96.9	31	<b>Fold:</b> LexA/Signal peptidase <b>Superfamily:</b> LexA/Signal peptidase <b>Family:</b> LexA-related

12	<a href="#">c3jsoA_</a>	 Alignment		96.8	30	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> classic protein with a new twist: crystal structure of a lexa2 repressor dna complex
13	<a href="#">c1jhhB_</a>	 Alignment		96.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> lexa s119a mutant
14	<a href="#">c3bdnB_</a>	 Alignment		96.2	30	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor
15	<a href="#">c2hnfA_</a>	 Alignment		96.0	25	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein ci101-229dm-k192a; <b>PDBTitle:</b> structure of a hyper-cleavable monomeric fragment of phage2 lambda repressor containing the cleavage site region
16	<a href="#">c2fjrB_</a>	 Alignment		92.8	7	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
17	<a href="#">d1hr0w_</a>	 Alignment		60.5	32	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
18	<a href="#">c6c00A_</a>	 Alignment		59.1	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> solution structure of translation initiation factor 1 from clostridium2 difficile
19	<a href="#">c2nchA_</a>	 Alignment		58.7	29	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> solution structure of translation initiation factor if1 from wolbachia2 endosymbiont strain trs of brugia malayi
20	<a href="#">c4ql5A_</a>	 Alignment		56.9	27	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4
21	<a href="#">c3pbiA_</a>	 Alignment	not modelled	49.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein; <b>PDBTitle:</b> structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
22	<a href="#">c3i4oA_</a>	 Alignment	not modelled	49.7	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
23	<a href="#">d1ah9a_</a>	 Alignment	not modelled	48.2	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
24	<a href="#">c4dqqa_</a>	 Alignment	not modelled	45.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative carbohydrate binding protein2 (bacova_03559) from bacteroides ovatus atcc 8483 at 1.50 a resolution
25	<a href="#">c4bpp0_</a>	 Alignment	not modelled	40.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> 0: <b>PDB Molecule:</b> translation initiation factor eif-1a family protein; <b>PDBTitle:</b> the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
26	<a href="#">c3j81i_</a>	 Alignment	not modelled	39.6	32	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> es8; <b>PDBTitle:</b> cryoem structure of a partial yeast 48s preinitiation complex
27	<a href="#">c2kogA_</a>	 Alignment	not modelled	37.9	4	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
28	<a href="#">d1v54d_</a>	 Alignment	not modelled	37.4	10	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV

29	<a href="#">c2y69Q_</a>	Alignment	not modelled	36.9	10	<b>PDB header:</b> electron transport <b>Chain:</b> Q: <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
30	<a href="#">c3hd7A_</a>	Alignment	not modelled	36.8	6	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
31	<a href="#">c2xivA_</a>	Alignment	not modelled	35.3	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical invasion protein; <b>PDBTitle:</b> structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
32	<a href="#">d1jz8a5</a>	Alignment	not modelled	31.1	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
33	<a href="#">d2ftxa1</a>	Alignment	not modelled	30.4	36	<b>Fold:</b> Kinetochore globular domain-like <b>Superfamily:</b> Kinetochore globular domain <b>Family:</b> Spc25-like
34	<a href="#">c2oqkA_</a>	Alignment	not modelled	30.4	32	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> putative translation initiation factor eif-1a; <b>PDBTitle:</b> crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
35	<a href="#">d1bhga2</a>	Alignment	not modelled	29.4	24	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> beta-Galactosidase/glucuronidase, N-terminal domain
36	<a href="#">c4hzbA_</a>	Alignment	not modelled	29.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
37	<a href="#">c2jv8A_</a>	Alignment	not modelled	26.6	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ne1242; <b>PDBTitle:</b> solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4
38	<a href="#">d1jt8a_</a>	Alignment	not modelled	26.4	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
39	<a href="#">d1d7qa_</a>	Alignment	not modelled	25.6	32	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
40	<a href="#">c5td8D_</a>	Alignment	not modelled	23.8	36	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> kinetochore protein spc25; <b>PDBTitle:</b> crystal structure of an extended dwarf ndc80 complex
41	<a href="#">d1knwa1</a>	Alignment	not modelled	23.5	14	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Eukaryotic ODC-like
42	<a href="#">c3w5aC_</a>	Alignment	not modelled	23.3	13	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> sarcolipin; <b>PDBTitle:</b> crystal structure of the calcium pump and sarcolipin from rabbit fast2 twitch skeletal muscle in the e1.mg2+ state
43	<a href="#">c4h1wB_</a>	Alignment	not modelled	23.3	13	<b>PDB header:</b> hydrolase/hydrolase regulator <b>Chain:</b> B: <b>PDB Molecule:</b> sarcolipin; <b>PDBTitle:</b> e1 structure of the (sr) ca2+-atpase in complex with sarcolipin
44	<a href="#">d1bhga3</a>	Alignment	not modelled	21.9	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
45	<a href="#">d2ix0a2</a>	Alignment	not modelled	21.3	47	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
46	<a href="#">d1jnpa_</a>	Alignment	not modelled	20.2	18	<b>Fold:</b> Oncogene products <b>Superfamily:</b> Oncogene products <b>Family:</b> Oncogene products
47	<a href="#">d1zvpa1</a>	Alignment	not modelled	20.0	40	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> VC0802-like
48	<a href="#">c4eqxA_</a>	Alignment	not modelled	19.6	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinasin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a cc1-fha tandem
49	<a href="#">c2vijA_</a>	Alignment	not modelled	18.0	43	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tailspike protein; <b>PDBTitle:</b> tailspike protein of e.coli bacteriophage hk620 in complex with2 hexasaccharide
50	<a href="#">c4eqjB_</a>	Alignment	not modelled	17.7	29	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinasin-like protein kif1a; <b>PDBTitle:</b> crystal structure of kif1a c-c1-fha
51	<a href="#">d1a1xa_</a>	Alignment	not modelled	17.7	21	<b>Fold:</b> Oncogene products <b>Superfamily:</b> Oncogene products <b>Family:</b> Oncogene products
52	<a href="#">c2rtsA_</a>	Alignment	not modelled	16.8	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> chitin binding domain1
53	<a href="#">d1yq2a5</a>	Alignment	not modelled	16.8	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
54	<a href="#">d1jsga_</a>	Alignment	not modelled	16.7	25	<b>Fold:</b> Oncogene products <b>Superfamily:</b> Oncogene products <b>Family:</b> Oncogene products
55	<a href="#">c1jlxB_</a>	Alignment	not modelled	16.6	32	<b>PDB header:</b> lectin <b>Chain:</b> B: <b>PDB Molecule:</b> agglutinin; <b>PDBTitle:</b> agglutinin in complex with t-disaccharide

56	<a href="#">d2qmma1</a>	Alignment	not modelled	16.3	21	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> AF1056-like
57	<a href="#">d2io8a2</a>	Alignment	not modelled	15.5	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> CHAP domain
58	<a href="#">c3i86A</a>	Alignment	not modelled	15.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
59	<a href="#">c4mnoA</a>	Alignment	not modelled	14.7	30	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 1a; <b>PDBTitle:</b> crystal structure of aif1a from pyrococcus abyssi
60	<a href="#">c2lzsE</a>	Alignment	not modelled	14.4	33	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> sec-independent protein translocase protein tata; <b>PDBTitle:</b> tata oligomer
61	<a href="#">c3j1rQ</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> Q: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
62	<a href="#">c3j1rR</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
63	<a href="#">c3j1rH</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
64	<a href="#">c3j1rD</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
65	<a href="#">c3j1rM</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> M: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
66	<a href="#">c3j1rB</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
67	<a href="#">c3j1rK</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> K: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
68	<a href="#">c3j1rG</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> G: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
69	<a href="#">c3j1rN</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
70	<a href="#">c3j1rE</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
71	<a href="#">c3j1rO</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> O: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
72	<a href="#">c3j1rI</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> I: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
73	<a href="#">c3j1rF</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
74	<a href="#">c3j1rT</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> T: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
75	<a href="#">c3j1rL</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> L: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
76	<a href="#">c3j1rA</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
77	<a href="#">c3j1rP</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> P: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
78	<a href="#">c3j1rC</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
79	<a href="#">c3j1rU</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
80	<a href="#">c3j1rJ</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> J: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
81	<a href="#">c3j1rS</a>	Alignment	not modelled	14.4	29	<b>PDB header:</b> cell adhesion, structural protein <b>Chain:</b> S: <b>PDB Molecule:</b> archaeal adhesion filament core; <b>PDBTitle:</b> filaments from iginococcus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices

82	<a href="#">c1jdmA_</a>	Alignment	not modelled	14.1	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosylipin; <b>PDBTitle:</b> nmr structure of sarcosylipin
83	<a href="#">c2pkpA_</a>	Alignment	not modelled	13.7	40	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> homoaconitase small subunit; <b>PDBTitle:</b> crystal structure of 3-isopropylmalate dehydratase (leud)2 from methanocaldococcus jannaschii dsm2661 (mj1271)
84	<a href="#">c2na9A_</a>	Alignment	not modelled	13.5	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
85	<a href="#">c4wo1A_</a>	Alignment	not modelled	13.4	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
86	<a href="#">c2l34B_</a>	Alignment	not modelled	13.4	16	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> structure of the dap12 transmembrane homodimer
87	<a href="#">c2pwyB_</a>	Alignment	not modelled	13.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (adenine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of a m1a58 trna methyltransferase
88	<a href="#">c3mt1B_</a>	Alignment	not modelled	13.1	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative carboxynorspermidine decarboxylase protein; <b>PDBTitle:</b> crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
89	<a href="#">c3nx6A_</a>	Alignment	not modelled	13.1	23	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> 10kda chaperonin; <b>PDBTitle:</b> crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
90	<a href="#">c4d7zA_</a>	Alignment	not modelled	13.0	38	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate 1-decarboxylase beta chain; <b>PDBTitle:</b> e. coli l-aspartate-alpha-decarboxylase mutant n72q to a resolution of 2 1.9 angstroms
91	<a href="#">c4wo1C_</a>	Alignment	not modelled	12.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
92	<a href="#">c4wo1A_</a>	Alignment	not modelled	12.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
93	<a href="#">c4wo1B_</a>	Alignment	not modelled	12.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
94	<a href="#">c4wo1D_</a>	Alignment	not modelled	12.9	16	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
95	<a href="#">c5djoB_</a>	Alignment	not modelled	12.9	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> kinesin-like protein; <b>PDBTitle:</b> crystal structure of the cc1-fha tandem of kinesin-3 kif13a
96	<a href="#">c3n29A_</a>	Alignment	not modelled	12.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxynorspermidine decarboxylase; <b>PDBTitle:</b> crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
97	<a href="#">c2mi2A_</a>	Alignment	not modelled	12.8	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sec-independent protein translocase protein tatb; <b>PDBTitle:</b> solution structure of the e. coli tatb protein in dpc micelles
98	<a href="#">c2pfuA_</a>	Alignment	not modelled	12.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biopolymer transport exbd protein; <b>PDBTitle:</b> nmr structure determination of the periplasmic domain of exbd from2 e.coli
99	<a href="#">c4wo1B_</a>	Alignment	not modelled	12.4	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> tyro protein tyrosine kinase-binding protein; <b>PDBTitle:</b> crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase