

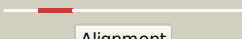

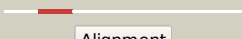





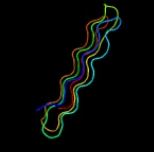


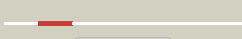
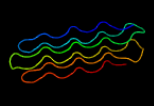

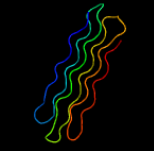



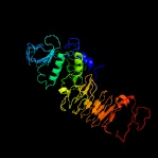
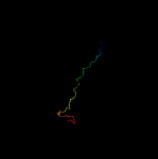
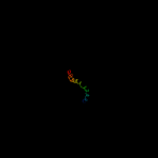
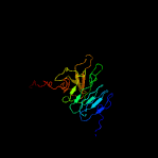

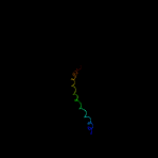
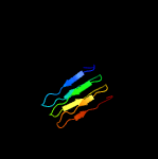
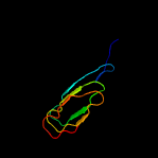


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0977_(PE_PGRS16)_1090377_1093148
 Date Wed Jul 31 22:05:04 BST 2019
 Unique Job ID bc42aa0231215a79

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		99.9	46	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
2	c2g38A_	 Alignment		99.9	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/pppe protein complex from mycobacterium tuberculosis
3	d2g38a1	 Alignment		99.9	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c1ygvA_	 Alignment		99.8	25	PDB header: structural protein/contractile protein Chain: A: PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule: rigid refinement
5	c1y0fB_	 Alignment		99.7	25	PDB header: structural protein/contractile protein Chain: B: PDB Molecule: collagen i alpha 2; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
6	c3hqvB_	 Alignment		99.5	26	PDB header: structural protein, contractile protein Chain: B: PDB Molecule: collagen alpha-2(i) chain; PDBTitle: low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
7	c2pneA_	 Alignment		98.1	34	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
8	c3boiB_	 Alignment		98.1	34	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
9	c3boiA_	 Alignment		98.1	34	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
10	c3bogB_	 Alignment		98.1	33	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
11	c3bogA_	 Alignment		98.1	33	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate

12	c4ehcA	Alignment		97.8	97	PDB header: hydrolase Chain: A: PDB Molecule: pe-pgrs family protein; PDBTitle: crystal structure of the c-terminal domain of rv0977 of mycobacterium2 tuberculosis
13	c1k7qA	Alignment		97.3	14	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
14	c1nayC	Alignment		96.3	29	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
15	c5ctdB	Alignment		96.3	38	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain,collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
16	c2ml3A	Alignment		96.1	20	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
17	c5ctdA	Alignment		96.0	38	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
18	c5ctiC	Alignment		95.9	36	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
19	c2zj6A	Alignment		95.5	28	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
20	d1kapp1	Alignment		94.6	31	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
21	c2ml2A	Alignment	not modelled	94.3	25	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
22	c1jiwP	Alignment	not modelled	94.2	20	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
23	d1k7ia1	Alignment	not modelled	93.9	21	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
24	c2agmA	Alignment	not modelled	93.7	29	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
25	c1satA	Alignment	not modelled	93.2	18	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
26	c2qubG	Alignment	not modelled	93.2	16	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
27	c1om8A	Alignment	not modelled	92.9	21	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
28	c5cxlA	Alignment	not modelled	92.1	32	PDB header: toxin Chain: A: PDB Molecule: bifunctional hemolysin/adenylate cyclase; PDBTitle: crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis

29	d1sata1	Alignment	not modelled	88.9	17	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
30	c3p4gD_	Alignment	not modelled	88.4	13	PDB header: antifreeze protein Chain: D: PDB Molecule: antifreeze protein; PDBTitle: x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
31	c3gvmA_	Alignment	not modelled	86.0	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
32	d1g9ka1	Alignment	not modelled	85.1	17	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
33	c2klwA_	Alignment	not modelled	82.7	27	PDB header: de novo protein Chain: A: PDB Molecule: (pkg)10; PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
34	d1wa8a1	Alignment	not modelled	79.4	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
35	c4lwsA_	Alignment	not modelled	76.2	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
36	c3zbhC_	Alignment	not modelled	74.6	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
37	c2cuoF_	Alignment	not modelled	72.4	30	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
38	c2cuoC_	Alignment	not modelled	72.4	30	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
39	c1k6fA_	Alignment	not modelled	69.4	34	PDB header: structural protein Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
40	c1k6fC_	Alignment	not modelled	69.4	34	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
41	c1k6fF_	Alignment	not modelled	69.4	34	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
42	c1k6fD_	Alignment	not modelled	69.4	34	PDB header: structural protein Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
43	c1k6fE_	Alignment	not modelled	69.4	34	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
44	c1k6fB_	Alignment	not modelled	69.4	34	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
45	c4iogD_	Alignment	not modelled	65.6	13	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
46	c5juhA_	Alignment	not modelled	64.2	31	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
47	c3ah9F_	Alignment	not modelled	63.7	29	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
48	c3ah9A_	Alignment	not modelled	63.4	28	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
49	c3ah9C_	Alignment	not modelled	63.1	27	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
50	c3ah9E_	Alignment	not modelled	63.1	27	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
51	c3ah9B_	Alignment	not modelled	63.1	27	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
52	c3ah9D_	Alignment	not modelled	62.3	32	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
53	c2cuoA_	Alignment	not modelled	55.2	31	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
54	c2cuoB_	Alignment	not modelled	55.2	31	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
55	c2cuoE_	Alignment	not modelled	55.2	31	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9

56	c2cuoD_	Alignment	not modelled	55.2	31	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
57	c3a0mF_	Alignment	not modelled	49.0	29	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
58	c4wj2A_	Alignment	not modelled	48.7	11	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
59	c4q1qA_	Alignment	not modelled	45.4	18	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tiba autotransporter; PDBTitle: crystal structure of tbc-catalyzed hyper-glycosylated tiba55-3502 fragment
60	c3abnA_	Alignment	not modelled	43.7	31	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
61	c4rglA_	Alignment	not modelled	38.2	23	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from <i>Desulfovibrio desulfuricans</i> g20 at 2.70 a resolution
62	c3admC_	Alignment	not modelled	38.0	32	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
63	c3admF_	Alignment	not modelled	36.6	31	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
64	c3admB_	Alignment	not modelled	36.6	31	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
65	c3admE_	Alignment	not modelled	36.6	31	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
66	c3admA_	Alignment	not modelled	36.6	31	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
67	c2ymbC_	Alignment	not modelled	32.7	15	PDB header: protein transport Chain: C: PDB Molecule: mit domain-containing protein 1; PDBTitle: structures of mitd1
68	c3abnC_	Alignment	not modelled	32.5	30	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
69	c2kg7B_	Alignment	not modelled	31.4	18	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
70	c3a1hF_	Alignment	not modelled	30.9	36	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
71	c1x1kA_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: A: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
72	c1x1kD_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: D: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
73	c2d3fF_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
74	c2d3fD_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
75	c2d3fE_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
76	c1x1kC_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
77	c1x1kB_	Alignment	not modelled	30.6	35	PDB header: structural protein Chain: B: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
78	c3a19D_	Alignment	not modelled	28.2	38	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
79	d3e9va1	Alignment	not modelled	27.5	20	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
						PDB header: structural protein

80	c3abnB_	Alignment	not modelled	25.6	29	Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
81	c2bnIE_	Alignment	not modelled	24.1	19	PDB header: stress-response Chain: E: PDB Molecule: modulator protein rsbr; PDBTitle: the structure of the n-terminal domain of rsbr
82	c2lyyB_	Alignment	not modelled	24.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
83	c3a0aC_	Alignment	not modelled	21.9	30	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
84	c5yanA_	Alignment	not modelled	21.1	33	PDB header: structural protein Chain: A: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
85	c3a0aB_	Alignment	not modelled	21.0	33	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
86	c3a0mC_	Alignment	not modelled	21.0	33	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
87	c2dyoB_	Alignment	not modelled	20.8	9	PDB header: protein turnover/protein turnover Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-57) complex
88	c2oqqB_	Alignment	not modelled	19.4	18	PDB header: transcription Chain: B: PDB Molecule: transcription factor hy5; PDBTitle: crystal structure of hy5 leucine zipper homodimer from arabidopsis2 thaliana
89	c4hrsB_	Alignment	not modelled	19.2	13	PDB header: hydrolase Chain: B: PDB Molecule: glutaryl-7-aminocephalosporanic acid acylase beta chain; PDBTitle: crystal structure of a class iii engineered cephalosporin acylase
90	c1m7IA_	Alignment	not modelled	19.1	38	PDB header: sugar binding protein Chain: A: PDB Molecule: pulmonary surfactant-associated protein d; PDBTitle: solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
91	c3admD_	Alignment	not modelled	19.1	28	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
92	c3a1hB_	Alignment	not modelled	18.4	32	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
93	c5tw9D_	Alignment	not modelled	17.6	18	PDB header: lipid-binding protein Chain: D: PDB Molecule: iron uptake system component efeo; PDBTitle: 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
94	c2q2fA_	Alignment	not modelled	16.9	22	PDB header: membrane protein Chain: A: PDB Molecule: selenoprotein s; PDBTitle: structure of the human selenoprotein s (vcp-interacting membrane2 protein)
95	c3a0mB_	Alignment	not modelled	16.8	30	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
96	c3a1hA_	Alignment	not modelled	16.7	30	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
97	c4knaA_	Alignment	not modelled	16.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: n-succinylglutamate 5-semialdehyde dehydrogenase; PDBTitle: crystal structure of an n-succinylglutamate 5-semialdehyde2 dehydrogenase from burkholderia thailandensis
98	c4x2eA_	Alignment	not modelled	15.9	19	PDB header: transferase Chain: A: PDB Molecule: fic family protein putative filamentation induced by camp PDBTitle: clostridium difficile wild type fic protein
99	c3fkeB_	Alignment	not modelled	15.8	17	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain