
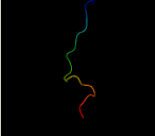

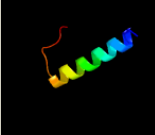



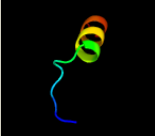



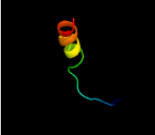





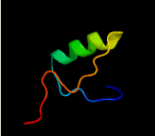




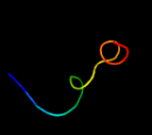
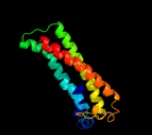
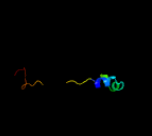
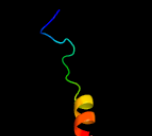


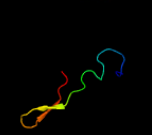




# Phyre2


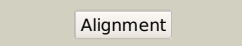
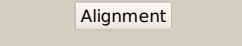
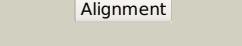
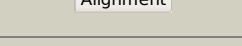
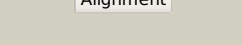


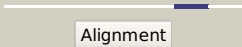
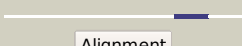

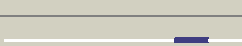



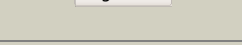
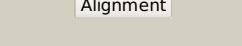
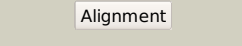
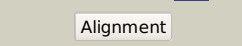
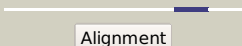

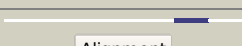
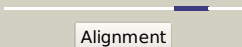
Email	mdejesus@rockefeller.edu
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Date	Fri Jul 26 01:50:09 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2lnhC_</a>	 Alignment		56.6	46	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> C; <b>PDB Molecule:</b> secreted effector protein espf(u); <b>PDBTitle:</b> enterohaemorrhagic e. coli (ehec) exploits a tryptophan switch to2 hijack host f-actin assembly
2	<a href="#">c2k9pA_</a>	 Alignment		42.0	41	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> pheromone alpha factor receptor; <b>PDBTitle:</b> structure of tm1_tm2 in lppg micelles
3	<a href="#">c4kppA_</a>	 Alignment		42.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax
4	<a href="#">c3t5xB_</a>	 Alignment		41.8	44	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> 26s proteasome complex subunit dss1; <b>PDBTitle:</b> pcid2:dss1 structure
5	<a href="#">c2w2eA_</a>	 Alignment		35.0	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> aquaporin pip2-7 7; <b>PDBTitle:</b> 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
6	<a href="#">c5gjqY_</a>	 Alignment		32.9	36	<b>PDB header:</b> hydrolase <b>Chain:</b> Y; <b>PDB Molecule:</b> 26s proteasome complex subunit dss1; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
7	<a href="#">d1j4na_</a>	 Alignment		29.0	14	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
8	<a href="#">c3eh4A_</a>	 Alignment		25.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome c oxidase subunit 1; <b>PDBTitle:</b> structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
9	<a href="#">c6gcsH_</a>	 Alignment		22.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H; <b>PDB Molecule:</b> 24-kda subunit (nuhm); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
10	<a href="#">d1h6ia_</a>	 Alignment		20.5	15	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
11	<a href="#">c6m97A_</a>	 Alignment		19.8	27	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1 <b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1

12	<a href="#">c1iyjC_</a>	Alignment		18.0	44	<b>PDB header:</b> gene regulation/antitumor protein <b>Chain:</b> C: <b>PDB Molecule:</b> deleted in split hand/split foot protein 1; <b>PDBTitle:</b> structure of a brca2-dss1 complex
13	<a href="#">d1xmea1</a>	Alignment		17.2	14	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
14	<a href="#">d2qlva1</a>	Alignment		16.3	22	<b>Fold:</b> TBP-like <b>Superfamily:</b> KA1-like <b>Family:</b> Ssp2 C-terminal domain-like
15	<a href="#">c2kncA_</a>	Alignment		15.4	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alpha-iiB-beta3 transmembrane-cytoplasmic2 heterocomplex
16	<a href="#">c2ia2D_</a>	Alignment		13.9	7	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
17	<a href="#">c2b6pA_</a>	Alignment		13.7	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
18	<a href="#">d1f2ri_</a>	Alignment		13.1	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> CAD domain
19	<a href="#">c2m59A_</a>	Alignment		13.1	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
20	<a href="#">c2m59B_</a>	Alignment		13.1	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2; <b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles
21	<a href="#">c4xydA_</a>	Alignment	not modelled	13.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide reductase subunit b; <b>PDBTitle:</b> nitric oxide reductase from roseobacter denitrificans (rdnor)
22	<a href="#">c3ld1A_</a>	Alignment	not modelled	11.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicase polyprotein 1a; <b>PDBTitle:</b> crystal structure of ibv nsp2a
23	<a href="#">c6hwhB_</a>	Alignment	not modelled	11.6	33	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
24	<a href="#">c2bbjB_</a>	Alignment	not modelled	10.7	19	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
25	<a href="#">c3aygA_</a>	Alignment	not modelled	10.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric oxide reductase; <b>PDBTitle:</b> crystal structure of nitric oxide reductase complex with hqno
26	<a href="#">c5l6nl_</a>	Alignment	not modelled	10.5	42	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> thrombin inhibitor madanin 1; <b>PDBTitle:</b> disulfated madanin-thrombin complex
27	<a href="#">c1ymgA_</a>	Alignment	not modelled	10.1	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> the channel architecture of aquaporin o at 2.2 angstrom resolution
28	<a href="#">d1ymga1</a>	Alignment	not modelled	10.1	14	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like

29	<a href="#">c5sxpG</a>	Alignment	not modelled	9.3	42	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> G: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase itchy homolog; <b>PDBTitle:</b> structural basis for the interaction between itch prr and beta-pix
30	<a href="#">c2jofA</a>	Alignment	not modelled	9.3	36	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> trp-cage; <b>PDBTitle:</b> the trp-cage: optimizing the stability of a globular2 miniprotein
31	<a href="#">c4v19U</a>	Alignment	not modelled	9.2	25	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> mitoribosomal protein bl20m, mrp120; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
32	<a href="#">d1vlaa</a>	Alignment	not modelled	9.1	24	<b>Fold:</b> OsmC-like <b>Superfamily:</b> OsmC-like <b>Family:</b> YhfA-like
33	<a href="#">d2f6ua1</a>	Alignment	not modelled	9.1	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
34	<a href="#">c4g7oN</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> transcription, transferase/dna <b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of thermus thermophilus transcription initiation2 complex containing 2 nt of rna
35	<a href="#">d1nmla2</a>	Alignment	not modelled	8.7	16	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
36	<a href="#">c2nuuF</a>	Alignment	not modelled	8.7	20	<b>PDB header:</b> transport protein/signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> ammonia channel; <b>PDBTitle:</b> regulating the escherichia coli ammonia channel: the crystal structure2 of the amtB-glnK complex
37	<a href="#">c5levA</a>	Alignment	not modelled	8.6	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--dolichyl-phosphate n- <b>PDBTitle:</b> crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminophosphotransferase (dpagt1) (v264g mutant)
38	<a href="#">d2qtva4</a>	Alignment	not modelled	8.5	19	<b>Fold:</b> Gelsolin-like <b>Superfamily:</b> C-terminal, gelsolin-like domain of Sec23/24 <b>Family:</b> C-terminal, gelsolin-like domain of Sec23/24
39	<a href="#">c3a0aE</a>	Alignment	not modelled	8.5	50	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
40	<a href="#">c6humP</a>	Alignment	not modelled	8.3	37	<b>PDB header:</b> proton transport <b>Chain:</b> P: <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit p <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
41	<a href="#">c4wqsD</a>	Alignment	not modelled	8.2	26	<b>PDB header:</b> transferase/dna/rna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> thermus thermophilus rna polymerase backtracked complex
42	<a href="#">c3a0aB</a>	Alignment	not modelled	8.1	62	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
43	<a href="#">d1s7ba</a>	Alignment	not modelled	8.1	16	<b>Fold:</b> Multidrug resistance efflux transporter EmrE <b>Superfamily:</b> Multidrug resistance efflux transporter EmrE <b>Family:</b> Multidrug resistance efflux transporter EmrE
44	<a href="#">c6eu6A</a>	Alignment	not modelled	8.1	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter; <b>PDBTitle:</b> sensor amt protein
45	<a href="#">c2jmvA</a>	Alignment	not modelled	8.1	46	<b>PDB header:</b> antiviral protein <b>Chain:</b> A: <b>PDB Molecule:</b> scytovirin; <b>PDBTitle:</b> solution structure of scytovirin refined against residual2 dipolar couplings
46	<a href="#">c3jqom</a>	Alignment	not modelled	8.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> M: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
47	<a href="#">c3jqol</a>	Alignment	not modelled	8.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> I: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
48	<a href="#">c3jqoF</a>	Alignment	not modelled	8.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
49	<a href="#">c3jqog</a>	Alignment	not modelled	8.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
50	<a href="#">c3jqoj</a>	Alignment	not modelled	8.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> J: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
51	<a href="#">c3jqoC</a>	Alignment	not modelled	8.1	32	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
52	<a href="#">c1k87A</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of e.coli puta (residues 1-669)
53	<a href="#">d2vy4a1</a>	Alignment	not modelled	8.1	43	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> CHHC finger

54	<a href="#">c3jqoR_</a>		Alignment	not modelled	8.0	32	<b>PDB header:</b> transport protein <b>Chain:</b> R: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
55	<a href="#">c3jqoO_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> O: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
56	<a href="#">c3jqod_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
57	<a href="#">c3jqoX_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> X: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
58	<a href="#">c3jqoa_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
59	<a href="#">c3zbiX_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> X: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
60	<a href="#">c3zbiO_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> O: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
61	<a href="#">c3zbiU_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> U: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
62	<a href="#">c3zbid_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
63	<a href="#">c3zbij_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> J: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
64	<a href="#">c3zbiR_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> R: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
65	<a href="#">c3zbim_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> M: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
66	<a href="#">c3jqoL_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> L: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
67	<a href="#">c3zbiC_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
68	<a href="#">c3zbil_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> I: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
69	<a href="#">c3zbiL_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> L: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
70	<a href="#">c3zbia_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
71	<a href="#">c3zbig_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> G: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
72	<a href="#">c3zbip_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> P: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
73	<a href="#">c3zbiF_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> cell adhesion <b>Chain:</b> F: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
74	<a href="#">c4qtnB_</a>		Alignment	not modelled	7.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinamide riboside transporter pnuc; <b>PDBTitle:</b> crystal structure of the vitamin b3 transporter pnuc
75	<a href="#">c3jqoU_</a>		Alignment	not modelled	7.9	32	<b>PDB header:</b> transport protein <b>Chain:</b> U: <b>PDB Molecule:</b> tran protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
							<b>PDB header:</b> transport protein

76	<a href="#">c3jqop_</a>	Alignment	not modelled	7.9	32	<b>Chain:</b> P: <b>PDB Molecule:</b> traf protein; <b>PDBTitle:</b> crystal structure of the outer membrane complex of a type iv secretion2 system
77	<a href="#">c2rmhA_</a>	Alignment	not modelled	7.8	38	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> urocortin-3; <b>PDBTitle:</b> human urocortin 3
78	<a href="#">c2g7uB_</a>	Alignment	not modelled	7.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
79	<a href="#">c2bruC_</a>	Alignment	not modelled	7.8	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
80	<a href="#">c5x22D_</a>	Alignment	not modelled	7.8	26	<b>PDB header:</b> transferase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of thermus thermophilus transcription initiation2 complex with gpa and cmppp
81	<a href="#">c3aoiN_</a>	Alignment	not modelled	7.7	26	<b>PDB header:</b> transcription, transferase/dna/rna <b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> rna polymerase-gfh1 complex (crystal type 2)
82	<a href="#">d1jlia_</a>	Alignment	not modelled	7.6	45	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Short-chain cytokines
83	<a href="#">c1ciiA_</a>	Alignment	not modelled	7.6	23	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
84	<a href="#">c1i6vD_</a>	Alignment	not modelled	7.4	26	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase; <b>PDBTitle:</b> thermus aquaticus core rna polymerase-rifampicin complex
85	<a href="#">d1i6vd_</a>	Alignment	not modelled	7.4	26	<b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Family:</b> RNA-polymerase beta-prime
86	<a href="#">d1d4oa_</a>	Alignment	not modelled	7.3	42	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
87	<a href="#">c3a0aF_</a>	Alignment	not modelled	7.3	62	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
88	<a href="#">c4ymuC_</a>	Alignment	not modelled	7.3	19	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> abc-type amino acid transport system, permease component; <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps
89	<a href="#">c3r4kD_</a>	Alignment	not modelled	7.3	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, iclr family; <b>PDBTitle:</b> crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
90	<a href="#">c1pt9B_</a>	Alignment	not modelled	7.2	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure analysis of the dii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
91	<a href="#">c5khuQ_</a>	Alignment	not modelled	7.2	24	<b>PDB header:</b> cell cycle <b>Chain:</b> Q: <b>PDB Molecule:</b> mitotic checkpoint serine/threonine-protein kinase bub1 <b>PDBTitle:</b> model of human anaphase-promoting complex/cyclosome (apc15 deletion2 mutant), in complex with the mitotic checkpoint complex (apc/c-cdc20-3 mcc) based on cryo em data at 4.8 angstrom resolution
92	<a href="#">c6cceD_</a>	Alignment	not modelled	7.2	32	<b>PDB header:</b> transcription/dna/antibiotic <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> crystal structure of a mycobacterium smegmatis rna polymerase2 transcription initiation complex with inhibitor kanglemycin a
93	<a href="#">c3a0aA_</a>	Alignment	not modelled	7.2	62	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
94	<a href="#">c6mdxA_</a>	Alignment	not modelled	7.1	40	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> spirt-like domain-containing protein spartan; <b>PDBTitle:</b> mechanism of protease dependent dpc repair
95	<a href="#">d1pnoa_</a>	Alignment	not modelled	7.1	33	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
96	<a href="#">c5xj0D_</a>	Alignment	not modelled	7.0	26	<b>PDB header:</b> transferase/transcription <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta'; <b>PDBTitle:</b> t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76
97	<a href="#">d1ynjd1</a>	Alignment	not modelled	7.0	26	<b>Fold:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Superfamily:</b> beta and beta-prime subunits of DNA dependent RNA-polymerase <b>Family:</b> RNA-polymerase beta-prime
98	<a href="#">c2o5jN_</a>	Alignment	not modelled	6.9	26	<b>PDB header:</b> transferase/dna-rna hybrid <b>Chain:</b> N: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase elongation2 complex with the ntp substrate analog
99	<a href="#">c3ajbB_</a>	Alignment	not modelled	6.8	55	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 19; <b>PDBTitle:</b> crystal structure of human pex3p in complex with n-

