


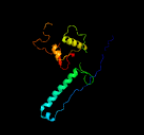

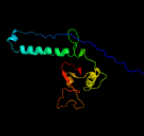



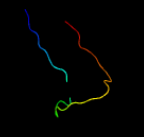

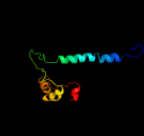

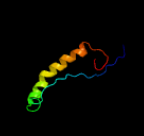

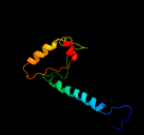





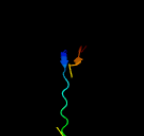
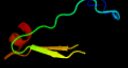


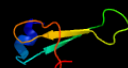
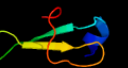
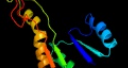
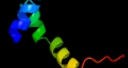

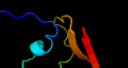


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1yueA_</a>	 Alignment		100.0	70	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> head vertex protein gp24; <b>PDBTitle:</b> bacteriophage t4 capsid vertex protein gp24
2	<a href="#">d2ft1a1</a>	 Alignment		96.3	17	<b>Fold:</b> Major capsid protein gp5 <b>Superfamily:</b> Major capsid protein gp5 <b>Family:</b> Major capsid protein gp5
3	<a href="#">c1if0A_</a>	 Alignment		94.8	17	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> protein (major capsid protein gp5); <b>PDBTitle:</b> pseudo-atomic model of bacteriophage hk97 procapsid2 (prohead ii)
4	<a href="#">c3j7wF_</a>	 Alignment		63.5	10	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> major capsid protein 10a; <b>PDBTitle:</b> capsid expansion mechanism of bacteriophage t7 revealed by multi-state2 atomic models derived from cryo-em reconstructions
5	<a href="#">d2j9ga1</a>	 Alignment		45.4	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
6	<a href="#">c4bm1A_</a>	 Alignment		43.0	12	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> major capsid protein; <b>PDBTitle:</b> c-alpha backbone trace of major capsid protein gp39 found2 in marine virus syn5.
7	<a href="#">c3p8qF_</a>	 Alignment		41.5	16	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> gp5, head protein; <b>PDBTitle:</b> hk97 prohead i encapsidating inactive virally encoded protease
8	<a href="#">c2xd8F_</a>	 Alignment		38.7	10	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> t7-like capsid protein; <b>PDBTitle:</b> capsid structure of the infectious prochlorococcus2 cyanophage p-ssp7
9	<a href="#">c1abzA_</a>	 Alignment		36.6	39	<b>PDB header:</b> de novo design <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-t-alpha; <b>PDBTitle:</b> alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
10	<a href="#">c4jvsA_</a>	 Alignment		27.4	31	<b>PDB header:</b> hydrolase activator/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of lepb gap domain from legionella drancourtii in2 complex with rab1-gdp and alf3
11	<a href="#">d1dqta_</a>	 Alignment		25.0	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)

12	<a href="#">c3jzfA_</a>	Alignment		21.4	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase from e. coli in2 complex with benzimidazoles series
13	<a href="#">d1gd6a_</a>	Alignment		19.8	15	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
14	<a href="#">c3feuA_</a>	Alignment		18.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
15	<a href="#">c1ym5A_</a>	Alignment		17.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 32.6 kda protein in dap2-slt2 <b>PDBTitle:</b> crystal structure of yhi9, the yeast member of the2 phenazine biosynthesis phzf enzyme superfamily.
16	<a href="#">d1qy9a1</a>	Alignment		16.0	19	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
17	<a href="#">c4di7A_</a>	Alignment		15.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amphi; <b>PDBTitle:</b> structure of a2-type ketoreductase of modular polyketide synthases
18	<a href="#">d1un2a_</a>	Alignment		15.9	12	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
19	<a href="#">d1p3qq_</a>	Alignment		15.9	16	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> CUE domain
20	<a href="#">c2rtsA_</a>	Alignment		14.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase; <b>PDBTitle:</b> chitin binding domain1
21	<a href="#">c2m0nA_</a>	Alignment	not modelled	13.9	58	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
22	<a href="#">c4dunA_</a>	Alignment	not modelled	13.7	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phenazine biosynthesis phzc/phzf protein; <b>PDBTitle:</b> 1.76a x-ray crystal structure of a putative phenazine biosynthesis2 phzc/phzf protein from clostridium difficile (strain 630)
23	<a href="#">c3bqwA_</a>	Alignment	not modelled	13.7	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative capsid protein of prophage; <b>PDBTitle:</b> crystal structure of the putative capsid protein of prophage (e.coli2 cft073)
24	<a href="#">c2fbdB_</a>	Alignment	not modelled	13.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lysozyme 1; <b>PDBTitle:</b> the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
25	<a href="#">c4an5F_</a>	Alignment	not modelled	13.0	18	<b>PDB header:</b> virus <b>Chain:</b> F: <b>PDB Molecule:</b> coat protein; <b>PDBTitle:</b> capsid structure and its stability at the late stages of2 bacteriophage spp1 assembly
26	<a href="#">d1dvoa_</a>	Alignment	not modelled	12.2	17	<b>Fold:</b> FinO-like <b>Superfamily:</b> FinO-like <b>Family:</b> FinO-like
27	<a href="#">c2e76G_</a>	Alignment	not modelled	12.2	39	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 5; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
28	<a href="#">c1u0kA_</a>	Alignment	not modelled	12.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gene product pa4716; <b>PDBTitle:</b> the structure of a predicted epimerase pa4716 from

						pseudomonas2 aeruginosa
29	<a href="#">d1iiza_</a>	Alignment	not modelled	11.7	21	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> C-type lysozyme
30	<a href="#">d2e2dc1</a>	Alignment	not modelled	11.0	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> TIMP-like <b>Family:</b> Tissue inhibitor of metalloproteinases, TIMP
31	<a href="#">c1vf5G_</a>	Alignment	not modelled	10.8	56	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> protein pet g; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
32	<a href="#">d1vf5g_</a>	Alignment	not modelled	10.8	56	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
33	<a href="#">c4l4xA_</a>	Alignment	not modelled	10.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> amphi; <b>PDBTitle:</b> an a2-type ketoreductase from a modular polyketide synthase
34	<a href="#">d2e74g1</a>	Alignment	not modelled	10.4	56	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
35	<a href="#">d1s7ja_</a>	Alignment	not modelled	10.3	20	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
36	<a href="#">c4v0bA_</a>	Alignment	not modelled	10.2	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> escherichia coli ftsh hexameric n-domain
37	<a href="#">d1ck1a1</a>	Alignment	not modelled	10.0	30	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Superantigen toxins, N-terminal domain
38	<a href="#">d1ulza1</a>	Alignment	not modelled	10.0	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
39	<a href="#">c2qb0D_</a>	Alignment	not modelled	9.9	21	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> D: <b>PDB Molecule:</b> tslam domain - lysozyme chimera; <b>PDBTitle:</b> structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
40	<a href="#">d1br9a_</a>	Alignment	not modelled	9.7	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> TIMP-like <b>Family:</b> Tissue inhibitor of metalloproteinases, TIMP
41	<a href="#">c2f40A_</a>	Alignment	not modelled	9.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pf1455; <b>PDBTitle:</b> structure of a novel protein from backbone-centered nmr data and nmr-2 assisted structure prediction
42	<a href="#">c4bduC_</a>	Alignment	not modelled	9.7	22	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> green fluorescent protein, apoptosis regulator bax; <b>PDBTitle:</b> bax bh3-in-groove dimer (gfp)
43	<a href="#">c3bjqA_</a>	Alignment	not modelled	9.6	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> phage-related protein; <b>PDBTitle:</b> crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
44	<a href="#">c2lkyA_</a>	Alignment	not modelled	9.5	42	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of msme_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysm.17112.b
45	<a href="#">c1qy9B_</a>	Alignment	not modelled	9.3	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ydde; <b>PDBTitle:</b> crystal structure of e. coli se-met protein ydde
46	<a href="#">d1p5ca_</a>	Alignment	not modelled	9.3	21	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Phage lysozyme
47	<a href="#">d1lrza2</a>	Alignment	not modelled	8.6	11	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> FemXAB nonribosomal peptidyltransferases
48	<a href="#">c3lvyB_</a>	Alignment	not modelled	8.5	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
49	<a href="#">c3kv1A_</a>	Alignment	not modelled	8.5	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor; <b>PDBTitle:</b> crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
50	<a href="#">c2imeA_</a>	Alignment	not modelled	8.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxychromene-2-carboxylate isomerase; <b>PDBTitle:</b> 2-hydroxychromene-2-carboxylate isomerase; a kappa class glutathione-2 s-transferase from pseudomonas putida
51	<a href="#">c4je3B_</a>	Alignment	not modelled	8.3	23	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> central kinetochore subunit chl4; <b>PDBTitle:</b> an iml3-chl4 heterodimer links the core centromere to factors required2 for accurate chromosome segregation
52	<a href="#">c1yzxB_</a>	Alignment	not modelled	8.3	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione s-transferase kappa 1; <b>PDBTitle:</b> crystal structure of human kappa class glutathione2 transferase
53	<a href="#">c2mhhA_</a>	Alignment	not modelled	8.3	29	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> polycystic kidney disease protein 2; <b>PDBTitle:</b> solution structure of a ef-hand domain from sea urchin polycystin-2
						<b>Fold:</b> Thioredoxin fold

54	<a href="#">d1r4wa_</a>	Alignment	not modelled	8.3	7	<b>Superfamily:</b> Thioredoxin-like <b>Family:</b> DsbA-like
55	<a href="#">d1gvpa_</a>	Alignment	not modelled	8.1	33	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Phage ssDNA-binding proteins
56	<a href="#">c5d50E_</a>	Alignment	not modelled	8.1	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> anti-repressor protein; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage
57	<a href="#">d1goia1</a>	Alignment	not modelled	8.1	29	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
58	<a href="#">c3ckiB_</a>	Alignment	not modelled	8.1	25	<b>PDB header:</b> hydrolase, hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> metalloproteinase inhibitor 3; <b>PDBTitle:</b> crystal structure of the tace-n-timp-3 complex
59	<a href="#">c1hr9D_</a>	Alignment	not modelled	7.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mitochondrial processing peptidase beta subunit; <b>PDBTitle:</b> yeast mitochondrial processing peptidase beta-e73q mutant2 complexed with malate dehydrogenase signal peptide
60	<a href="#">c2o4wA_</a>	Alignment	not modelled	7.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysozyme; <b>PDBTitle:</b> t4 lysozyme circular permutant
61	<a href="#">c4zonB_</a>	Alignment	not modelled	7.5	20	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> verruculogen synthase; <b>PDBTitle:</b> structure of ftmox1 with fumitremorgen b complex
62	<a href="#">d1hr6b1</a>	Alignment	not modelled	7.4	29	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> MPP-like
63	<a href="#">d1evsa_</a>	Alignment	not modelled	7.3	36	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Long-chain cytokines
64	<a href="#">c1y4eA_</a>	Alignment	not modelled	7.2	63	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/hydrogen exchanger 1; <b>PDBTitle:</b> nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
65	<a href="#">d1ztxe1</a>	Alignment	not modelled	7.1	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Class II viral fusion proteins C-terminal domain
66	<a href="#">d2v9va1</a>	Alignment	not modelled	7.0	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
67	<a href="#">c3ol4B_</a>	Alignment	not modelled	7.0	55	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
68	<a href="#">c5aj3h_</a>	Alignment	not modelled	6.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the small subunit of the mammalian mitoribosome
69	<a href="#">c2dp3A_</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
70	<a href="#">c2jz2A_</a>	Alignment	not modelled	6.8	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ssl0352 protein; <b>PDBTitle:</b> solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
71	<a href="#">d1ttja_</a>	Alignment	not modelled	6.7	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
72	<a href="#">c4x22A_</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of leptospira interrogans triosephosphate isomerase2 (litim)
73	<a href="#">c3h93A_</a>	Alignment	not modelled	6.6	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> thiol:disulfide interchange protein dsba; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa dsba
74	<a href="#">c3zljC_</a>	Alignment	not modelled	6.5	44	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair2 protein muts d835r mutant in complex with gt mismatched dna
75	<a href="#">d1w96a1</a>	Alignment	not modelled	6.5	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> BC C-terminal domain-like
76	<a href="#">c5d2eA_</a>	Alignment	not modelled	6.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mlne; <b>PDBTitle:</b> crystal structure of an n-terminal ketoreductase from macrolactin2 assembly line
77	<a href="#">d3cx5a1</a>	Alignment	not modelled	6.3	31	<b>Fold:</b> LuxS/MPP-like metallohydrolase <b>Superfamily:</b> LuxS/MPP-like metallohydrolase <b>Family:</b> MPP-like
78	<a href="#">c4naoA_</a>	Alignment	not modelled	6.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxygenase; <b>PDBTitle:</b> crystal structure of eash
79	<a href="#">c2kz3A_</a>	Alignment	not modelled	6.2	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein rad51l3; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
80	<a href="#">c5daqA_</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytanoyl-coa dioxygenase family protein (afu_orthologue

						<b>PDBTitle:</b> fe(ii)/(alpha)ketoglutarate-dependent dioxygenase asqj in complex with2 4-methoxycyclopeptin <b>PDB header:</b> hydrolase activator <b>Chain:</b> B: <b>PDB Molecule:</b> effector protein b; <b>PDBTitle:</b> crystal structure of n-terminal 618-residue fragment of lepb from2 legionella pneumophila
81	<a href="#">c4jw1B_</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> actin cytoskeleton-regulatory complex protein sla1; <b>PDBTitle:</b> crystal structure of sla1 homology domain 2
82	<a href="#">c3idwA_</a>	Alignment	not modelled	5.9	28	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair2 protein muts d835r mutant in complex with gt mismatched dna
83	<a href="#">c3zljD_</a>	Alignment	not modelled	5.8	44	<b>Fold:</b> Methionine synthase activation domain-like <b>Superfamily:</b> Methionine synthase activation domain-like <b>Family:</b> Methionine synthase SAM-binding domain
84	<a href="#">d1mska_</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
85	<a href="#">d1kv5a_</a>	Alignment	not modelled	5.7	27	<b>Fold:</b> Complement control module/SCR domain <b>Superfamily:</b> Complement control module/SCR domain <b>Family:</b> Complement control module/SCR domain
86	<a href="#">d2b5id1</a>	Alignment	not modelled	5.7	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> structure of a diaminopimelate epimerase from acinetobacter baumannii
87	<a href="#">c5ha4A_</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> gene regulation <b>Chain:</b> H: <b>PDB Molecule:</b> nanos, isoform b; <b>PDBTitle:</b> drosophila nanos nbr peptide bound to the not module2 of the human ccr4-not complex
88	<a href="#">c5fu7H_</a>	Alignment	not modelled	5.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Triosephosphate isomerase (TIM) <b>Family:</b> Triosephosphate isomerase (TIM)
89	<a href="#">d1r2ra_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> triosephosphate isomerase; <b>PDBTitle:</b> crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
90	<a href="#">c3m9yB_</a>	Alignment	not modelled	5.6	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> TIMP-like <b>Family:</b> Tissue inhibitor of metalloproteinases, TIMP
91	<a href="#">d1ueab_</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chitinase c; <b>PDBTitle:</b> solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
92	<a href="#">c2d49A_</a>	Alignment	not modelled	5.5	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
93	<a href="#">d1olta_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ectd; <b>PDBTitle:</b> crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
94	<a href="#">c3emrA_</a>	Alignment	not modelled	5.3	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit ul89 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain, mn soaked
95	<a href="#">c3n4qA_</a>	Alignment	not modelled	5.3	30	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structure of mouse orc1 bah domain bound to h4k20me2
96	<a href="#">c4dowA_</a>	Alignment	not modelled	5.3	13	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
97	<a href="#">d1ed7a_</a>	Alignment	not modelled	5.2	25	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> the solution structure of the ftsh periplasmic n-domain
98	<a href="#">c2muyA_</a>	Alignment	not modelled	5.2	6	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna damage response b protein; <b>PDBTitle:</b> crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis
99	<a href="#">c3kdvB_</a>	Alignment	not modelled	5.2	31	