





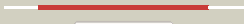















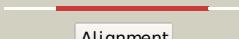

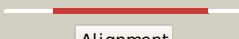















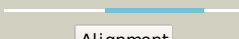
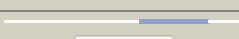
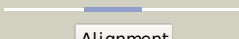


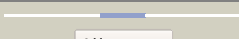





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2l26A_</a>	 Alignment		100.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein rv0899/mt0922; <b>PDBTitle:</b> rv0899 from mycobacterium tuberculosis contains two separated domains
2	<a href="#">c2kgwA_</a>	 Alignment		100.0	31	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein a; <b>PDBTitle:</b> solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
3	<a href="#">c3td4D_</a>	 Alignment		100.0	38	<b>PDB header:</b> membrane protein,peptide binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> outer membrane protein omp38; <b>PDBTitle:</b> crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
4	<a href="#">d2aizp1</a>	 Alignment		100.0	23	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> OmpA-like <b>Family:</b> OmpA-like
5	<a href="#">c2k1sA_</a>	 Alignment		100.0	32	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane lipoprotein yiad; <b>PDBTitle:</b> solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
6	<a href="#">c3khnB_</a>	 Alignment		100.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> motb protein, putative; <b>PDBTitle:</b> crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
7	<a href="#">d2hqsc1</a>	 Alignment		100.0	24	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> OmpA-like <b>Family:</b> OmpA-like
8	<a href="#">c1rlmA_</a>	 Alignment		100.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein class 4; <b>PDBTitle:</b> structure of the ompa-like domain of rmpm from neisseria2 meningitidis
9	<a href="#">d1rlma_</a>	 Alignment		100.0	36	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> OmpA-like <b>Family:</b> OmpA-like
10	<a href="#">c3cyqM_</a>	 Alignment		100.0	22	<b>PDB header:</b> membrane protein <b>Chain:</b> M: <b>PDB Molecule:</b> chemotaxis protein motb; <b>PDBTitle:</b> the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
11	<a href="#">c2zvyB_</a>	 Alignment		100.0	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> chemotaxis protein motb; <b>PDBTitle:</b> structure of the periplasmic domain of motb from salmonella2 (crystal form ii)

12	<a href="#">c3ltdA</a>	 Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein, ompa family protein; <b>PDBTitle:</b> crystal structure of an outer membrane protein(ompA)from2 legionella pneumophila
13	<a href="#">c3oonA</a>	 Alignment		99.9	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein (tpn50); <b>PDBTitle:</b> the structure of an outer membrane protein from borrelia burgdorferi2 b31
14	<a href="#">c2zovA</a>	 Alignment		99.9	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein motb; <b>PDBTitle:</b> structure of the periplasmic domain of motb from salmonella2 (crystal form i)
15	<a href="#">c2zf8A</a>	 Alignment		99.8	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> component of sodium-driven polar flagellar motor; <b>PDBTitle:</b> crystal structure of moty
16	<a href="#">d1tba</a>	 Alignment		56.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
17	<a href="#">d1taa</a>	 Alignment		49.5	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
18	<a href="#">c3ngmB</a>	 Alignment		45.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of lipase from gibberella zeae
19	<a href="#">c3o0dF</a>	 Alignment		41.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> triacylglycerol lipase; <b>PDBTitle:</b> crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
20	<a href="#">d1uwca</a>	 Alignment		31.8	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
21	<a href="#">c3g7nA</a>	 Alignment	not modelled	31.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
22	<a href="#">d1qy7a</a>	 Alignment	not modelled	29.3	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
23	<a href="#">c3ds8A</a>	 Alignment	not modelled	24.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crysatl structure of the gene lin2722 products from listeria2 innocua
24	<a href="#">d1uzhc1</a>	 Alignment	not modelled	24.2	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
25	<a href="#">d1rbli</a>	 Alignment	not modelled	23.9	19	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
26	<a href="#">c1ir6A</a>	 Alignment	not modelled	22.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease recj; <b>PDBTitle:</b> crystal structure of exonuclease recj bound to manganese
27	<a href="#">d1ir6a</a>	 Alignment	not modelled	22.3	17	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Exonuclease Recj
28	<a href="#">c2rd5D</a>	 Alignment	not modelled	22.2	17	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> pii protein; <b>PDBTitle:</b> structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
29	<a href="#">d1svdm1</a>	 Alignment	not modelled	22.0	4	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit

30	<a href="#">c2r6hC_</a>	Alignment	not modelled	19.4	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:ubiquinone oxidoreductase, na translocating, f <b>PDBTitle:</b> crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
31	<a href="#">d8rucI_</a>	Alignment	not modelled	18.9	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
32	<a href="#">c2oghA_</a>	Alignment	not modelled	18.3	13	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor eif-1; <b>PDBTitle:</b> solution structure of yeast eif1
33	<a href="#">d1ej7s_</a>	Alignment	not modelled	18.3	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
34	<a href="#">d3tgla_</a>	Alignment	not modelled	17.7	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
35	<a href="#">d1ir1s_</a>	Alignment	not modelled	17.1	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
36	<a href="#">d2if1a_</a>	Alignment	not modelled	17.0	13	<b>Fold:</b> eIF1-like <b>Superfamily:</b> eIF1-like <b>Family:</b> eIF1-like
37	<a href="#">d1wdds_</a>	Alignment	not modelled	16.8	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
38	<a href="#">d1bwvs_</a>	Alignment	not modelled	16.6	9	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
39	<a href="#">d1lgva_</a>	Alignment	not modelled	16.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
40	<a href="#">d2v6ai1</a>	Alignment	not modelled	14.7	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
41	<a href="#">d1bxni_</a>	Alignment	not modelled	12.7	3	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
42	<a href="#">d1sxra_</a>	Alignment	not modelled	12.7	11	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
43	<a href="#">c1nauA_</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> hormone/growth factor <b>Chain:</b> A: <b>PDB Molecule:</b> glucagon; <b>PDBTitle:</b> nmr solution structure of the glucagon antagonist [desHis1,2 desPhe6, glu9]glucagon amide in the presence of 3 perdeuterated dodecylphosphocholine micelles
44	<a href="#">d2ckca1</a>	Alignment	not modelled	11.7	10	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
45	<a href="#">c2ckcA_</a>	Alignment	not modelled	11.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 7; <b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
46	<a href="#">d1gvha3</a>	Alignment	not modelled	11.1	15	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Flavohemoglobin, C-terminal domain
47	<a href="#">d1gk8i_</a>	Alignment	not modelled	11.0	10	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
48	<a href="#">d2piia_</a>	Alignment	not modelled	10.7	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
49	<a href="#">d1uzdc1</a>	Alignment	not modelled	10.3	10	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
50	<a href="#">c1s2jA_</a>	Alignment	not modelled	10.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan recognition protein sa cg11709-pa; <b>PDBTitle:</b> crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
51	<a href="#">d1d4oa_</a>	Alignment	not modelled	9.8	19	<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)
52	<a href="#">d2v0ea1</a>	Alignment	not modelled	8.9	8	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
53	<a href="#">c1pt9B_</a>	Alignment	not modelled	8.9	19	<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 diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
54	<a href="#">d1tvca2</a>	Alignment	not modelled	8.3	11	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like <b>PDB header:</b> hydrolase

55	<a href="#">c3b9eA</a>	Alignment	not modelled	8.1	9	<b>Chain:</b> A: <b>PDB Molecule:</b> chitinase a; <b>PDBTitle:</b> crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
56	<a href="#">c3bzqA</a>	Alignment	not modelled	7.2	15	<b>PDB header:</b> signaling protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein p-ii; <b>PDBTitle:</b> high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
57	<a href="#">c3rxyA</a>	Alignment	not modelled	6.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nif3 protein; <b>PDBTitle:</b> crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
58	<a href="#">d2gova1</a>	Alignment	not modelled	6.6	10	<b>Fold:</b> Probable bacterial effector-binding domain <b>Superfamily:</b> Probable bacterial effector-binding domain <b>Family:</b> SOUL heme-binding protein
59	<a href="#">c1gvhA</a>	Alignment	not modelled	6.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheomprotein; <b>PDBTitle:</b> the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
60	<a href="#">c3devB</a>	Alignment	not modelled	6.5	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> sh1221; <b>PDBTitle:</b> crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
61	<a href="#">c3mhyC</a>	Alignment	not modelled	6.2	13	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> pii-like protein pz; <b>PDBTitle:</b> a new pii protein structure
62	<a href="#">c2ckaA</a>	Alignment	not modelled	6.0	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chromodomain-helicase-dna-binding protein 8; <b>PDBTitle:</b> solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
63	<a href="#">d2ckaa1</a>	Alignment	not modelled	6.0	8	<b>Fold:</b> GYF/BRK domain-like <b>Superfamily:</b> BRK domain-like <b>Family:</b> BRK domain-like
64	<a href="#">dlzpdA1</a>	Alignment	not modelled	6.0	13	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
65	<a href="#">d1e32a3</a>	Alignment	not modelled	5.8	19	<b>Fold:</b> Cdc48 domain 2-like <b>Superfamily:</b> Cdc48 domain 2-like <b>Family:</b> Cdc48 domain 2-like
66	<a href="#">c3dmaA</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase-related protein; <b>PDBTitle:</b> crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
67	<a href="#">dlcqx3</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Flavoheomoglobin, C-terminal domain