



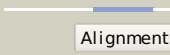

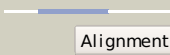



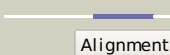





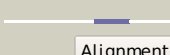

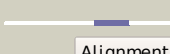

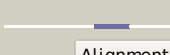


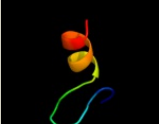


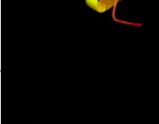


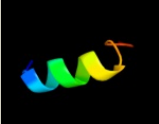



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h92A_	 Alignment		24.0	55	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized atp-binding protein mjcl15; PDBTitle: the crystal structure of one domain of the protein with unknown2 function from methanocaldococcus jannaschii
2	c3pvdA_	 Alignment		22.4	22	PDB header: viral protein Chain: A: PDB Molecule: capsid; PDBTitle: crystal structure of p domain dimer of norovirus va207 complexed with 2 3'-sialyl-lewis x tetrasaccharide
3	c2z15A_	 Alignment		20.4	39	PDB header: viral protein Chain: A: PDB Molecule: 58 kd capsid protein; PDBTitle: atomic resolution structural characterization of 2 recognition of histo-blood group antigen by norwalk virus
4	c3pm5B_	 Alignment		20.1	32	PDB header: oxidoreductase Chain: B: PDB Molecule: benzoyl-coa oxygenase component b; PDBTitle: crystal structure of boxb in mixed valent state with bound benzoyl-coa
5	c3lq6A_	 Alignment		17.8	39	PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structure of murine norovirus protruding (p) domain
6	c2obtA_	 Alignment		16.8	28	PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structures of p domain of norovirus va387 in 2 complex with blood group trisaccharides type b
7	c2vy2A_	 Alignment		16.8	40	PDB header: transcription Chain: A: PDB Molecule: protein leafy; PDBTitle: structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
8	c3q6iA_	 Alignment		13.8	100	PDB header: unknown function Chain: A: PDB Molecule: putative outer membrane protein, part of carbohydrate PDBTitle: crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
9	c1mgrA_	 Alignment		13.7	50	PDB header: hydrolase Chain: A: PDB Molecule: alpha-d-glucuronidase; PDBTitle: the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 steartothermophilus t-6
10	d1l8na1	 Alignment		13.6	50	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
11	c3bjoA_	 Alignment		13.0	45	PDB header: nucleotide binding protein Chain: A: PDB Molecule: uncharacterized atp-binding protein mj1010; PDBTitle: crystal structure of the c-terminal domain of a possible atp-binding2 protein from methanocaldococcus jannaschii dsm 2661

12	c2hl2A_	Alignment		12.8	40	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
13	d2i5nh2	Alignment		9.0	32	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
14	dlw36c3	Alignment		8.9	23	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecC), C-terminal domain
15	d3cjrbl	Alignment		8.0	47	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein L11, C-terminal domain Family: Ribosomal protein L11, C-terminal domain
16	dlh41a1	Alignment		7.6	50	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
17	clgqkB_	Alignment		7.3	50	PDB header: hydrolase Chain: B: PDB Molecule: alpha-d-glucuronidase; PDBTitle: structure of pseudomonas cellulosa alpha-d-glucuronidase2 complexed with glucuronic acid
18	c3q38A_	Alignment		7.2	19	PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: crystal structure of p domain from norwalk virus strain vietnam 026 in2 complex with hbga type b (triglycan)
19	clztoA_	Alignment		6.5	50	PDB header: potassium channel Chain: A: PDB Molecule: potassium channel protein rck4; PDBTitle: inactivation gate of potassium channel rck4, nmr, 82 structures
20	c2vzjB_	Alignment		5.7	67	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 167aa long hypothetical dntpase; PDBTitle: crystal structure of dctp deaminase from sulfolobus tokodaii
21	c3cu2A_	Alignment	not modelled	5.3	9	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
22	c3rmsA_	Alignment	not modelled	5.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein svir_20580 from2 saccharomonospora viridis