





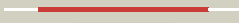





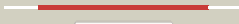



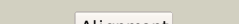


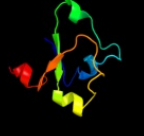
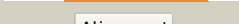



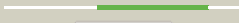

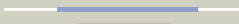
















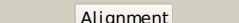


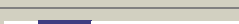
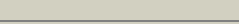


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2d1pc1	 Alignment		100.0	100	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrH-like
2	d2hy5c1	 Alignment		100.0	35	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrH-like
3	dlx9aa_	 Alignment		100.0	28	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrH-like
4	d2d1pb1	 Alignment		99.2	20	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
5	dljx7a_	 Alignment		98.7	18	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
6	d2hy5b1	 Alignment		98.7	24	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
7	d2hy5a1	 Alignment		98.6	15	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
8	d2d1pa1	 Alignment		98.4	14	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
9	c3mc3A_	 Alignment		96.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsre/dsrf-like family protein; PDBTitle: crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
10	dl11sa_	 Alignment		88.3	15	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
11	c2qs7D_	 Alignment		88.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfolobus solfataricus p2 at 2.09 a resolution

12	c2pd2A_		Alignment		67.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st0148; PDBTitle: crystal structure of (st0148) conserved hypothetical from sulfobolus2 tokodaii strain7
13	c3pnxF_		Alignment		51.0	14	PDB header: transferase Chain: F: PDB Molecule: putative sulfurtransferase dsre; PDBTitle: crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
14	c2pk0C_		Alignment		24.2	25	PDB header: signaling protein Chain: C: PDB Molecule: serine/threonine protein phosphatase stp1; PDBTitle: structure of the s. agalactiae serine/threonine phosphatase at 2.652 resolution
15	c3pu9A_		Alignment		21.6	24	PDB header: transferase Chain: A: PDB Molecule: protein serine/threonine phosphatase; PDBTitle: crystal structure of serine/threonine phosphatase sphaerobacter2 thermophilus dsm 20745
16	c3t9qB_		Alignment		11.8	40	PDB header: hydrolase Chain: B: PDB Molecule: stage ii sporulation protein e; PDBTitle: structure of the phosphatase domain of the cell fate determinant2 spoIIE from bacillus subtilis (mn presoaked)
17	d1txoa_		Alignment		11.5	27	Fold: PP2C-like Superfamily: PP2C-like Family: PP2C-like
18	c1eg4A_		Alignment		11.1	26	PDB header: structural protein Chain: A: PDB Molecule: dystrophin; PDBTitle: structure of a dystrophin ww domain fragment in complex2 with a beta-dystroglycan peptide
19	c2j82A_		Alignment		10.2	37	PDB header: hydrolase Chain: A: PDB Molecule: protein serine-threonine phosphatase; PDBTitle: structural analysis of the pp2c family phosphatase tpha2 from thermosynechococcus elongatus
20	c2jfsA_		Alignment		9.0	22	PDB header: hydrolase Chain: A: PDB Molecule: ser-thr phosphatase mspp; PDBTitle: crystal structure of the ppm ser-thr phosphatase mspp from2 mycobacterium smegmatis in complex with cacodylate
21	c2cm1A_		Alignment	not modelled	7.7	33	PDB header: hydrolase Chain: A: PDB Molecule: serine threonine protein phosphatase pstp; PDBTitle: crystal structure of the catalytic domain of serine2 threonine protein phosphatase pstp in complex with3 2 manganese ions.
22	d1e8ca2		Alignment	not modelled	7.7	17	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
23	c3rnrB_		Alignment	not modelled	6.9	40	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: stage ii sporulation e family protein; PDBTitle: crystal structure of stage ii sporulation e family protein from2 thermanaerovibrio acidaminovorans
24	c1dbgA_		Alignment	not modelled	6.8	13	PDB header: lyase Chain: A: PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
25	c3h4sE_		Alignment	not modelled	6.7	29	PDB header: motor protein/calcium binding protein Chain: E: PDB Molecule: kcbp interacting ca2+-binding protein; PDBTitle: structure of the complex of a mitotic kinesin with its2 calcium binding regulator
26	c3epmB_		Alignment	not modelled	6.3	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic
27	c2wtzC_		Alignment	not modelled	5.6	17	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis
28	c2i18A_		Alignment	not modelled	5.6	18	PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein; PDBTitle: the refined structure of c-terminal domain of an ef-hand2

					calcium binding protein from entamoeba histolytica	
29	d1xm7a_	<div><div></div><div>Alignment</div></div>	not modelled	5.5	27	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666