

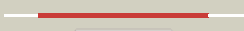



























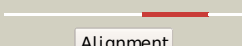

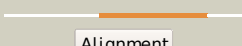

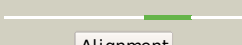

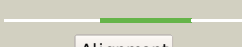




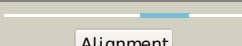


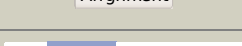
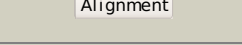
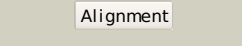




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k1gA_	 Alignment		100.0	48	PDB header: lipoprotein Chain: A: PDB Molecule: lipoprotein spr; PDBTitle: solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
2	c2fg0B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
3	c3h41A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: nlp/p60 family protein; PDBTitle: crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
4	d2evra2	 Alignment		100.0	30	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
5	c3nfpB_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
6	c2xivA_	 Alignment		100.0	23	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
7	c3pbiA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
8	c3i86A_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
9	c3gt2A_	 Alignment		100.0	26	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
10	c3m1uB_	 Alignment		99.9	26	PDB header: hydrolase Chain: B: PDB Molecule: putative gamma-d-glutamyl-l-diamino acid endopeptidase; PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dву_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
11	c2p1gA_	 Alignment		99.5	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative xylanase; PDBTitle: crystal structure of a putative xylanase from bacteroides fragilis

12	d2im9a1	 Alignment		97.8	30	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Lpg0564-like
13	c2im9A_	 Alignment		97.8	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
14	d2if6a1	 Alignment		97.6	15	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Yiix-like
15	c2kya_	 Alignment		97.5	26	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution struture of the h-rev107 n-terminal domain
16	c3kw0D_	 Alignment		97.4	23	PDB header: hydrolase Chain: D: PDB Molecule: cysteine peptidase; PDBTitle: crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
17	d2io8a2	 Alignment		88.6	14	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: CHAP domain
18	c2vpmB_	 Alignment		56.9	13	PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase
19	c2ioaA_	 Alignment		53.8	17	PDB header: ligase, hydrolase Chain: A: PDB Molecule: bifunctional glutathionylspermidine PDBTitle: e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
20	d2g2xa1	 Alignment		40.7	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
21	d2ar1a1	 Alignment	not modelled	32.4	15	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
22	c3eopB_	 Alignment	not modelled	31.2	12	PDB header: unknown function Chain: B: PDB Molecule: thymocyte nuclear protein 1; PDBTitle: crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
23	d2evea1	 Alignment	not modelled	29.4	21	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
24	d2gbsa1	 Alignment	not modelled	26.8	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
25	d1bg6a1	 Alignment	not modelled	22.6	22	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
26	c2bcmB_	 Alignment	not modelled	19.5	41	PDB header: cell adhesion Chain: B: PDB Molecule: f1845 fimbrial protein; PDBTitle: daae adhesion
27	d1zcea1	 Alignment	not modelled	18.9	22	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
28	c3kopB_	 Alignment	not modelled	9.8	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
29	c2hivB_	 Alignment	not modelled	7.8	12	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi;

29	c5vjAB_	Alignment	not modelled	7.8	12	PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
30	d2ba0a2	Alignment	not modelled	6.0	23	Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like
31	d2hd9a1	Alignment	not modelled	5.7	12	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
32	d1ut1a_	Alignment	not modelled	5.7	37	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Dr-family adhesin
33	d2vera1	Alignment	not modelled	5.6	37	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Dr-family adhesin