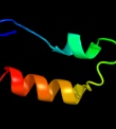
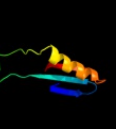
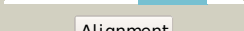
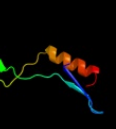


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vldA_	 Alignment		88.9	20	PDB header: hydrolase Chain: A: PDB Molecule: upf0286 protein pyrab01260; PDBTitle: crystal structure of a repair endonuclease from pyrococcus2 abyssi
2	d1xmx_	 Alignment		70.7	13	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899
3	d2foka4	 Alignment		69.0	17	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease FokI, C-terminal (catalytic) domain
4	c2wj0B_	 Alignment		64.5	18	PDB header: hydrolase/dna Chain: B: PDB Molecule: archaeal hjc; PDBTitle: crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
5	c1foka_	 Alignment		62.2	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (foki restriction endonucleas); PDBTitle: structure of restriction endonuclease foki bound to dna
6	c3a9fA_	 Alignment		56.6	12	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the c-terminal domain of cytochrome cz2 from chlorobium tepidum
7	c1y88A_	 Alignment		52.7	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1548; PDBTitle: crystal structure of protein of unknown function af1548
8	d1hh1a_	 Alignment		50.5	14	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
9	d1ob8a_	 Alignment		39.4	16	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
10	d1y88a2	 Alignment		36.7	6	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: MRR-like
11	d1gefa_	 Alignment		33.5	14	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like

12	c2fhyL_	Alignment		32.5	21	PDB header: hydrolase Chain: L: PDB Molecule: fructose-1,6-bisphosphatase 1; PDBTitle: structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
13	d1spia_	Alignment		30.1	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
14	d1nuwa_	Alignment		28.9	25	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	c2gq1A_	Alignment		28.8	18	PDB header: hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
16	d1bk4a_	Alignment		28.6	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
17	d1ftaa_	Alignment		28.2	21	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
18	c2e52A_	Alignment		21.5	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: type ii restriction enzyme hindiii; PDBTitle: crystal structural analysis of hindiii restriction endonuclease in2 complex with cognate dna at 2.0 angstrom resolution
19	c3h4rA_	Alignment		17.9	16	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
20	c2l2oA_	Alignment		15.4	6	PDB header: unknown function Chain: A: PDB Molecule: upf0727 protein c6orf115; PDBTitle: solution structure of human hspc280 protein
21	c3h1tA_	Alignment	not modelled	12.9	22	PDB header: hydrolase Chain: A: PDB Molecule: type i site-specific restriction-modification PDBTitle: the fragment structure of a putative hsdR subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
22	d1c3ha_	Alignment	not modelled	12.5	30	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
23	d1d9qa_	Alignment	not modelled	11.9	22	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
24	c2krhA_	Alignment	not modelled	10.8	9	PDB header: actin-binding protein Chain: A: PDB Molecule: actin-binding rho-activating protein; PDBTitle: structure of the c-terminal actin binding domain of abra
25	d2bu3a1	Alignment	not modelled	7.9	12	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Phytochelatin synthase
26	d1w36b3	Alignment	not modelled	5.9	16	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
27	d1pk6a_	Alignment	not modelled	5.5	50	Fold: TNF-like Superfamily: TNF-like Family: TNF-like