
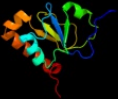





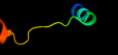





















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1em8b_	 Alignment		100.0	100	Fold: DNA polymerase III psi subunit Superfamily: DNA polymerase III psi subunit Family: DNA polymerase III psi subunit
2	c3sxuB_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit psi; PDBTitle: structure of the e. coli ssb-dna polymerase iii interface
3	c3gliP_	 Alignment		98.4	100	PDB header: transferase/dna Chain: P: PDB Molecule: dna polymerase iii subunit psi; PDBTitle: crystal structure of the e. coli clamp loader bound to2 primer-template dna and psi peptide
4	c3gliO_	 Alignment		98.4	100	PDB header: transferase/dna Chain: O: PDB Molecule: dna polymerase iii subunit psi; PDBTitle: crystal structure of the e. coli clamp loader bound to2 primer-template dna and psi peptide
5	d1ui0a_	 Alignment		24.1	18	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
6	d1vk2a_	 Alignment		15.4	21	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
7	c2kboA_	 Alignment		15.1	17	PDB header: hydrolase Chain: A: PDB Molecule: dna dc->du-editing enzyme apobec-3g; PDBTitle: structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
8	c2br6A_	 Alignment		14.7	17	PDB header: hydrolase Chain: A: PDB Molecule: aiia-like protein; PDBTitle: crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
9	c3mk4A_	 Alignment		12.3	17	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal biogenesis factor 3; PDBTitle: x-ray structure of human pex3 in complex with a pex19 derived peptide
10	d1tafa_	 Alignment		11.4	15	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
11	c2g80C_	 Alignment		10.9	13	PDB header: hydrolase Chain: C: PDB Molecule: protein utr4; PDBTitle: crystal structure of utr4 protein (unknown transcript 4 protein)2 (yel038w) from saccharomyces cerevisiae at 2.28 a resolution

12	c2j8pA_	Alignment		7.7	69	PDB header: nuclear protein Chain: A: PDB Molecule: cleavage stimulation factor 64 kda subunit; PDBTitle: nmr structure of c-terminal domain of human cstf-64
13	d1cmxa_	Alignment		7.0	23	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
14	d2etla1	Alignment		6.3	25	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin carboxyl-terminal hydrolase UCH-L
15	c3o8wA_	Alignment		6.0	16	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen regulatory protein p-ii (glnb-1); PDBTitle: archaeoglobus fulgidus glnk1
16	c2k29A_	Alignment		5.9	30	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb

17

[c2p5xB_](#)

Alignment



5.6

29

PDB header: structural genomics, unknown function
Chain: B: **PDB Molecule:** n-acetylserotonin o-methyltransferase-like protein;
PDB Title: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein