




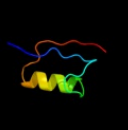

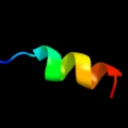














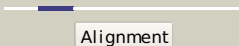

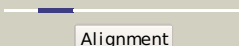
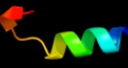


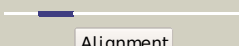

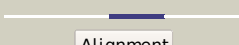

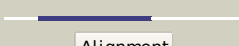







Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A8S9
Date	Thu Jan 5 11:08:38 GMT 2012
Unique Job ID	642802a13464f03c

Detailed template information

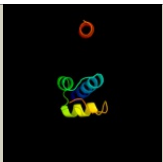
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g8ea_	 Alignment		100.0	100	Fold: Flagellar transcriptional activator FlhD Superfamily: Flagellar transcriptional activator FlhD Family: Flagellar transcriptional activator FlhD
2	d1g8eb_	 Alignment		100.0	100	Fold: Flagellar transcriptional activator FlhD Superfamily: Flagellar transcriptional activator FlhD Family: Flagellar transcriptional activator FlhD
3	d1x1ma_	 Alignment		18.3	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
4	c2kq5A_	 Alignment		16.9	36	PDB header: unknown function Chain: A: PDB Molecule: avirulence protein; PDBTitle: solution nmr structure of a section of the repeat domain of the type2 iii effector protein ptha
5	d2fx0a2	 Alignment		16.0	7	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
6	d1b4ua_	 Alignment		11.7	6	Fold: LigA subunit of an aromatic-ring-opening dioxygenase LigAB Superfamily: LigA subunit of an aromatic-ring-opening dioxygenase LigAB Family: LigA subunit of an aromatic-ring-opening dioxygenase LigAB
7	d3e46a1	 Alignment		10.1	23	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
8	d1qt1a_	 Alignment		8.1	22	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
9	c3m91B_	 Alignment		8.0	42	PDB header: hydrolase regulator Chain: B: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa
10	d2glka1	 Alignment		7.9	22	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
11	d1au7a2	 Alignment		7.8	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain

12	c3hgfA_		Alignment		7.6	45	PDB header: nucleotide binding protein Chain: A: PDB Molecule: rhoptry protein fragment; PDBTitle: expression, purification, spectroscopical and2 crystallographical studies of segments of the nucleotide3 binding domain of the reticulocyte binding protein py235 of4 plasmodium yoelii
13	d1dd3a1		Alignment		7.3	28	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
14	d1bxca_		Alignment		6.7	30	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
15	c3m9dl_		Alignment		6.5	42	PDB header: chaperone Chain: I: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain
16	c2fh0A_		Alignment		5.9	23	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 16.0 kda protein in abf2-chl12 PDBTitle: nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
17	c2i56A_		Alignment		5.6	15	PDB header: isomerase, metal-binding protein Chain: A: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
18	c2e8mA_		Alignment		5.6	29	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
19	c3eq1A_		Alignment		5.5	10	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at2 2.8a resolution

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[c2avuF](#)

Alignment



5.4

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PDB header:transcription activator
Chain: F: **PDB Molecule:**flagellar transcriptional activator flhA;
PDBTitle: structure of the escherichia coli flhdc complex, a2
prokaryotic heteromeric regulator of transcription