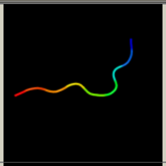
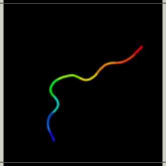
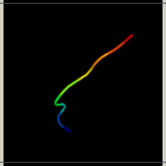
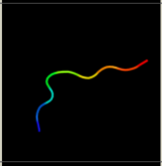
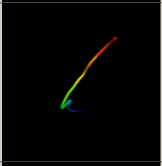
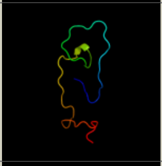
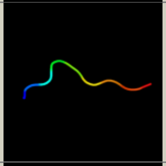
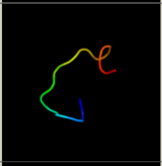
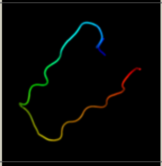
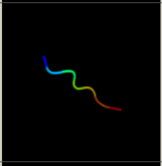
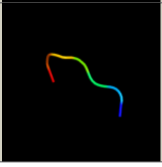
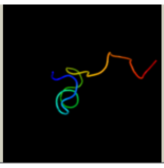
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P08339
Date	Thu Jan 5 11:01:11 GMT 2012
Unique Job ID	d8d1658deff2e7d6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nvpC_	Alignment		43.2	78	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia beta chain; **PDBTitle:** human tfiia/tbp/dna complex
2	d1nvpc_	Alignment		43.2	78	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
3	d1nh2c_	Alignment		42.0	56	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
4	c1nh2C_	Alignment		42.0	56	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
5	d1ytfc_	Alignment		40.1	56	**Fold:**Transcription factor IIA (TFIIA), beta-barrel domain **Superfamily:**Transcription factor IIA (TFIIA), beta-barrel domain **Family:**Transcription factor IIA (TFIIA), beta-barrel domain
6	c3eatX_	Alignment		34.2	27	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
7	c1rm1C_	Alignment		28.7	56	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
8	d2vy4a1	Alignment		24.1	40	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**CHHC finger
9	c3pvjB_	Alignment		9.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
10	d3c96a2	Alignment		8.0	43	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
11	d1x3ha2	Alignment		7.9	57	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

12	d1m06f_	Alignment		7.0	55	**Fold:** Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:** ssDNA viruses **Family:** Microviridae-like VP