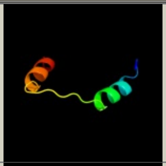
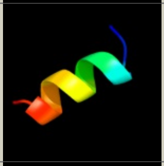
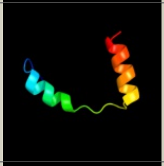
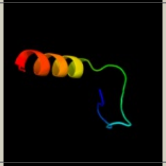
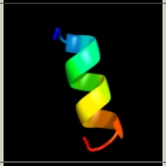
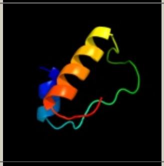
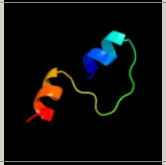
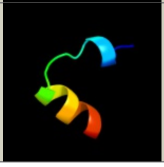
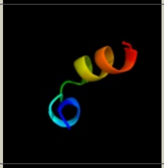
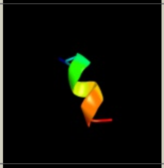
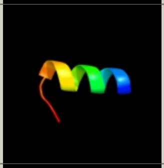
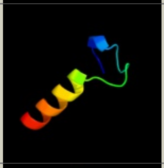
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76545
Date	Thu Jan 5 12:24:21 GMT 2012
Unique Job ID	49db092b810e553d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1giqa2	Alignment		15.6	24	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
2	d1fova_	Alignment		11.6	43	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
3	d1jhba_	Alignment		8.5	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
4	c3l4nA_	Alignment		8.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6
5	d1qs1a1	Alignment		8.0	35	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
6	c3fveA_	Alignment		7.7	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**diaminopimelate epimerase; **PDBTitle:** crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
7	d1t1va_	Alignment		7.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
8	d1ejxc2	Alignment		6.8	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
9	d2hy5c1	Alignment		6.6	22	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
10	c3hymE_	Alignment		6.6	70	**PDB header:**cell cycle, ligase **Chain:** E: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
11	c3ogmB_	Alignment		6.5	33	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronatine-insensitive protein 1; **PDBTitle:** structure of coi1-ask1 in complex with coronatine and the jaz1 degron

12	d1ktea_	Alignment		6.4	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
13	c3oglD_	Alignment		6.3	33	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**coronatine-insensitive protein 1; **PDBTitle:** structure of coi1-ask1 in complex with ja-isoleucine and the jaz12 degron
14	c3hymK_	Alignment		6.2	70	**PDB header:**cell cycle, ligase **Chain:** K: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
15	c3ljbA_	Alignment		6.2	12	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**interferon-induced gtp-binding protein mx1; **PDBTitle:** structural basis of oligomerisation in the mxa stalk
16	d1qb5d_	Alignment		6.1	60	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
17	c2wulB_	Alignment		6.1	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin related protein 5; **PDBTitle:** crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
18	d2gkea2	Alignment		6.0	28	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**Diaminopimelate epimerase
19	c2hzfA_	Alignment		5.9	31	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
20	d1knya1	Alignment		5.9	43	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Kanamycin nucleotidyltransferase (KNTase), C-terminal domain
21	c3hymA_	Alignment	not modelled	5.9	70	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
22	c3hymI_	Alignment	not modelled	5.9	70	**PDB header:**cell cycle, ligase **Chain:** I: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
23	c2ht9A_	Alignment	not modelled	5.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
24	d2f6mb1	Alignment	not modelled	5.4	29	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS28 N-terminal domain
25	d1p3qq_	Alignment	not modelled	5.3	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
26	c3hymC_	Alignment	not modelled	5.3	70	**PDB header:**cell cycle, ligase **Chain:** C: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
27	d1r45a_	Alignment	not modelled	5.3	29	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
28	c2e7pC_	Alignment	not modelled	5.2	31	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from

						populus2 tremula x tremuloides
29	c2cazB_	Alignment	not modelled	5.1	29	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** escrt-i core
30	d2cazb1	Alignment	not modelled	5.1	29	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS28 N-terminal domain
31	c3hymG_	Alignment	not modelled	5.1	70	**PDB header:**cell cycle, ligase **Chain:** G: **PDB Molecule:**anaphase-promoting complex subunit cdc26; **PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure