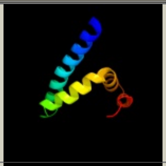
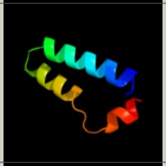
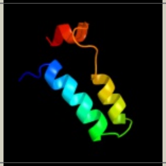
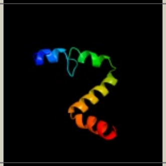
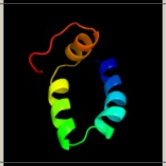
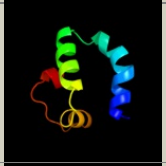
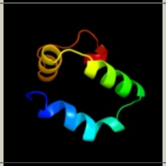
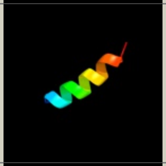
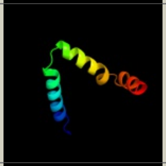
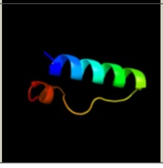
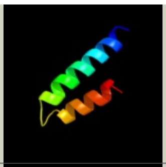
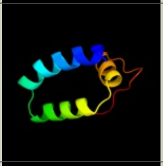
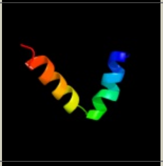
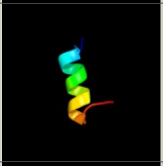
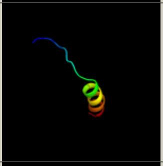
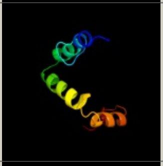
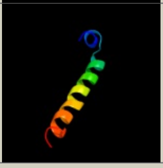
Email	l.a.kelley@imperial.ac.uk
Description	P0ACY9
Date	Thu Jan 5 11:19:27 GMT 2012
Unique Job ID	4c5940d08162aa02

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ermD_	Alignment		99.9	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved protein with unknown function2 from pseudomonas syringae pv. tomato str. dc3000
2	d1vf6c_	Alignment		52.6	20	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
3	c1vf6C_	Alignment		52.6	20	**PDB header:**protein binding/protein transport **Chain:** C: **PDB Molecule:**maguk p55 subfamily member 5; **PDBTitle:** 2.1 angstrom crystal structure of the pals-1-l27n and patj2 l27 heterodimer complex
4	d1y76b1	Alignment		51.2	23	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
5	d1r45a_	Alignment		45.5	15	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
6	d1puza_	Alignment		40.8	12	**Fold:**YgfY-like **Superfamily:**YgfY-like **Family:**YgfY-like
7	c2jr5A_	Alignment		33.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0350 protein vc_2471; **PDBTitle:** solution structure of upf0350 protein vc_2471. northeast2 structural genomics target vcr36
8	c1x6iB_	Alignment		32.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ygfy; **PDBTitle:** crystal structure of ygfy from escherichia coli
9	d1fcdc1	Alignment		21.0	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
10	c3bw8B_	Alignment		18.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mono-adp-ribosyltransferase c3; **PDBTitle:** crystal structure of the clostridium limosum c3 exoenzyme
11	d1f46a_	Alignment		16.7	13	**Fold:**TBP-like **Superfamily:**Cell-division protein ZipA, C-terminal domain **Family:**Cell-division protein ZipA, C-terminal domain

12	c2kubA_	Alignment		16.5	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** solution structure of the alpha subdomain of the major non-repeat unit2 of fap1 fimbriae of streptococcus parasanguis
13	c2lm4A_	Alignment		16.3	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**succinate dehydrogenase assembly factor 2, mitochondrial; **PDBTitle:** solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a
14	c3rguA_	Alignment		16.3	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** structure of fap-nra at ph 5.0
15	d1fcdc2	Alignment		16.3	20	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
16	d1kx7a_	Alignment		16.1	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
17	d1wh7a_	Alignment		14.8	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
18	d1ojqa_	Alignment		14.7	15	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
19	d1c75a_	Alignment		14.0	41	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
20	c3cs5B_	Alignment		13.4	22	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942
21	d1vima_	Alignment	not modelled	12.2	8	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
22	d1cora_	Alignment	not modelled	11.5	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
23	c2bovB_	Alignment	not modelled	11.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mono-adp-ribosyltransferase c3; **PDBTitle:** molecular recognition of an adp-ribosylating clostridium2 botulinum c3 exoenzyme by rala gtpase
24	d2c8aa1	Alignment	not modelled	11.0	17	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
25	d1lqta1	Alignment	not modelled	9.9	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
26	d1h1oa1	Alignment	not modelled	8.3	22	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
27	c1u6hB_	Alignment	not modelled	8.3	40	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** vinculin head (0-258) in complex with the talin vinculin2 binding site 2 (849-879)
28	c1qs2A_	Alignment	not modelled	7.9	26	**PDB header:**toxin **Chain:** A: **PDB Molecule:**adp-ribosyltransferase; **PDBTitle:** crystal structure of vip2 with nad
29	d1urfa_	Alignment	not modelled	6.6	22	**Fold:**Long alpha-hairpin **Superfamily:**HR1 repeat

						Family:HR1 repeat
30	c2c9eA_	Alignment	not modelled	6.2	50	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**peridinin-chlorophyll a protein; **PDBTitle:** peridinin-chlorophyll a protein, high-salt form
31	d351ca_	Alignment	not modelled	6.0	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
32	c2d0sA_	Alignment	not modelled	5.4	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
33	c2kr1A_	Alignment	not modelled	5.4	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin protein ligase e3a; **PDBTitle:** solution nmr structure of zinc binding n-terminal domain of ubiquitin-2 protein ligase e3a from homo sapiens. northeast structural genomics3 consortium (nesg) target hr3662
34	c1skoA_	Alignment	not modelled	5.2	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase 1 **PDBTitle:** mp1-p14 complex
35	c1qs1D_	Alignment	not modelled	5.1	24	**PDB header:**toxin **Chain:** D: **PDB Molecule:**adp-ribosyltransferase; **PDBTitle:** crystal structure of vegetative insecticidal protein2 (vip2)