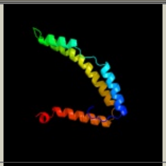
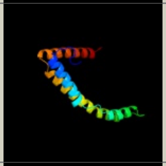
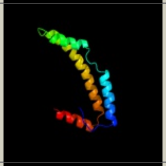
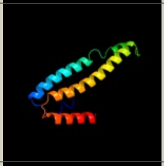
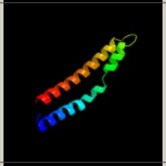
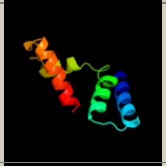
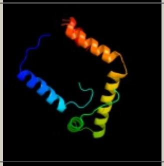
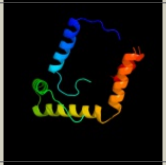
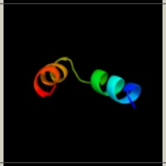
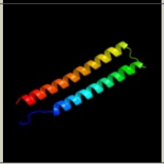
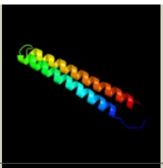
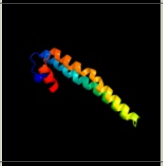
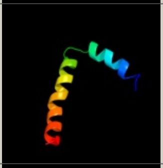
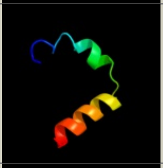
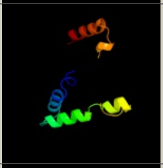
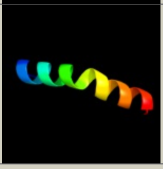
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AE85
Date	Thu Jan 5 11:22:46 GMT 2012
Unique Job ID	5c85a20df6173c80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3itfA_	Alignment		99.9	93	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein
2	c3qzcA_	Alignment		99.9	100	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic protein cpxp; **PDBTitle:** structure of the periplasmic stress response protein cpxp
3	c3o39A_	Alignment		99.8	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**periplasmic protein related to spheroblast formation; **PDBTitle:** crystal structure of spy
4	c3epvB_	Alignment		99.7	8	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
5	c3oeoD_	Alignment		99.7	30	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**spheroplast protein y; **PDBTitle:** the crystal structure e. coli spy
6	c3layF_	Alignment		98.6	17	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
7	c2qguA_	Alignment		82.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
8	d3cmna1	Alignment		61.1	20	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Caur0242-like
9	c3cmnA_	Alignment		57.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of a putative hydrolase with a novel fold2 from chloroflexus aurantiacus
10	c2i9lL_	Alignment		54.3	28	**PDB header:**immune system/viral protein **Chain:** L: **PDB Molecule:**virion membrane protein m25; **PDBTitle:** structure of fab 7d11 from a neutralizing antibody against the2 poxvirus l1 protein
11	d1ek8a_	Alignment		44.5	21	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF

12	d1dd5a_	Alignment		41.2	16	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
13	c3g6iA_	Alignment		39.9	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative outer membrane protein, part of carbohydrate **PDBTitle:** crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
14	c2crjA_	Alignment		37.7	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
15	c2ctoA_	Alignment		37.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**novel protein; **PDBTitle:** solution structure of the hmg box like domain from human2 hypothetical protein flj14904
16	c2an7A_	Alignment		36.8	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
17	d1q44a_	Alignment		34.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
18	d1olma1	Alignment		34.4	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
19	c2k5jB_	Alignment		33.4	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
20	d1pcfa_	Alignment		32.6	30	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
21	c1o6uA_	Alignment	not modelled	31.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sec14-like protein 2; **PDBTitle:** the crystal structure of human supernatant protein factor
22	c3ieeA_	Alignment	not modelled	30.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of hypothetical protein bf3319 from bacteroides2 fragilis (yp_212931.1) from bacteroides fragilis nctc 9343 at 1.70 a3 resolution
23	c2eqzA_	Alignment	not modelled	30.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group protein b3; **PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3
24	c2co9A_	Alignment	not modelled	29.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
25	c1y698_	Alignment	not modelled	27.8	19	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**ribosome recycling factor; **PDBTitle:** rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
26	c3b7qA_	Alignment	not modelled	27.7	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**uncharacterized protein ykl091c; **PDBTitle:** crystal structure of yeast sec14 homolog sfh1 in complex with2 phosphatidylcholine
27	c1zd1B_	Alignment	not modelled	27.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
28	c2e6oA_	Alignment	not modelled	26.6	5	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** solution structure of the hmg box domain from human

						hmg-box2 transcription factor 1
29	c3fghA_	Alignment	not modelled	26.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
30	c3lf9A_	Alignment	not modelled	26.0	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**4e10_d0_1is1a_001_c (t161); **PDBTitle:** crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
31	c1wr1B_	Alignment	not modelled	25.5	26	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
32	d1hsma_	Alignment	not modelled	25.0	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
33	c2h8kA_	Alignment	not modelled	24.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
34	d1akha_	Alignment	not modelled	24.4	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
35	d1wqga1	Alignment	not modelled	24.4	21	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
36	d1k99a_	Alignment	not modelled	24.0	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
37	d1i11a_	Alignment	not modelled	22.6	10	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
38	d1v63a_	Alignment	not modelled	22.4	9	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
39	d1q20a_	Alignment	not modelled	21.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
40	d1g3ma_	Alignment	not modelled	21.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
41	d1eh1a_	Alignment	not modelled	21.6	13	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
42	c2x5qA_	Alignment	not modelled	21.6	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso1986; **PDBTitle:** crystal structure of hypothetical protein sso1986 from2 sulfolobus solfataricus p2
43	c2gwhA_	Alignment	not modelled	21.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
44	c1hryA_	Alignment	not modelled	20.9	16	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**human sry; **PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multid-dimensional heteronuclear-edited and-filtered nmr
45	c1hrzA_	Alignment	not modelled	20.9	16	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**human sry; **PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multi-dimensional heteronuclear-edited and-filtered nmr
46	d1i94m_	Alignment	not modelled	20.2	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
47	d2gzka2	Alignment	not modelled	20.1	15	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
48	c2amiA_	Alignment	not modelled	19.3	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
49	c3rh3A_	Alignment	not modelled	18.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized duf3829-like protein; **PDBTitle:** crystal structure of an uncharacterized duf3829-like protein (bt_1908)2 from bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
50	d1ckta_	Alignment	not modelled	18.8	5	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
51	d1v65a_	Alignment	not modelled	18.4	19	**Fold:**KRAB domain (Kruppel-associated box) **Superfamily:**KRAB domain (Kruppel-associated box) **Family:**KRAB domain (Kruppel-associated box)
52	c1hmfA_	Alignment	not modelled	17.7	11	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein fragment-b; **PDBTitle:** structure of the hmg box motif in the b-domain of hmg1
53	d1hmfa_	Alignment	not modelled	17.7	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
54	c1wz6A_	Alignment	not modelled	17.5	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hmg-box transcription factor bbx; **PDBTitle:** solution structure of the hmg_box domain of murine bobby2 sox homolog
						Fold:RRF/tRNA synthetase additional domain-like

55	d1is1a_	Alignment	not modelled	17.4	16	**Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
56	d1lwma_	Alignment	not modelled	17.2	18	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
57	d1jebb_	Alignment	not modelled	17.2	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
58	c2zvpX_	Alignment	not modelled	16.8	20	**PDB header:**transferase **Chain:** X: **PDB Molecule:**tyrosine-ester sulfotransferase; **PDBTitle:** crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
59	d3d1kb1	Alignment	not modelled	16.7	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
60	c1j3xA_	Alignment	not modelled	16.6	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**high mobility group protein 2; **PDBTitle:** solution structure of the n-terminal domain of the hmgb2
61	d1j3xa_	Alignment	not modelled	16.6	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
62	d2uubm1	Alignment	not modelled	16.4	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
63	d1j99a_	Alignment	not modelled	16.1	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
64	c3u2bC_	Alignment	not modelled	16.1	10	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription factor sox-4; **PDBTitle:** structure of the sox4 hmg domain bound to dna
65	d1auaa1	Alignment	not modelled	15.8	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
66	d1gt0d_	Alignment	not modelled	15.8	10	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
67	c2j8pA_	Alignment	not modelled	15.7	28	**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
68	d1j3da_	Alignment	not modelled	15.6	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
69	d1ls6a_	Alignment	not modelled	15.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
70	c3u3oA_	Alignment	not modelled	15.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1a1; **PDBTitle:** crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
71	c2da4A_	Alignment	not modelled	15.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
72	c2yulA_	Alignment	not modelled	14.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sox-17; **PDBTitle:** solution structure of the hmg box of human transcription2 factor sox-17
73	d1hmja_	Alignment	not modelled	14.1	6	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
74	c2d7lA_	Alignment	not modelled	14.0	25	**PDB header:**gene regulation, dna binding protein **Chain:** A: **PDB Molecule:**wd repeat and hmg-box dna binding protein 1; **PDBTitle:** solution structure of the hmg box domain from human wd2 repeat and hmg-box dna binding protein 1
75	d3bfxa1	Alignment	not modelled	13.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
76	c2kgrA_	Alignment	not modelled	13.7	0	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
77	d1aaba_	Alignment	not modelled	13.7	3	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
78	c1aabA_	Alignment	not modelled	13.7	3	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein; **PDBTitle:** nmr structure of rat hmg1 hmga fragment
79	c2kz5A_	Alignment	not modelled	13.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
80	c1q1qA_	Alignment	not modelled	13.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase family, cytosolic, 2b, member 1 **PDBTitle:** crystal structure of human pregnenolone sulfotransferase2 (sult2b1a) in the presence of pap
						Fold:HMG-box

81	d2lefa_	Alignment	not modelled	13.2	11	**Superfamily:**HMG-box **Family:**HMG-box
82	c2cs1A_	Alignment	not modelled	13.1	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pms1 protein homolog 1; **PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein
83	d1a9we_	Alignment	not modelled	13.1	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
84	d2e9xa1	Alignment	not modelled	13.0	15	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**PSF1 N-terminal domain-like
85	c3crqA_	Alignment	not modelled	12.8	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
86	d1hbrb_	Alignment	not modelled	12.7	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
87	d2a3ra1	Alignment	not modelled	12.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
88	c3ptjA_	Alignment	not modelled	12.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0603 protein at1g54780, chloroplastic; **PDBTitle:** structural and functional analysis of arabidopsis thaliana thylakoid2 lumen protein attlp18.3
89	d1aqua_	Alignment	not modelled	12.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
90	d1uuja_	Alignment	not modelled	12.3	33	**Fold:**Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain **Superfamily:**Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain **Family:**Lissencephaly-1 protein (Lis-1, PAF-AH alpha) N-terminal domain
91	d1v64a_	Alignment	not modelled	12.2	18	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
92	d1wova1	Alignment	not modelled	12.1	13	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**Eukaryotic type heme oxygenase
93	d1fmja_	Alignment	not modelled	12.0	5	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
94	d1s7ea1	Alignment	not modelled	12.0	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
95	d1qpwb_	Alignment	not modelled	12.0	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
96	c2kqxA_	Alignment	not modelled	11.8	17	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
97	d1wh7a_	Alignment	not modelled	11.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	d1fi6a_	Alignment	not modelled	11.6	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
99	c2q9qC_	Alignment	not modelled	11.5	15	**PDB header:**replication **Chain:** C: **PDB Molecule:**dna replication complex gins protein psf1; **PDBTitle:** the crystal structure of full length human gins complex