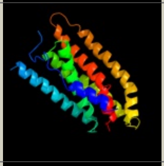
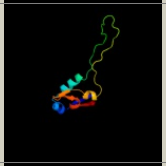
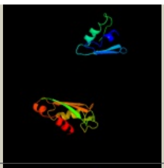
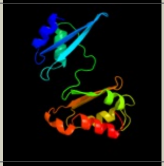
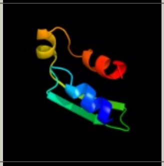
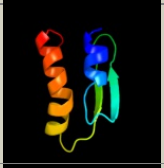
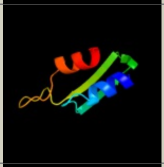
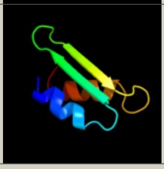
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P31224
Date	Thu Jan 5 11:47:22 GMT 2012
Unique Job ID	6b373747e88d0410

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1oy8A_	Alignment		100.0	100	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
2	c3k07A_	Alignment		100.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation efflux system protein cusa; **PDBTitle:** crystal structure of cusa
3	c3aqpB_	Alignment		100.0	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
4	d1iwga8	Alignment		100.0	87	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
5	d1iwga7	Alignment		100.0	89	**Fold:**Multidrug efflux transporter AcrB transmembrane domain **Superfamily:**Multidrug efflux transporter AcrB transmembrane domain **Family:**Multidrug efflux transporter AcrB transmembrane domain
6	d1iwga1	Alignment		99.9	100	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
7	d1iwga2	Alignment		99.7	63	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
8	d1iwga5	Alignment		99.7	100	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
9	d1iwga6	Alignment		99.3	100	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
10	d1iwga3	Alignment		99.1	100	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
11	d1iwga4	Alignment		98.0	100	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains

12	c2ropA_	Alignment		95.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
13	c2ew9A_	Alignment		93.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
14	d1s6ua_	Alignment		90.6	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
15	d2aw0a_	Alignment		89.8	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
16	d1cpza_	Alignment		89.5	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
17	d1q8la_	Alignment		89.2	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
18	d2qifa1	Alignment		88.9	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	c3dxsX_	Alignment		87.9	20	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
20	c1yjrA_	Alignment		87.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
21	c2l3mA_	Alignment	not modelled	87.3	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
22	d1kvja_	Alignment	not modelled	86.6	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1p6ta1	Alignment	not modelled	86.4	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	c2ga7A_	Alignment	not modelled	86.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
25	d1osda_	Alignment	not modelled	85.6	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	c2ldiA_	Alignment	not modelled	85.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
27	c2yvxD_	Alignment	not modelled	85.4	12	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
28	d1p6ta2	Alignment	not modelled	85.0	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
29	c2kt2A	Alignment	not modelled	84.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase;

29		Alignment	not modelled	84.0	18	**PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
30	c1yg0A_	Alignment	not modelled	83.9	9	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
31	c2kkhA_	Alignment	not modelled	83.9	9	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
32	c1y3kA_	Alignment	not modelled	80.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
33	d1afia_	Alignment	not modelled	79.4	14	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c2rmlA_	Alignment	not modelled	78.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
35	c2ofhX_	Alignment	not modelled	76.3	15	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
36	d1qupa2	Alignment	not modelled	75.8	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
37	c1jk9D_	Alignment	not modelled	70.5	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
38	c2k2pA_	Alignment	not modelled	70.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
39	d1mwza_	Alignment	not modelled	69.6	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
40	d2ggpb1	Alignment	not modelled	68.7	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
41	d1sb6a_	Alignment	not modelled	68.0	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
42	c2gcfA_	Alignment	not modelled	67.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
43	c2rogA_	Alignment	not modelled	61.9	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
44	c2crlA_	Alignment	not modelled	58.9	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
45	c2aj1A_	Alignment	not modelled	58.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
46	c1qupA_	Alignment	not modelled	55.4	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
47	d1cc8a_	Alignment	not modelled	53.1	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
48	d2vv5a2	Alignment	not modelled	52.6	15	**Fold:**Ferredoxin-like **Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain **Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain
49	c3j09A_	Alignment	not modelled	47.2	15	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
50	d2yvxa3	Alignment	not modelled	41.7	13	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
51	c2kyzA_	Alignment	not modelled	37.2	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
52	d2nwwa1	Alignment	not modelled	34.0	8	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
53	c1yj7A_	Alignment	not modelled	33.0	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
54	d2cu6a1	Alignment	not modelled	24.5	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like

55	c3c6fD_	Alignment	not modelled	20.5	3	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yetf protein; **PDBTitle:** crystal structure of protein bsu07140 from bacillus subtilis
56	c2kncA_	Alignment	not modelled	18.3	2	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
57	d1pw4a_	Alignment	not modelled	17.8	9	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
58	d1uwda_	Alignment	not modelled	17.5	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
59	c2yy3B_	Alignment	not modelled	16.7	9	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-beta; **PDBTitle:** crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii
60	c1ciiA_	Alignment	not modelled	16.4	17	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
61	d1ek8a_	Alignment	not modelled	15.0	21	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
62	c2jnvA_	Alignment	not modelled	13.0	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
63	c3fryB_	Alignment	not modelled	12.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable copper-exporting p-type atpase a; **PDBTitle:** crystal structure of the copa c-terminal metal binding domain
64	d1qmga1	Alignment	not modelled	11.7	25	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
65	d1jb0i_	Alignment	not modelled	10.5	19	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
66	c1a87A_	Alignment	not modelled	10.3	13	**PDB header:**bacteriocin **Chain:** A: **PDB Molecule:**colicin n; **PDBTitle:** colicin n
67	d1a87a_	Alignment	not modelled	10.3	13	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
68	d1dd5a_	Alignment	not modelled	10.2	16	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
69	d2cfxa2	Alignment	not modelled	10.2	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
70	c2i88A_	Alignment	not modelled	10.1	6	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1
71	d1is1a_	Alignment	not modelled	10.0	16	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
72	d1fe0a_	Alignment	not modelled	9.7	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
73	d1wqga1	Alignment	not modelled	9.2	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
74	c3qlbA_	Alignment	not modelled	9.0	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**enantio-pyochelin receptor; **PDBTitle:** enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin
75	c3g7sA_	Alignment	not modelled	9.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
76	c2hdiA_	Alignment	not modelled	9.0	33	**PDB header:**protein transport,antimicrobial protein **Chain:** A: **PDB Molecule:**colicin i receptor; **PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
77	d2b3ya2	Alignment	not modelled	8.9	43	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
78	d2cg4a2	Alignment	not modelled	8.8	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
79	d1nwaa_	Alignment	not modelled	8.7	24	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
80	c1nwaA_	Alignment	not modelled	8.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2

						sulfoxide reductase a in complex with protein-bound3 methionine
81	c2i8bB_	Alignment	not modelled	8.6	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**minor nucleoprotein vp30; **PDBTitle:** crystal structure of the c-terminal domain of ebola virus vp30
82	d1eh1a_	Alignment	not modelled	8.4	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
83	c2yg8B_	Alignment	not modelled	8.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative; **PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
84	d2phcb2	Alignment	not modelled	8.3	19	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
85	d1lr0a_	Alignment	not modelled	7.9	13	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
86	d2cyya2	Alignment	not modelled	7.9	2	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
87	d1bvsa2	Alignment	not modelled	7.8	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
88	c3bdeA_	Alignment	not modelled	7.8	3	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mll5499 protein; **PDBTitle:** crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
89	d1s7ba_	Alignment	not modelled	7.7	18	**Fold:**Multidrug resistance efflux transporter EmrE **Superfamily:**Multidrug resistance efflux transporter EmrE **Family:**Multidrug resistance efflux transporter EmrE
90	d1h3da2	Alignment	not modelled	7.6	19	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
91	c3lkxB_	Alignment	not modelled	7.6	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha; **PDBTitle:** human nac dimerization domain
92	c3lnoA_	Alignment	not modelled	7.5	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
93	c2h5xA_	Alignment	not modelled	7.5	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
94	c1d8lA_	Alignment	not modelled	7.5	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
95	c2k9pA_	Alignment	not modelled	7.4	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles
96	d1wiha_	Alignment	not modelled	7.4	15	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
97	c3ibwA_	Alignment	not modelled	7.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
98	c2ki0A_	Alignment	not modelled	7.4	6	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
99	d1ydxa2	Alignment	not modelled	7.3	11	**Fold:**DNA methylase specificity domain **Superfamily:**DNA methylase specificity domain **Family:**Type I restriction modification DNA specificity domain