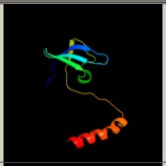
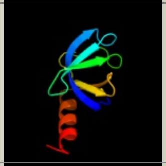
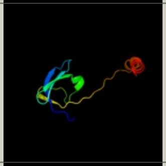
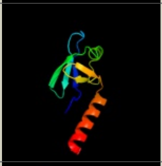
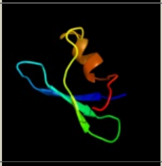
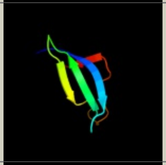
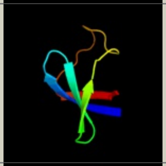
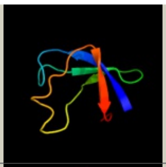
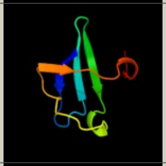
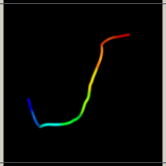
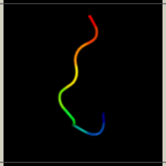
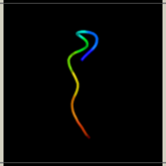
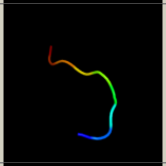
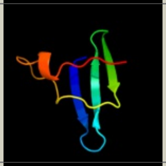
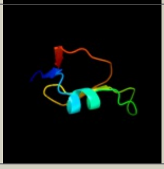
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AAM7
Date	Thu Jan 5 11:13:19 GMT 2012
Unique Job ID	8ba12a15c4edb1d4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d3rA_	Alignment		100.0	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
2	d2ot2a1	Alignment		99.9	57	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
3	d3d3ra1	Alignment		99.9	32	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
4	d2z1ca1	Alignment		99.9	38	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
5	d1rl2a2	Alignment		80.6	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
6	c2rcnA_	Alignment		67.5	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
7	d1vqoa2	Alignment		66.7	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
8	c4a2iV_	Alignment		65.4	26	**PDB header:**ribosome/hydrolase **Chain:** V: **PDB Molecule:**putative ribosome biogenesis gtpase rsga; **PDBTitle:** cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
9	d2zjra2	Alignment		56.1	34	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	c1u0lB_	Alignment		55.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
11	c2dgyA_	Alignment		54.3	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein

12	c2yv5A_	Alignment		54.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
13	c3mxnB_	Alignment		53.7	18	**PDB header:**replication **Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2; **PDBTitle:** crystal structure of the rmi core complex
14	c1g0dA_	Alignment		43.4	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** crystal structure of red sea bream transglutaminase
15	c1kv3F_	Alignment		42.5	44	**PDB header:**transferase **Chain:** F: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** human tissue transglutaminase in gdp bound form
16	c1l9mB_	Alignment		42.3	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-glutamine glutamyltransferase e3; **PDBTitle:** three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
17	c1f13A_	Alignment		40.0	33	**PDB header:**coagulation factor **Chain:** A: **PDB Molecule:**cellular coagulation factor xiii zymogen; **PDBTitle:** recombinant human cellular coagulation factor xiii
18	c2oqkA_	Alignment		39.7	34	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
19	d2j01d2	Alignment		37.2	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
20	d1ny4a_	Alignment		35.6	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
21	d2qamc2	Alignment	not modelled	35.4	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	d1jt8a_	Alignment	not modelled	34.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
23	d1g0da4	Alignment	not modelled	33.7	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
24	d1d7qa_	Alignment	not modelled	33.3	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
25	d1njjb1	Alignment	not modelled	33.1	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
26	d2q3za4	Alignment	not modelled	32.8	44	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
27	d1ex0a4	Alignment	not modelled	31.3	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
28	c1t9hA_	Alignment	not modelled	31.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
29	d1vjja4	Alignment	not modelled	29.6	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases

						Family: Transglutaminase core
30	c2xzm1_	Alignment	not modelled	29.1	19	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**ribosomal protein s28e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
31	d2toda1	Alignment	not modelled	28.4	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
32	c1rl2A_	Alignment	not modelled	28.3	17	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**protein (ribosomal protein l2); **PDBTitle:** ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
33	d1d7ka1	Alignment	not modelled	27.1	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
34	d1ne3a_	Alignment	not modelled	26.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
35	c1njjC_	Alignment	not modelled	23.3	33	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine2 decarboxylase bound to d-ornithine and to g418
36	c3i4oA_	Alignment	not modelled	22.8	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
37	c3fp9E_	Alignment	not modelled	22.8	24	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
38	d1f3ta1	Alignment	not modelled	22.3	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
39	c2hc8A_	Alignment	not modelled	22.2	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
40	c1oy5B_	Alignment	not modelled	20.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
41	d1u0la1	Alignment	not modelled	19.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
42	d1knwa1	Alignment	not modelled	19.5	25	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
43	c2qghA_	Alignment	not modelled	19.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
44	d1t9ha1	Alignment	not modelled	19.1	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
45	d7odca1	Alignment	not modelled	18.6	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
46	d1oy5a_	Alignment	not modelled	18.3	22	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
47	c1xniI_	Alignment	not modelled	17.8	19	**PDB header:**cell cycle **Chain:** I: **PDB Molecule:**tumor suppressor p53-binding protein 1; **PDBTitle:** tandem tudor domain of 53bp1
48	d1twia1	Alignment	not modelled	17.8	8	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
49	c2p3eA_	Alignment	not modelled	16.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus
50	c1kqsA_	Alignment	not modelled	16.5	24	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**ribosomal protein l2; **PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
51	c2nvaH_	Alignment	not modelled	15.5	33	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
52	c1knwA_	Alignment	not modelled	14.9	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
53	d3pnpa_	Alignment	not modelled	14.4	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
54	c2yxxA_	Alignment	not modelled	14.3	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa)
55	c1yr3A_	Alignment	not modelled	13.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene

56	d1p3ha_	Alignment	not modelled	13.6	28	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
57	d1p3qq_	Alignment	not modelled	13.5	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
58	c1w4sA_	Alignment	not modelled	13.4	38	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**polybromo 1 protein; **PDBTitle:** crystal structure of the proximal bah domain of polybromo
59	d1aono_	Alignment	not modelled	13.3	24	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
60	d1cb0a_	Alignment	not modelled	13.2	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
61	d1fr3a_	Alignment	not modelled	12.9	11	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
62	d2id1a1	Alignment	not modelled	12.8	27	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
63	d1uala_	Alignment	not modelled	12.7	38	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
64	d2a7ya1	Alignment	not modelled	12.6	22	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Rv2302-like
65	c2a7yA_	Alignment	not modelled	12.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2302/mt2359; **PDBTitle:** solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
66	d1vmka_	Alignment	not modelled	12.5	30	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
67	c2akwB_	Alignment	not modelled	12.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
68	c2pljA_	Alignment	not modelled	11.7	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
69	c2k29A_	Alignment	not modelled	11.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
70	d1ntga_	Alignment	not modelled	11.4	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Myf domain
71	d1pqwa_	Alignment	not modelled	11.3	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
72	c3n29A_	Alignment	not modelled	11.2	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase; **PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
73	c3knuD_	Alignment	not modelled	11.2	33	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
74	d1g2oa_	Alignment	not modelled	11.1	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
75	c3upsA_	Alignment	not modelled	11.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
76	c3quvB_	Alignment	not modelled	10.9	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
77	c3khsB_	Alignment	not modelled	10.8	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
78	d1v3va2	Alignment	not modelled	10.8	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
79	c2j66A_	Alignment	not modelled	10.7	45	**PDB header:**lyase **Chain:** A: **PDB Molecule:**btrk; **PDBTitle:** structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
80	c3ky7A_	Alignment	not modelled	10.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
81	c3e6eC_	Alignment	not modelled	10.6	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
82	d2fzwa2	Alignment	not modelled	10.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Alcohol dehydrogenase-like, C-terminal domain
83	d1p9pa_	Alignment	not modelled	10.5	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
84	c1ltlE_	Alignment	not modelled	10.4	22	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
85	c2equA_	Alignment	not modelled	10.4	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
86	c1tufA_	Alignment	not modelled	10.4	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
87	c3iefA_	Alignment	not modelled	10.3	22	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
88	c3ggsA_	Alignment	not modelled	10.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
89	c3mt1B_	Alignment	not modelled	10.2	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
90	c2p4sA_	Alignment	not modelled	10.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
91	d2fsqa1	Alignment	not modelled	10.0	6	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**Atu0111-like
92	d2hd3a1	Alignment	not modelled	10.0	33	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
93	d2qw7a1	Alignment	not modelled	9.9	24	**Fold:**OB-fold **Superfamily:**EutN/CcmL-like **Family:**EutN/CcmL-like
94	c3oo2A_	Alignment	not modelled	9.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
95	d2soba_	Alignment	not modelled	9.7	9	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
96	d1ltla_	Alignment	not modelled	9.6	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
97	d2nn6h1	Alignment	not modelled	9.5	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
98	c2opkC_	Alignment	not modelled	9.4	27	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
99	c2zkra_	Alignment	not modelled	9.4	25	**PDB header:**ribosomal protein/rna **Chain:** A: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map