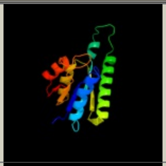
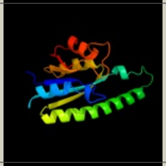
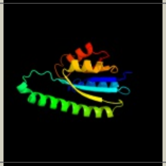
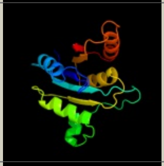
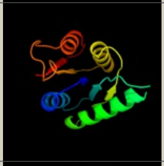
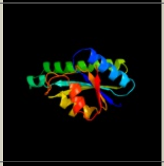
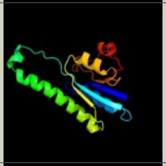
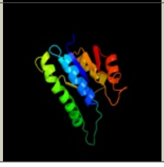
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P39177
Date	Thu Jan 5 11:58:24 GMT 2012
Unique Job ID	6a8a16253a1957c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hgmD_	Alignment		99.9	24	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
2	d1mjha_	Alignment		99.9	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
3	c3s3tD_	Alignment		99.9	22	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
4	c3dloC_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
5	d1jmva_	Alignment		99.9	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
6	c3fh0A_	Alignment		99.9	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative universal stress protein kpn_01444; **PDBTitle:** crystal structure of putative universal stress protein kpn_01444 -2 atpase
7	d2z3va1	Alignment		99.9	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
8	c3fg9B_	Alignment		99.9	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of universal stress protein uspa family; **PDBTitle:** the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
9	c2dumD_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
10	c3idfA_	Alignment		99.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
11	c2pfsA_	Alignment		99.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea

12	d2gm3a1	Alignment		99.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
13	d1tq8a_	Alignment		99.9	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
14	d1q77a_	Alignment		99.8	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
15	c3loqA_	Alignment		99.8	25	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
16	c3olqA_	Alignment		99.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein e; **PDBTitle:** the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
17	c3mt0A_	Alignment		99.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
18	c2jaxA_	Alignment		99.7	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein tb31.7; **PDBTitle:** universal stress protein rv2623 from mycobaterium2 tuberculosis
19	c3ab8B_	Alignment		99.6	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
20	d1g5qa_	Alignment		84.4	14	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
21	c2ejbA_	Alignment	not modelled	60.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
22	d2iela1	Alignment	not modelled	57.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
23	d1p3y1_	Alignment	not modelled	48.2	9	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
24	c3tvsA_	Alignment	not modelled	41.7	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome-1; **PDBTitle:** structure of full-length drosophila cryptochrome
25	c3qjgD_	Alignment	not modelled	41.2	6	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
26	c3zquA_	Alignment	not modelled	36.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
27	c2yxbA_	Alignment	not modelled	34.8	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
28	d1f0ka_	Alignment	not modelled	26.6	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG

29	c3lqkA_	Alignment	not modelled	26.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
30	c1a3wB_	Alignment	not modelled	19.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
31	c1pklB_	Alignment	not modelled	19.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
32	c3mcuF_	Alignment	not modelled	19.1	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dipicolinate synthase, b chain; **PDBTitle:** crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
33	c3dnfB_	Alignment	not modelled	18.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
34	c3a2kB_	Alignment	not modelled	18.7	16	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
35	c3e0vB_	Alignment	not modelled	18.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
36	d1wy5a1	Alignment	not modelled	18.0	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
37	d3clsc1	Alignment	not modelled	17.8	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
38	c1mvlA_	Alignment	not modelled	16.3	3	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
39	d1mvla_	Alignment	not modelled	16.3	3	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
40	d1t6aa_	Alignment	not modelled	15.1	28	**Fold:**TBP-like **Superfamily:**Rbstp2229 protein **Family:**Rbstp2229 protein
41	d1vbka1	Alignment	not modelled	14.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
42	c1t5aB_	Alignment	not modelled	14.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
43	c2vgbB_	Alignment	not modelled	13.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
44	d1lfda_	Alignment	not modelled	12.9	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
45	d1nu0a_	Alignment	not modelled	12.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
46	d1u11a_	Alignment	not modelled	11.9	18	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
47	d2dbsa1	Alignment	not modelled	11.6	32	**Fold:**TTHC002-like **Superfamily:**TTHC002-like **Family:**TTHC002-like
48	c2e21A_	Alignment	not modelled	11.3	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
49	c3g40A_	Alignment	not modelled	10.9	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**na-k-cl cotransporter; **PDBTitle:** crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
50	d1sbza_	Alignment	not modelled	10.5	15	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
51	c2fw9A_	Alignment	not modelled	10.5	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
52	c3ma8A_	Alignment	not modelled	10.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
						Fold: Flavodoxin-like

53	d1xmpa_	Alignment	not modelled	10.3	22	**Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
54	c3lp6D_	Alignment	not modelled	9.9	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
55	d1to6a_	Alignment	not modelled	9.2	19	**Fold:**Glycerate kinase I **Superfamily:**Glycerate kinase I **Family:**Glycerate kinase I
56	d1o4va_	Alignment	not modelled	9.1	18	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
57	c3orsD_	Alignment	not modelled	8.8	16	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
58	c1aqfB_	Alignment	not modelled	8.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
59	c3ke8A_	Alignment	not modelled	8.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
60	c3kh0A_	Alignment	not modelled	8.5	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ral guanine nucleotide dissociation stimulator; **PDBTitle:** crystal structure of the ras-association (ra) domain of2 ralgds
61	d1ulza2	Alignment	not modelled	8.3	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
62	c1ulzA_	Alignment	not modelled	8.2	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
63	d1efvb_	Alignment	not modelled	8.1	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
64	c1cf3A_	Alignment	not modelled	8.0	21	**PDB header:**oxidoreductase(flavoprotein) **Chain:** A: **PDB Molecule:**protein (glucose oxidase); **PDBTitle:** glucose oxidase from apergillus niger
65	c2wdfA_	Alignment	not modelled	8.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
66	c2ywxA_	Alignment	not modelled	7.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
67	c2pjuD_	Alignment	not modelled	7.8	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
68	c1ni5A_	Alignment	not modelled	7.8	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
69	d1o94c_	Alignment	not modelled	7.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
70	d1nmpa_	Alignment	not modelled	7.3	14	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
71	d2rgfa_	Alignment	not modelled	7.3	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
72	c2auhB_	Alignment	not modelled	7.2	11	**PDB header:**transferase/signaling protein **Chain:** B: **PDB Molecule:**growth factor receptor-bound protein 14; **PDBTitle:** crystal structure of the grb14 bps region in complex with2 the insulin receptor tyrosine kinase
73	d1qzua_	Alignment	not modelled	7.2	15	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
74	d1cf3a1	Alignment	not modelled	7.1	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
75	d2j9ga2	Alignment	not modelled	6.8	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
76	d2pjua1	Alignment	not modelled	6.7	11	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
						Fold: Adenine nucleotide alpha hydrolase-like

77	d1ni5a1	Alignment	not modelled	6.6	11	**Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
78	d1qcza_	Alignment	not modelled	6.6	22	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
79	d2b3aa1	Alignment	not modelled	6.6	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
80	c2nydB_	Alignment	not modelled	6.5	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
81	d2g0ta1	Alignment	not modelled	6.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
82	d1gpea1	Alignment	not modelled	6.1	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
83	d1ylqa1	Alignment	not modelled	5.9	24	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Catalytic subunit of bi-partite nucleotidyltransferase
84	d2a1fa1	Alignment	not modelled	5.7	12	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
85	c3cwcB_	Alignment	not modelled	5.6	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
86	d1qf6a1	Alignment	not modelled	5.6	14	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
87	d1vhxa_	Alignment	not modelled	5.5	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
88	d2j07a2	Alignment	not modelled	5.5	19	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
89	c1gpeA_	Alignment	not modelled	5.5	18	**PDB header:**oxidoreductase(flavoprotein) **Chain:** A: **PDB Molecule:**protein (glucose oxidase); **PDBTitle:** glucose oxidase from penicillium amagasakiense
90	d1rlfa_	Alignment	not modelled	5.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
91	c3khdC_	Alignment	not modelled	5.4	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
92	d1rvga_	Alignment	not modelled	5.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
93	c3u02C_	Alignment	not modelled	5.3	57	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative transcription-associated protein tfiis; **PDBTitle:** crystal structure of the trna modifier tias from pyrococcus furiosus,2 northeast structural genomics consortium target pfr225
94	d2hy5b1	Alignment	not modelled	5.3	13	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
95	d1vm6a3	Alignment	not modelled	5.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d1fmfa_	Alignment	not modelled	5.2	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain