Phyre^2

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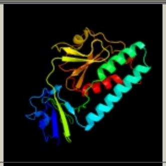
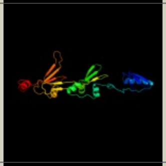
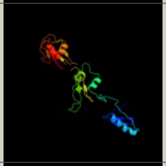
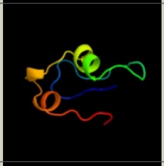
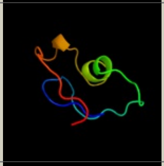
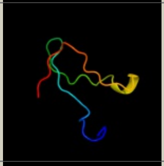
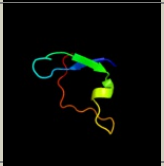
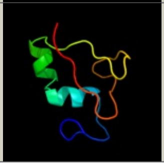
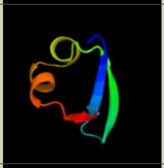
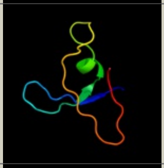
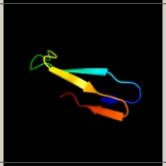
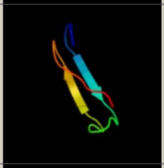
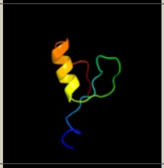
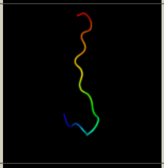
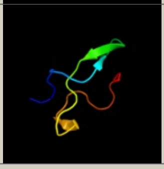
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p42D_	Alignment		100.0	43	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**predicted protein; **PDBTitle:** structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
2	c2j58G_	Alignment		99.6	18	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza; **PDBTitle:** the structure of wza
3	c2w8iG_	Alignment		99.5	17	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza; **PDBTitle:** crystal structure of wza24-345.
4	d2fug13	Alignment		77.6	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Nqo1 middle domain-like **Family:**Nqo1 middle domain-like
5	c2fugA_	Alignment		60.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
6	c3ixzA_	Alignment		59.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
7	c3b8eC_	Alignment		57.3	21	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
8	c3rfuC_	Alignment		51.0	17	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
9	c3ibmB_	Alignment		45.5	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
10	c2zxeA_	Alignment		44.8	21	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
11	d1rwsa_	Alignment		37.2	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS

12	c2vldA_	Alignment		35.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
13	c3j08A_	Alignment		34.5	36	**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
14	c2hc8A_	Alignment		33.4	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
15	d1lr5a_	Alignment		29.9	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
16	c3jzvA_	Alignment		29.4	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
17	c3b8cB_	Alignment		28.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
18	c2r32A_	Alignment		27.3	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
19	d1uika1	Alignment		26.7	6	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
20	c1mhsA_	Alignment		26.4	30	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
21	c2kytA_	Alignment	not modelled	26.1	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
22	c3kgzA_	Alignment	not modelled	26.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
23	d1d1la_	Alignment	not modelled	24.4	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
24	c3ff4A_	Alignment	not modelled	23.3	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
25	d1vj2a_	Alignment	not modelled	23.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
26	c2xdvA_	Alignment	not modelled	22.8	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
27	d1uija1	Alignment	not modelled	22.6	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
28	d1p9ka_	Alignment	not modelled	22.5	12	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
29	d2cu3a1	Alignment	not modelled	22.3	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS

						Family: ThiS
30	d3bu7a1	Alignment	not modelled	22.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
31	c3bu7A_	Alignment	not modelled	22.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure and biochemical characterization of gdosp,2 a gentisate 1,2-dioxygenase from silicibacter pomeroyi
32	c2vpvA_	Alignment	not modelled	22.0	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p
33	d2d40a1	Alignment	not modelled	21.8	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
34	c3s7eB_	Alignment	not modelled	21.2	11	**PDB header:**allergen **Chain:** B: **PDB Molecule:**allergen ara h 1, clone p41b; **PDBTitle:** crystal structure of ara h 1
35	d1sq4a_	Alignment	not modelled	21.2	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
36	d1dgwa_	Alignment	not modelled	21.2	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
37	d1uija2	Alignment	not modelled	20.8	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
38	d1y7ma2	Alignment	not modelled	20.0	4	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
39	d1b2pa_	Alignment	not modelled	19.8	23	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
40	c3kd4A_	Alignment	not modelled	19.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative protease; **PDBTitle:** crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
41	d1rc6a_	Alignment	not modelled	19.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
42	d1uika2	Alignment	not modelled	19.0	9	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
43	c3c3vA_	Alignment	not modelled	18.9	14	**PDB header:**allergen **Chain:** A: **PDB Molecule:**arachin arah3 isoform; **PDBTitle:** crystal structure of peanut major allergen ara h 3
44	c3cewA_	Alignment	not modelled	18.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
45	d1fxza2	Alignment	not modelled	18.3	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
46	d1j58a_	Alignment	not modelled	17.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
47	d1od5a2	Alignment	not modelled	17.2	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
48	d1dlpa1	Alignment	not modelled	17.1	22	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
49	c2cauA_	Alignment	not modelled	17.1	9	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**protein (canavalin); **PDBTitle:** canavalin from jack bean
50	c3k2oB_	Alignment	not modelled	16.3	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
51	c2d40C_	Alignment	not modelled	16.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative gentisate 1,2-dioxygenase; **PDBTitle:** crystal structure of z3393 from escherichia coli o157:h7
52	c3dwmA_	Alignment	not modelled	16.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
53	d1vrba1	Alignment	not modelled	16.0	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
54	d4croa_	Alignment	not modelled	16.0	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
55	c2oa2A_	Alignment	not modelled	15.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2720 protein; **PDBTitle:** crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
56	c3mezA_	Alignment	not modelled	15.4	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**mannose-specific lectin 3 chain 1; **PDBTitle:** x-ray structural analysis of a mannose specific lectin

						from dutch2 crocus (crocus vernus)
57	c3j09A_	Alignment	not modelled	15.3	36	**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
58	c2q30C_	Alignment	not modelled	15.1	10	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
59	c2kijA_	Alignment	not modelled	14.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
60	c3cwiA_	Alignment	not modelled	14.8	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
61	d2phda1	Alignment	not modelled	14.3	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
62	d1sfna_	Alignment	not modelled	14.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
63	c1fxzC_	Alignment	not modelled	14.1	14	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
64	c1sefA_	Alignment	not modelled	14.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of cupin domain protein ef2996 from enterococcus2 faecalis
65	d1sefa_	Alignment	not modelled	14.0	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
66	c2oh2B_	Alignment	not modelled	13.6	13	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
67	d1a6fa_	Alignment	not modelled	13.1	6	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
68	d1h9ma1	Alignment	not modelled	12.9	16	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
69	c2e9qA_	Alignment	not modelled	12.8	12	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
70	c1uijA_	Alignment	not modelled	12.7	5	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**beta subunit of beta conglycinin; **PDBTitle:** crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
71	c1h9mB_	Alignment	not modelled	12.7	16	**PDB header:**binding protein **Chain:** B: **PDB Molecule:**molybdenum-binding-protein; **PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
72	c1cauB_	Alignment	not modelled	12.1	15	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
73	c3ehkC_	Alignment	not modelled	11.9	18	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**prunin; **PDBTitle:** crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
74	c2oqkA_	Alignment	not modelled	11.9	25	**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
75	c3kglB_	Alignment	not modelled	11.9	8	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
76	c2vqaC_	Alignment	not modelled	11.5	12	**PDB header:**metal-binding protein **Chain:** C: **PDB Molecule:**sll1358 protein; **PDBTitle:** protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.
77	c3h7yA_	Alignment	not modelled	11.5	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**bacilysin biosynthesis protein bacb; **PDBTitle:** crystal structure of bacb, an enzyme involved in bacilysin synthesis,2 in tetragonal form
78	d1zrra1	Alignment	not modelled	11.5	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
79	c3al6A_	Alignment	not modelled	11.3	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
80	c3kscD_	Alignment	not modelled	11.3	16	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
81	c1ue7A_	Alignment	not modelled	11.3	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
						PDB header:metal binding protein

82	c3d82A_	Alignment	not modelled	11.2	7	**Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
83	d1guta_	Alignment	not modelled	11.2	7	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
84	c2pfwB_	Alignment	not modelled	11.1	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
85	d1h2ka_	Alignment	not modelled	11.0	30	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
86	c2kl0A_	Alignment	not modelled	11.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
87	d1d6ta_	Alignment	not modelled	11.0	12	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**RNase P protein
88	c3uyjA_	Alignment	not modelled	10.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
89	c2pijB_	Alignment	not modelled	10.7	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
90	d1hr0w_	Alignment	not modelled	10.7	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
91	d1ah9a_	Alignment	not modelled	10.7	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	c2hj1A_	Alignment	not modelled	10.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
93	d2hj1a1	Alignment	not modelled	10.6	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
94	c2i45C_	Alignment	not modelled	10.6	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
95	d2arca_	Alignment	not modelled	10.6	21	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
96	c2opkC_	Alignment	not modelled	10.6	13	**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
97	c2gu9B_	Alignment	not modelled	10.5	25	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
98	d1hyoa2	Alignment	not modelled	10.5	14	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
99	c1kskA_	Alignment	not modelled	10.4	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua