Phyre^2

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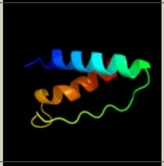
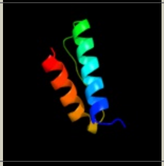
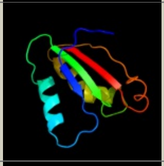
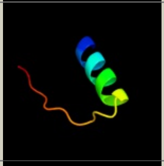
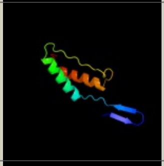
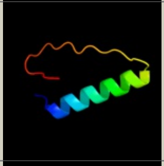
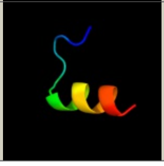
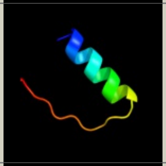
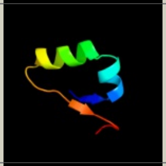
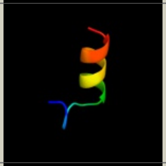
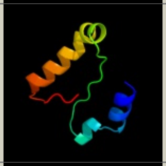
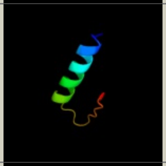
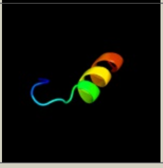
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qd7X_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
2	c2zqeA_	Alignment		99.9	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
3	d2d9ia1	Alignment		99.7	19	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain
4	c2vkcA_	Alignment		99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nedd4-binding protein 2; **PDBTitle:** solution structure of the b3bp smr domain
5	c3no4A_	Alignment		66.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
6	d1v7za_	Alignment		66.5	10	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
7	d1jdqa_	Alignment		50.8	11	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
8	c2fmoA_	Alignment		43.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methylenetetrahydrofolate reductase; **PDBTitle:** ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
9	c1x0lB_	Alignment		38.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoisocitrate dehydrogenase; **PDBTitle:** crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
10	c3lubE_	Alignment		36.6	16	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
11	d1pyya2	Alignment		35.9	6	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain

12	d1b5ta_	Alignment		35.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
13	d1v93a_	Alignment		33.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
14	d2odka1	Alignment		33.1	12	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
15	d2obba1	Alignment		31.3	3	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
16	d1k25a2	Alignment		30.7	6	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
17	c3ouvA_	Alignment		29.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase; **PDBTitle:** semet derivative of l512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb
18	d1d3ya_	Alignment		26.7	15	**Fold:**DNA topoisomerase IV, alpha subunit **Superfamily:**DNA topoisomerase IV, alpha subunit **Family:**DNA topoisomerase IV, alpha subunit
19	c3e0jF_	Alignment		26.2	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna polymerase subunit delta-3; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
20	d1rp5a2	Alignment		24.9	6	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
21	d1xpja_	Alignment	not modelled	24.7	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
22	c3fmxX_	Alignment	not modelled	24.5	6	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**tartrate dehydrogenase/decarboxylase; **PDBTitle:** crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
23	d2a6qb1	Alignment	not modelled	23.8	15	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
24	c3fdjA_	Alignment	not modelled	23.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.
25	c2q2eA_	Alignment	not modelled	21.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type ii dna topoisomerase vi subunit a; **PDBTitle:** crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
26	c3aysA_	Alignment	not modelled	21.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose
27	d1dcja_	Alignment	not modelled	20.9	15	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
28	c3e0fA_	Alignment	not modelled	20.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphoesterase; **PDBTitle:** crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis

						atcc 15703 at 2.40 a3 resolution
29	d2c0ha1	Alignment	not modelled	20.3	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
30	c3blxL_	Alignment	not modelled	20.0	12	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 2; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
31	d2c2la2	Alignment	not modelled	18.8	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
32	c3pzqA_	Alignment	not modelled	18.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family **PDBTitle:** structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
33	d1r57a_	Alignment	not modelled	18.0	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
34	c3k5wA_	Alignment	not modelled	17.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
35	c2odkD_	Alignment	not modelled	16.9	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
36	d1m65a_	Alignment	not modelled	16.1	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
37	c1mwoA_	Alignment	not modelled	15.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
38	c1jdaA_	Alignment	not modelled	15.4	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
39	c2g7zB_	Alignment	not modelled	15.2	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
40	d1e43a2	Alignment	not modelled	14.9	5	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	c1bplA_	Alignment	not modelled	14.8	10	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
42	c1m7xC_	Alignment	not modelled	14.8	37	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
43	c2wjeA_	Alignment	not modelled	14.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
44	d1pava_	Alignment	not modelled	14.4	8	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
45	c1jaeA_	Alignment	not modelled	14.2	10	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
46	d1g8fa3	Alignment	not modelled	14.0	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
47	c3ndyA_	Alignment	not modelled	13.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase d; **PDBTitle:** the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
48	c2zbkA_	Alignment	not modelled	13.6	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**type ii dna topoisomerase vi subunit a; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
49	c3mmwB_	Alignment	not modelled	13.5	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
50	d1hx0a2	Alignment	not modelled	13.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	c3ll4B_	Alignment	not modelled	13.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ykr043c; **PDBTitle:** structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
52	c2ns6A_	Alignment	not modelled	13.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
53	d1gcya2	Alignment	not modelled	12.6	5	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
54	d1vjza_	Alignment	not modelled	12.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases

55	d1ceoa_	Alignment	not modelled	12.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
56	d1avaa2	Alignment	not modelled	12.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
57	d3dhpa2	Alignment	not modelled	12.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
58	c1jd7A_	Alignment	not modelled	12.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
59	d1gjwa2	Alignment	not modelled	12.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	c1bagA_	Alignment	not modelled	11.9	10	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
61	c2kueA_	Alignment	not modelled	11.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase pknb; **PDBTitle:** nmr structure of the pasta domain 2 and 3 of mycobacterium2 tuberculosis of pknb
62	c3k35D_	Alignment	not modelled	11.8	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
63	c3eozB_	Alignment	not modelled	11.6	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
64	d2csba1	Alignment	not modelled	11.4	6	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
65	c1q14A_	Alignment	not modelled	11.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
66	c3icgD_	Alignment	not modelled	11.1	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
67	c3m07A_	Alignment	not modelled	11.1	37	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative alpha amylase; **PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
68	c2kudA_	Alignment	not modelled	10.9	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase pknb; **PDBTitle:** nmr structure of the pasta domain 1 and 2 of mycobacterium2 tuberculosis of pknb
69	d1g94a2	Alignment	not modelled	10.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	c3qy6A_	Alignment	not modelled	10.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase ywqe; **PDBTitle:** crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
71	c3blpX_	Alignment	not modelled	10.7	10	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
72	d1jaea2	Alignment	not modelled	10.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	d2gjpa2	Alignment	not modelled	10.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	c1wpcA_	Alignment	not modelled	10.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
75	c1qhoA_	Alignment	not modelled	10.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
76	c2yb1A_	Alignment	not modelled	10.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
77	c2zc3F_	Alignment	not modelled	10.4	0	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**penicillin-binding protein 2x; **PDBTitle:** penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae
78	d1m7xa3	Alignment	not modelled	10.3	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
79	c3jugA_	Alignment	not modelled	10.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-mannanase; **PDBTitle:** crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
80	c2x4bA_	Alignment	not modelled	10.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin

81	d1ua7a2	Alignment	not modelled	10.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	d1ob0a2	Alignment	not modelled	10.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
83	c2ya0A_	Alignment	not modelled	10.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
84	c1ehaA_	Alignment	not modelled	10.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
85	c3lupA_	Alignment	not modelled	9.9	19	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
86	d2isba1	Alignment	not modelled	9.9	31	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
87	c3amlA_	Alignment	not modelled	9.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
88	c3bmwA_	Alignment	not modelled	9.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
89	d1uf3a_	Alignment	not modelled	9.6	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
90	c1cygA_	Alignment	not modelled	9.4	15	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
91	d1cyga4	Alignment	not modelled	9.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	d1bqca_	Alignment	not modelled	9.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
93	c1bf2A_	Alignment	not modelled	9.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
94	d1ltqa1	Alignment	not modelled	9.3	8	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
95	d2pb1a1	Alignment	not modelled	9.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
96	d2a6qa1	Alignment	not modelled	9.2	15	**Fold:**YefM-like **Superfamily:**YefM-like **Family:**YefM-like
97	d1uuqa_	Alignment	not modelled	9.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
98	c1uz4A_	Alignment	not modelled	9.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
99	d1mxga2	Alignment	not modelled	9.1	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain