Phyre^2

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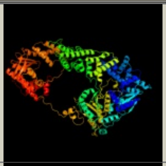
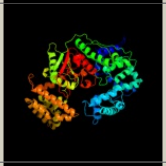
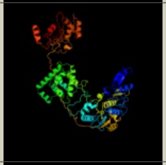
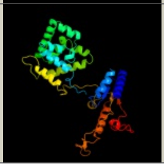
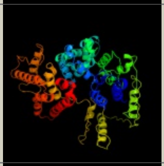
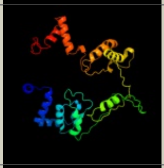
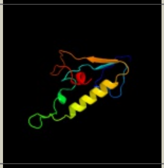
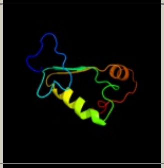
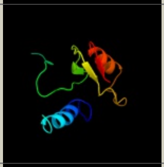
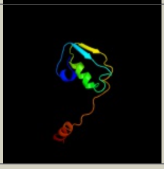
Description	P07648
Date	Thu Jan 5 11:00:26 GMT 2012
Unique Job ID	ca5204c70eaf15db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w36F_	Alignment		100.0	100	**PDB header:**recombination **Chain:** F: **PDB Molecule:**exodeoxyribonuclease v gamma chain; **PDBTitle:** recbcd:dna complex
2	d1w36c2	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
3	d1w36c1	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
4	d1w36c3	Alignment		100.0	100	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Exodeoxyribonuclease V beta chain (RecC), C-terminal domain
5	d1uaaa2	Alignment		100.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
6	c2is6B_	Alignment		100.0	15	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of uvrd-dna-adpmgf3 ternary complex
7	c1uaaB_	Alignment		100.0	14	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (atp-dependent dna helicase rep.); **PDBTitle:** e. coli rep helicase/dna complex
8	d1pjra2	Alignment		100.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
9	c1w36E_	Alignment		100.0	13	**PDB header:**recombination **Chain:** E: **PDB Molecule:**exodeoxyribonuclease v beta chain; **PDBTitle:** recbcd:dna complex
10	c3lfuA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase ii; **PDBTitle:** crystal structure of e. coli uvrd
11	d1w36b2	Alignment		99.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain

12	c1pjrA_	Alignment		99.9	13	**PDB header:**helicase **Chain:** A: **PDB Molecule:**pcra; **PDBTitle:** structure of dna helicase
13	c2pjrF_	Alignment		99.8	13	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
14	c1qhhB_	Alignment		99.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
15	c2pjrB_	Alignment		99.2	23	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
16	c1qhhD_	Alignment		99.1	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
17	c3dmnA_	Alignment		98.7	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dna helicase; **PDBTitle:** the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
18	d1w36d2	Alignment		98.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
19	c1w36G_	Alignment		95.3	18	**PDB header:**recombination **Chain:** G: **PDB Molecule:**exodeoxyribonuclease v alpha chain; **PDBTitle:** recbcd:dna complex
20	c3e1sA_	Alignment		94.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
21	c2gk7A_	Alignment	not modelled	91.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** structural and functional insights into the human upf1 helicase core
22	c2xzlA_	Alignment	not modelled	82.6	17	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
23	c2wjyA_	Alignment	not modelled	74.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
24	d1zrra1	Alignment	not modelled	61.8	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
25	d1vr3a1	Alignment	not modelled	61.2	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
26	c2l2qA_	Alignment	not modelled	56.1	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
27	d1vzva_	Alignment	not modelled	51.0	17	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
						PDB header:transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc

28	c3nbmA_	Alignment	not modelled	39.5	11	components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
29	c3h4rA_	Alignment	not modelled	30.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease 8; **PDBTitle:** crystal structure of e. coli rece exonuclease
30	d1at3a_	Alignment	not modelled	30.5	19	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
31	d1etea_	Alignment	not modelled	30.0	21	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
32	c3nctC_	Alignment	not modelled	19.8	22	**PDB header:**dna binding protein, chaperone **Chain:** C: **PDB Molecule:**protein psib; **PDBTitle:** x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
33	d1wnaa1	Alignment	not modelled	19.5	28	**Fold:**TTHA1528-like **Superfamily:**TTHA1528-like **Family:**TTHA1528-like
34	c1qhhA_	Alignment	not modelled	18.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
35	d1t1ea2	Alignment	not modelled	17.2	17	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
36	d2o8ra3	Alignment	not modelled	15.4	11	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
37	d1l5wa_	Alignment	not modelled	14.8	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
38	d1p2fa1	Alignment	not modelled	14.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
39	c3edyA_	Alignment	not modelled	14.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure of the precursor form of human tripeptidyl-peptidase2 1
40	c3l0aA_	Alignment	not modelled	14.3	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative exonuclease; **PDBTitle:** crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
41	d2bcqa3	Alignment	not modelled	14.2	15	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
42	c1eg4A_	Alignment	not modelled	13.6	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**dystrophin; **PDBTitle:** structure of a dystrophin ww domain fragment in complex2 with a beta-dystroglycan peptide
43	c1dipA_	Alignment	not modelled	12.4	29	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
44	d2cfua2	Alignment	not modelled	11.5	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
45	d2vo9a1	Alignment	not modelled	11.4	16	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanY-like
46	c1oywA_	Alignment	not modelled	11.2	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
47	c2zxxA_	Alignment	not modelled	11.2	29	**PDB header:**cell cycle/replication **Chain:** A: **PDB Molecule:**geminin; **PDBTitle:** crystal structure of cdt1/geminin complex
48	d2h5na1	Alignment	not modelled	11.0	21	**Fold:**TerB-like **Superfamily:**TerB-like **Family:**PG1108-like
49	d1x52a1	Alignment	not modelled	10.9	33	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
50	d2guka1	Alignment	not modelled	10.5	13	**Fold:**PG1857-like **Superfamily:**PG1857-like **Family:**PG1857-like
51	d1pjqa3	Alignment	not modelled	10.5	12	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
52	d1lb2b_	Alignment	not modelled	10.4	14	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
53	d1oywa2	Alignment	not modelled	10.2	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
54	c2vo9C_	Alignment	not modelled	10.1	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**l-alanyl-d-glutamate peptidase; **PDBTitle:** crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500

55	c3qy9C_	Alignment	not modelled	10.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** the crystal structure of dihydrodipicolinate reductase from2 staphylococcus aureus
56	d1pjra1	Alignment	not modelled	10.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
57	d1iiba_	Alignment	not modelled	9.9	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
58	c3dmqA_	Alignment	not modelled	9.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna polymerase-associated protein rapa; **PDBTitle:** crystal structure of rapa, a swi2/snf2 protein that2 recycles rna polymerase during transcription
59	c2v1xB_	Alignment	not modelled	9.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
60	c3agjD_	Alignment	not modelled	9.4	20	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
61	c3agjB_	Alignment	not modelled	9.4	20	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
62	d1tdja3	Alignment	not modelled	9.4	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
63	c1vjqB_	Alignment	not modelled	9.3	20	**PDB header:**structural genomics, de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
64	c2d1uA_	Alignment	not modelled	9.2	26	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution strcuture of the periplasmic signaling domain of2 feca from escherichia coli
65	c1w5cT_	Alignment	not modelled	9.0	23	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**cytochrome c-550; **PDBTitle:** photosystem ii from thermosynechococcus elongatus
66	d1dt9a3	Alignment	not modelled	9.0	13	**Fold:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Superfamily:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Family:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
67	d2gj4a1	Alignment	not modelled	8.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
68	d2vgna3	Alignment	not modelled	8.9	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
69	c3i7tA_	Alignment	not modelled	8.7	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
70	d1qzma_	Alignment	not modelled	8.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
71	c3ijpA_	Alignment	not modelled	8.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
72	c2cfuA_	Alignment	not modelled	8.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
73	c2wvrB_	Alignment	not modelled	8.4	29	**PDB header:**replication **Chain:** B: **PDB Molecule:**geminin; **PDBTitle:** human cdt1:geminin complex
74	d1v6ta_	Alignment	not modelled	8.4	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
75	c3ddsB_	Alignment	not modelled	8.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form; **PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
76	d1kgsa1	Alignment	not modelled	8.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
77	c2pmuD_	Alignment	not modelled	8.0	14	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
78	c1t1eA_	Alignment	not modelled	7.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**kumamolisin; **PDBTitle:** high resolution crystal structure of the intact pro-2 kumamolisin, a sedolisin type proteinase (previously3 called kumamolysin or kscp)
79	c3ee6A_	Alignment	not modelled	7.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure analysis of tripeptidyl peptidase -i

80	d2fcla1	Alignment	not modelled	7.7	19	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**TM1012-like
81	c3e20C_	Alignment	not modelled	7.7	12	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
82	d2pbka1	Alignment	not modelled	7.6	26	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
83	c2o8rA_	Alignment	not modelled	7.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
84	c3lmeE_	Alignment	not modelled	7.5	24	**PDB header:**translation **Chain:** E: **PDB Molecule:**possible translation initiation inhibitor; **PDBTitle:** structure of probable translation initiation inhibitor from2 (rpa2473) from rhodopseudomonas palustris
85	d1vm6a3	Alignment	not modelled	7.4	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
86	c1p65A_	Alignment	not modelled	7.3	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** crystal structure of the nucleocapsid protein of porcine reproductive2 and respiratory syndrome virus (prrsv)
87	d1p65a_	Alignment	not modelled	7.3	24	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Arterivirus nucleocapsid protein
88	d2aala1	Alignment	not modelled	7.2	20	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
89	d1nrga_	Alignment	not modelled	6.9	12	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
90	c1nrgA_	Alignment	not modelled	6.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate oxidase; **PDBTitle:** structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
91	d1mz4a_	Alignment	not modelled	6.8	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
92	d1cooa_	Alignment	not modelled	6.7	13	**Fold:**SAM domain-like **Superfamily:**C-terminal domain of RNA polymerase alpha subunit **Family:**C-terminal domain of RNA polymerase alpha subunit
93	c1um9D_	Alignment	not modelled	6.7	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**2-oxo acid dehydrogenase beta subunit; **PDBTitle:** branched-chain 2-oxo acid dehydrogenase (e1) from thermus2 thermophilus hb8 in apo-form
94	c2vgmA_	Alignment	not modelled	6.7	27	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dom34; **PDBTitle:** structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
95	d2ns0a1	Alignment	not modelled	6.7	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RHA1 ro06458-like
96	c2ph0A_	Alignment	not modelled	6.7	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q6d2t7_erwct protein from erwinia2 carotovora. nesg target ewr41.
97	c1xdoB_	Alignment	not modelled	6.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
98	c2qrvC_	Alignment	not modelled	6.6	14	**PDB header:**transferase/transferase regulator **Chain:** C: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3-like; **PDBTitle:** structure of dnmt3a-dnmt3l c-terminal domain complex
99	d1uaaa1	Alignment	not modelled	6.6	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain