Phyre^2

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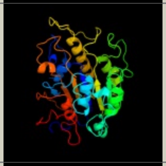
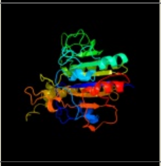
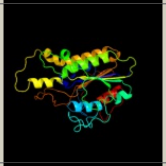
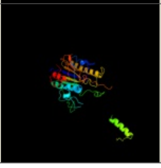
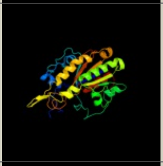
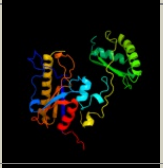
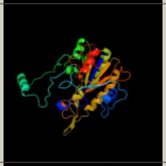
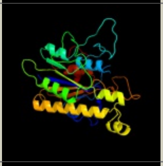
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w5tA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
2	c2w8dB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid synthase 2; **PDBTitle:** distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis
3	c3lxqB_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
4	d1fsua_	Alignment		100.0	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
5	c3ed4A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
6	c2qzuA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
7	d1auka_	Alignment		100.0	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
8	d1hdha_	Alignment		100.0	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
9	c2vqrA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase; **PDBTitle:** crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
10	c3b5qB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
11	d1p49a_	Alignment		100.0	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase

12	d1o98a2	Alignment		100.0	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
13	d2i09a1	Alignment		99.9	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
14	c2zktB_	Alignment		99.9	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
15	c3m8yC_	Alignment		99.9	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
16	c2gsoB_	Alignment		99.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
17	c3q3qA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
18	c2i09A_	Alignment		99.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
19	c2xr9A_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
20	c2xrgA_	Alignment		99.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
21	c3szzA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
22	d1ei6a_	Alignment	not modelled	99.5	11	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
23	c1o98A_	Alignment	not modelled	99.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
24	c3igzB_	Alignment	not modelled	99.1	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
25	c2d1gB_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
26	c2iucB_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	d1y6va1	Alignment	not modelled	98.8	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
28	c3a52A_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.

29	c2w0yB_	Alignment	not modelled	98.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
30	c2x98A_	Alignment	not modelled	98.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
31	c3e2dB_	Alignment	not modelled	98.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
32	d1zeda1	Alignment	not modelled	98.4	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
33	c1ew2A_	Alignment	not modelled	98.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
34	d1k7ha_	Alignment	not modelled	98.3	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
35	c3iddA_	Alignment	not modelled	54.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	d3sila_	Alignment	not modelled	31.5	33	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
37	c3pr9A_	Alignment	not modelled	30.8	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
38	c2kr7A_	Alignment	not modelled	27.3	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
39	d1b4ub_	Alignment	not modelled	23.3	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
40	c2kfwA_	Alignment	not modelled	22.3	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
41	d1ix5a_	Alignment	not modelled	20.7	35	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
42	c3bh2C_	Alignment	not modelled	20.4	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**acetoacetate decarboxylase; **PDBTitle:** structural studies of acetoacetate decarboxylase
43	c2xoaA_	Alignment	not modelled	17.7	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
44	c2o1sC_	Alignment	not modelled	16.4	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate synthase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
45	c3g8lD_	Alignment	not modelled	15.5	10	**PDB header:**immune system **Chain:** D: **PDB Molecule:**lectin-related nk cell receptor ly49l1; **PDBTitle:** crystal structure of murine natural killer cell receptor,2 ly49l4
46	c3ippA_	Alignment	not modelled	15.3	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
47	d2z1aa2	Alignment	not modelled	14.2	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
48	c3prdA_	Alignment	not modelled	14.0	25	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
49	d2jn4a1	Alignment	not modelled	13.8	13	**Fold:**NifT/FixU barrel-like **Superfamily:**NifT/FixU-like **Family:**NifT/FixU
50	c2jn4A_	Alignment	not modelled	13.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein fixu, nift; **PDBTitle:** solution nmr structure of protein rp4601 from2 rhodopseudomonas palustris. northeast structural genomics3 consortium target rpt2; ontario center for structural4 proteomics target rp4601.
51	d2bdea1	Alignment	not modelled	13.4	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**5' nucleotidase-like
52	c2qy1B_	Alignment	not modelled	13.3	43	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pectate lyase ii; **PDBTitle:** pectate lyase a31g/r236f from xanthomonas campestris
53	c2jtqA_	Alignment	not modelled	13.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
54	c2k8iA_	Alignment	not modelled	12.8	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase;

						PDBTitle: solution structure of e.coli slyd
55	d2hkja2	Alignment	not modelled	12.7	5	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
56	d1v4aa2	Alignment	not modelled	12.5	40	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GlnE-like domain
57	c2vbeA_	Alignment	not modelled	12.5	36	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike-protein; **PDBTitle:** tailspike protein of bacteriophage sf6
58	c3o2qB_	Alignment	not modelled	12.5	53	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
59	c3o2sB_	Alignment	not modelled	12.3	53	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
60	d2g50a3	Alignment	not modelled	11.7	31	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
61	d2r6gf1	Alignment	not modelled	11.5	19	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
62	c3bgtD_	Alignment	not modelled	11.3	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable acetoacetate decarboxylase; **PDBTitle:** structural studies of acetoacetate decarboxylase
63	c1okgA_	Alignment	not modelled	11.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
64	c3lmyA_	Alignment	not modelled	10.8	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase subunit beta; **PDBTitle:** the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
65	d1xo1a2	Alignment	not modelled	10.8	20	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
66	c2o30A_	Alignment	not modelled	10.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nuclear movement protein; **PDBTitle:** nuclear movement protein from e. cuniculi gb-m1
67	d1usha2	Alignment	not modelled	10.6	10	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
68	c2vk7A_	Alignment	not modelled	10.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-alpha-sialidase; **PDBTitle:** the structure of clostridium perfringens nani sialidase and2 its catalytic intermediates
69	d1pe9a_	Alignment	not modelled	10.2	43	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
70	d2nxfa1	Alignment	not modelled	10.1	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
71	c2ihnA_	Alignment	not modelled	10.1	14	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
72	d1a3xa3	Alignment	not modelled	10.0	23	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
73	d1pcla_	Alignment	not modelled	9.9	57	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
74	d1qhma_	Alignment	not modelled	9.9	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
75	c2oslP_	Alignment	not modelled	9.8	22	**PDB header:**immune system **Chain:** P: **PDB Molecule:**b-lymphocyte antigen cd20; **PDBTitle:** crystal structure of rituximab fab in complex with an2 epitope peptide
76	c3cgnA_	Alignment	not modelled	9.8	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
77	d2cnza1	Alignment	not modelled	9.6	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
78	d2co3a1	Alignment	not modelled	9.5	21	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
79	c3k7dA_	Alignment	not modelled	9.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate-ammonia-ligase adenylyltransferase; **PDBTitle:** c-terminal (adenylylation) domain of e.coli glutamine synthetase2 adenylyltransferase
80	d1g0da1	Alignment	not modelled	9.2	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain

81	d1tfra2	Alignment	not modelled	9.2	24	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
82	c2xmoB_	Alignment	not modelled	9.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
83	d1fx0a3	Alignment	not modelled	8.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
84	c2v4oB_	Alignment	not modelled	8.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
85	c2qfaC_	Alignment	not modelled	8.7	31	**PDB header:**cell cycle/cell cycle/cell cycle **Chain:** C: **PDB Molecule:**inner centromere protein; **PDBTitle:** crystal structure of a survivin-borealin-incenp core complex
86	c1oftC_	Alignment	not modelled	8.4	17	**PDB header:**bacterial cell division inhibitor **Chain:** C: **PDB Molecule:**hypothetical protein pa3008; **PDBTitle:** crystal structure of sula from pseudomonas aeruginosa
87	c2oslQ_	Alignment	not modelled	8.3	24	**PDB header:**immune system **Chain:** Q: **PDB Molecule:**b-lymphocyte antigen cd20; **PDBTitle:** crystal structure of rituximab fab in complex with an2 epitope peptide
88	c2rhqA_	Alignment	not modelled	8.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase alpha chain; **PDBTitle:** phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
89	d2nvpa1	Alignment	not modelled	8.1	13	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
90	c2jcmA_	Alignment	not modelled	8.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic purine 5'-nucleotidase; **PDBTitle:** crystal structure of human cytosolic 5'-nucleotidase ii in2 complex with beryllium trifluoride
91	d1idka_	Alignment	not modelled	7.9	43	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectin lyase
92	d1okga1	Alignment	not modelled	7.9	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
93	c1vblA_	Alignment	not modelled	7.8	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase 47; **PDBTitle:** structure of the thermostable pectate lyase pl 47
94	c2kyaA_	Alignment	not modelled	7.8	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**patellamide protein; **PDBTitle:** solution structure of the leader sequence of the patellamide precursor2 peptide, pate1-34
95	c2zxeB_	Alignment	not modelled	7.8	25	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**na+,k+-atpase beta subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
96	d1skyb3	Alignment	not modelled	7.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
97	d2nuja1	Alignment	not modelled	7.7	7	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**4HBT-like
98	c3d1pA_	Alignment	not modelled	7.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase yor285w; **PDBTitle:** atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
99	d1ofua2	Alignment	not modelled	7.6	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain