Phyre2

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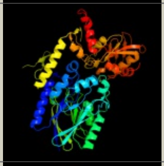
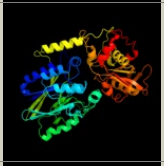
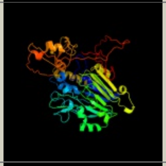
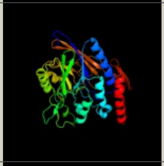
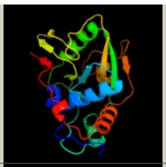
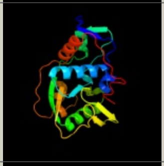
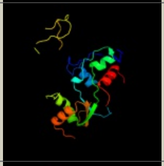
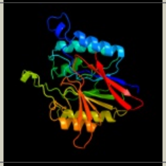
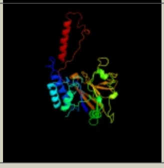
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1oidA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
2	c2z1aA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
3	c2wdfA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
4	c3zu0A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
5	c3ivdA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotidase; **PDBTitle:** putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
6	c3qfkA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
7	c3c9fB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
8	c3jyfB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- **PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
9	d1usha2	Alignment		100.0	100	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
10	c3gveB_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
11	d2z1aa2	Alignment		100.0	29	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain

12	d1usha1	Alignment		100.0	100	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
13	d3c9fa2	Alignment		100.0	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
14	d2z1aa1	Alignment		100.0	33	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
15	d1t71a_	Alignment		100.0	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
16	d1t70a_	Alignment		100.0	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
17	d2z06a1	Alignment		99.9	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
18	d3c9fa1	Alignment		99.9	10	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
19	c2xmoB_	Alignment		99.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
20	c3t1iC_	Alignment		99.6	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
21	c3ib7A_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
22	d1ii7a_	Alignment	not modelled	99.5	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
23	c3qg5D_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
24	c3av0A_	Alignment	not modelled	99.5	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
25	d2yvta1	Alignment	not modelled	99.4	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
26	c3auzA_	Alignment	not modelled	99.4	14	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
27	d1utea_	Alignment	not modelled	99.4	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
28	d1uf3a_	Alignment	not modelled	99.4	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
29	c2q8uA_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative;

29	c2q8dA_	Alignment	not modelled	99.4	15	**PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
30	d1qhwa_	Alignment	not modelled	99.3	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
31	c1qhwA_	Alignment	not modelled	99.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (purple acid phosphatase); **PDBTitle:** purple acid phosphatase from rat bone
32	c1kbpB_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase (phosphoric monoester) **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** kidney bean purple acid phosphatase
33	c1xzwB_	Alignment	not modelled	99.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** sweet potato purple acid phosphatase/phosphate complex
34	d2qfra2	Alignment	not modelled	99.3	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
35	d1xzwa2	Alignment	not modelled	99.3	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
36	d3d03a1	Alignment	not modelled	99.2	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
37	d2nxfa1	Alignment	not modelled	99.2	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
38	d2hy1a1	Alignment	not modelled	99.0	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
39	c2hy1A_	Alignment	not modelled	99.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
40	d1s3la_	Alignment	not modelled	98.9	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
41	c1s3mA_	Alignment	not modelled	98.9	22	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
42	c3rl4A_	Alignment	not modelled	98.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
43	c3qfnA_	Alignment	not modelled	98.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
44	d1su1a_	Alignment	not modelled	98.6	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
45	c1su1A_	Alignment	not modelled	98.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
46	d2a22a1	Alignment	not modelled	98.6	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
47	c2kknA_	Alignment	not modelled	98.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of thermotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
48	d1z2wa1	Alignment	not modelled	98.6	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
49	d1xm7a_	Alignment	not modelled	98.5	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
50	d1nnwa_	Alignment	not modelled	98.4	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Phosphoesterase-related
51	d3ck2a1	Alignment	not modelled	98.4	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
52	c3rqzC_	Alignment	not modelled	98.3	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
53	c2dfjA_	Alignment	not modelled	97.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
54	c2qjcA_	Alignment	not modelled	96.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase
55	c2zbmA_	Alignment	not modelled	96.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase; **PDBTitle:** crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
						Fold: Metallo-dependent phosphatases

56	d1g5ba_	Alignment	not modelled	96.0	24	**Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
57	c3icfB_	Alignment	not modelled	93.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase t; **PDBTitle:** structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
58	d3c5wc1	Alignment	not modelled	93.0	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
59	d1s70a_	Alignment	not modelled	92.9	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
60	d1s95a_	Alignment	not modelled	92.8	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
61	d1jk7a_	Alignment	not modelled	92.6	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
62	c1wao4_	Alignment	not modelled	91.1	22	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
63	c2jogA_	Alignment	not modelled	91.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
64	c1auiA_	Alignment	not modelled	87.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b; **PDBTitle:** human calcineurin heterodimer
65	d1auia_	Alignment	not modelled	87.3	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
66	d2p6ba1	Alignment	not modelled	86.2	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
67	c2p6bC_	Alignment	not modelled	83.8	20	**PDB header:**hydrolase/hydrolase regulator **Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide
68	d1vp8a_	Alignment	not modelled	39.6	19	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
69	c2eq5D_	Alignment	not modelled	39.6	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
70	d1ptma_	Alignment	not modelled	30.2	21	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
71	c3t0pB_	Alignment	not modelled	29.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii, beta subunit; **PDBTitle:** crystal structure of a putative dna polymerase iii beta subunit2 (eubrec_0002; ere_29750) from eubacterium rectale atcc 33656 at 2.263 a resolution
72	c1vlvA_	Alignment	not modelled	29.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
73	c3sdsA_	Alignment	not modelled	23.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
74	c2p2gD_	Alignment	not modelled	23.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
75	d1t57a_	Alignment	not modelled	23.6	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
76	d1vpka1	Alignment	not modelled	19.6	22	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
77	d1djqa1	Alignment	not modelled	18.2	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
78	c1fvoB_	Alignment	not modelled	17.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
79	c2bpbA_	Alignment	not modelled	16.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit a; **PDBTitle:** sulfite dehydrogenase from starkeya novella
80	c2qs0A_	Alignment	not modelled	16.6	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**quinolinate synthetase a; **PDBTitle:** quinolinate synthase from pyrococcus furiosus
81	d1vjda_	Alignment	not modelled	15.6	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase

82	c1vpkA_	Alignment	not modelled	14.8	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii, beta subunit; **PDBTitle:** crystal structure of dna polymerase iii, beta subunit (tm0262) from2 thermotoga maritima at 2.00 a resolution
83	d1pv8a_	Alignment	not modelled	14.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
84	d1r8ka_	Alignment	not modelled	14.0	26	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
85	d1ltka_	Alignment	not modelled	13.9	27	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
86	c3pg8B_	Alignment	not modelled	13.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
87	d2hawa1	Alignment	not modelled	13.3	16	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
88	c2ixaA_	Alignment	not modelled	13.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
89	c2eb0B_	Alignment	not modelled	13.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**manganese-dependent inorganic pyrophosphatase; **PDBTitle:** crystal structure of methanococcus jannaschii putative family ii2 inorganic pyrophosphatase
90	c2pjuD_	Alignment	not modelled	13.0	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
91	d1ok7a1	Alignment	not modelled	13.0	16	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
92	d1phpa_	Alignment	not modelled	11.9	28	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
93	c2w37A_	Alignment	not modelled	11.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
94	d7reqa2	Alignment	not modelled	11.5	12	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
95	d1v6sa_	Alignment	not modelled	11.3	16	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
96	c2hi1A_	Alignment	not modelled	10.8	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
97	c1unnA_	Alignment	not modelled	10.7	9	**PDB header:**beta-clamp **Chain:** A: **PDB Molecule:**dna polymerase iii beta subunit; **PDBTitle:** complex of beta-clamp processivity factor and little finger2 domain of poliv
98	d1vpka2	Alignment	not modelled	10.4	8	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
99	c3opyL_	Alignment	not modelled	10.4	25	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6-phosphofructo-1-kinase gamma-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state