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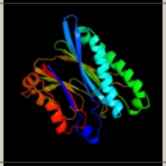
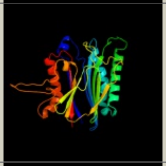
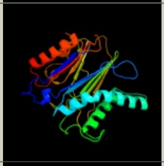
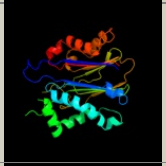
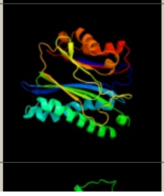
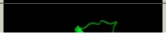
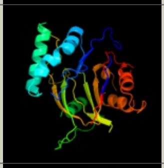
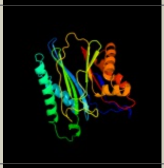
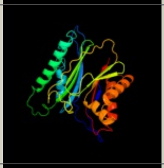
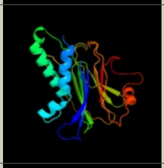
Description	P76395
Date	Thu Jan 5 12:22:33 GMT 2012
Unique Job ID	4eecc6d5947d364b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1a6qA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase 2c; **PDBTitle:** crystal structure of the protein serine/threonine phosphatase 2c at 22 a resolution
2	d1txoa_	Alignment		100.0	16	**Fold:**PP2C-like **Superfamily:**PP2C-like **Family:**PP2C-like
3	c2pk0C_	Alignment		100.0	15	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**serine/threonine protein phosphatase stp1; **PDBTitle:** structure of the s. agalactiae serine/threonine phosphatase at 2.652 resolution
4	d1a6qa2	Alignment		100.0	16	**Fold:**PP2C-like **Superfamily:**PP2C-like **Family:**PP2C-like
5	c3kdjB_	Alignment		100.0	15	**PDB header:**hydrolase/hormone receptor **Chain:** B: **PDB Molecule:**protein phosphatase 2c 56; **PDBTitle:** complex structure of (+)-aba-bound pyl1 and abi1
6	c2i44A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine-threonine phosphatase 2c; **PDBTitle:** crystal structure of serine-threonine phosphatase 2c from2 toxoplasma gondii
7	c2cm1A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine threonine protein phosphatase pstp; **PDBTitle:** crystal structure of the catalytic domain of serine2 threonine protein phosphatase pstp in complex with3 2 manganese ions.
8	c3kb3B_	Alignment		100.0	15	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**protein phosphatase 2c 16; **PDBTitle:** crystal structure of abscisic acid-bound pyl2 in complex with hab1
9	c2jfsA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ser-thr phosphatase mspp; **PDBTitle:** crystal structure of the ppm ser-thr phosphatase mspp from2 mycobacterium smegmatis in complex with cacodylate
10	c2i0oA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ser/thr phosphatase; **PDBTitle:** crystal structure of anopheles gambiae ser/thr phosphatase complexed2 with zn2+
11	c2iq1A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein phosphatase 2c kappa, ppm1k; **PDBTitle:** crystal structure of human ppm1k
						

12	c2irmA_	Alignment		100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase kinase 7 **PDBTitle:** crystal structure of mitogen-activated protein kinase kinase kinase 72 interacting protein 1 from anopheles gambiae
13	c2isnB_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nysgxrc-8828z, phosphatase; **PDBTitle:** crystal structure of a phosphatase from a pathogenic strain toxoplasma2 gondii
14	c2pnqA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]]-phosphatase **PDBTitle:** crystal structure of pyruvate dehydrogenase phosphatase 12 (pdp1)
15	c2j82A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein serine-threonine phosphatase; **PDBTitle:** structural analysis of the pp2c family phosphatase tppha2 from thermosynechococcus elongatus
16	c2pomA_	Alignment		99.9	12	**PDB header:**signaling protein/metal binding protein **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase kinase 7- **PDBTitle:** tab1 with manganese ion
17	c2j4oA_	Alignment		99.9	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase kinase **PDBTitle:** structure of tab1
18	c3rnrB_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**stage ii sporulation e family protein; **PDBTitle:** crystal structure of stage ii sporulation e family protein from2 thermanaerovibrio acidaminovorans
19	c3d8kD_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein phosphatase 2c; **PDBTitle:** crsytal structure of a phosphatase from a toxoplasma gondii
20	c3pu9A_	Alignment		99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein serine/threonine phosphatase; **PDBTitle:** crystal structure of serine/threonine phosphatase sphaerobacter2 thermophilus dsm 20745
21	c3t9qB_	Alignment	not modelled	99.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**stage ii sporulation protein e; **PDBTitle:** structure of the phosphatase domain of the cell fate determinant2 spoiie from bacillus subtilis (mn presoaked)
22	c3ke6A_	Alignment	not modelled	98.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein rv1364c/mt1410; **PDBTitle:** the crystal structure of the rsbu and rsbw domains of rv1364c from2 mycobacterium tuberculosis
23	c3es2A_	Alignment	not modelled	98.7	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of the c-terminal phosphatase domain of p.2 aeruginonsa rssb
24	c3eq2A_	Alignment	not modelled	28.8	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
25	c1rfoC_	Alignment	not modelled	10.1	25	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**whisker antigen control protein; **PDBTitle:** trimeric foldon of the t4 phagehead fibritin
26	c3iddA_	Alignment	not modelled	6.7	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
27	c3m8yC_	Alignment	not modelled	5.7	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
28	c3q4fG_	Alignment	not modelled	5.6	14	**PDB header:**dna binding protein/protein binding **Chain:** G: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of xrcc4/xlf-cernunnos complex

29	c3mudA_	Alignment	not modelled	5.4	14	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**dna repair protein xrcc4, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
30	c2zktB_	Alignment	not modelled	5.4	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
31	c3sr2A_	Alignment	not modelled	5.4	14	**PDB header:**dna binding protein/protein binding **Chain:** A: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of human xlf-xrcc4 complex
32	d1ik9a1	Alignment	not modelled	5.3	14	**Fold:**XRCC4, N-terminal domain **Superfamily:**XRCC4, N-terminal domain **Family:**XRCC4, N-terminal domain
33	c1avyA_	Alignment	not modelled	5.3	25	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)