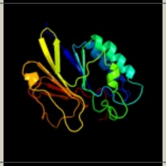
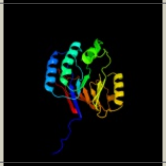
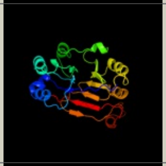
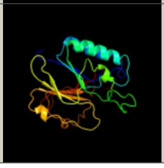
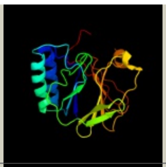
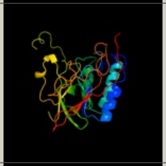
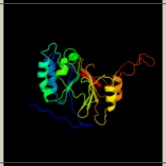
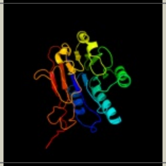
Phyre^2

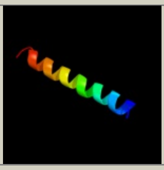
Email	l.a.kelley@imperial.ac.uk
Description	P37049
Date	Thu Jan 5 11:54:38 GMT 2012
Unique Job ID	c4d9df75dfd7c843

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xmoB_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
2	c3av0A_	Alignment		99.9	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
3	c3ib7A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
4	c3t1iC_	Alignment		99.9	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
5	d1xzwa2	Alignment		99.9	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
6	d3d03a1	Alignment		99.9	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
7	d2yvta1	Alignment		99.9	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
8	c2hy1A_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
9	d2hy1a1	Alignment		99.9	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
10	d2qfra2	Alignment		99.9	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
11	c3auzA_	Alignment		99.9	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese

12	d1ii7a_	Alignment		99.8	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
13	c3qg5D_	Alignment		99.8	17	**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
14	c1kbpB_	Alignment		99.8	14	**PDB header:**hydrolase (phosphoric monoester) **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** kidney bean purple acid phosphatase
15	d1uf3a_	Alignment		99.8	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
16	c2q8uA_	Alignment		99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
17	c1xzwB_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** sweet potato purple acid phosphatase/phosphate complex
18	c3rl4A_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
19	d2nxfa1	Alignment		99.7	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
20	d1s3la_	Alignment		99.7	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
21	c1s3mA_	Alignment	not modelled	99.7	23	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
22	d2z1aa2	Alignment	not modelled	99.7	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
23	d1usha2	Alignment	not modelled	99.7	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
24	d1utea_	Alignment	not modelled	99.7	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
25	c1qhwA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (purple acid phosphatase); **PDBTitle:** purple acid phosphatase from rat bone
26	d1qhwa_	Alignment	not modelled	99.7	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
27	c1oidA_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
28	c2z1aA_	Alignment	not modelled	99.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
						PDB header:hydrolase

29	c3qfnA_	Alignment	not modelled	99.6	20	**Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
30	d2a22a1	Alignment	not modelled	99.6	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
31	d1z2wa1	Alignment	not modelled	99.6	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
32	c3rqzC_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
33	d1xm7a_	Alignment	not modelled	99.5	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
34	c3ivdA_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotidase; **PDBTitle:** putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
35	c1su1A_	Alignment	not modelled	99.5	22	**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
36	d1su1a_	Alignment	not modelled	99.5	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
37	c3qfkA_	Alignment	not modelled	99.5	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
38	d3ck2a1	Alignment	not modelled	99.5	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
39	c3zu0A_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
40	c2wdfA_	Alignment	not modelled	99.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
41	d1nnwa_	Alignment	not modelled	99.4	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Phosphoesterase-related
42	c2kknA_	Alignment	not modelled	99.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
43	d3c9fa2	Alignment	not modelled	99.4	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
44	c3gveB_	Alignment	not modelled	99.3	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
45	c3jyfB_	Alignment	not modelled	99.2	19	**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
46	c3c9fB_	Alignment	not modelled	99.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
47	d1t71a_	Alignment	not modelled	99.0	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
48	d2z06a1	Alignment	not modelled	98.8	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
49	d1t70a_	Alignment	not modelled	98.8	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
50	c2qjcA_	Alignment	not modelled	98.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase
51	d1g5ba_	Alignment	not modelled	98.4	25	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
52	c2dfjA_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
53	c2zbmA_	Alignment	not modelled	98.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase; **PDBTitle:** crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
54	d1jk7a_	Alignment	not modelled	98.0	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases

						Family: Protein serine/threonine phosphatase
55	d3c5wc1	Alignment	not modelled	97.9	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
56	d1s70a_	Alignment	not modelled	97.8	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
57	c2jogA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
58	c3icfB_	Alignment	not modelled	97.8	15	**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
59	d1s95a_	Alignment	not modelled	97.8	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
60	c3e0jG_	Alignment	not modelled	97.8	14	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
61	d1auia_	Alignment	not modelled	97.8	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
62	c1auiA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b; **PDBTitle:** human calcineurin heterodimer
63	d2p6ba1	Alignment	not modelled	97.7	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
64	c2p6bC_	Alignment	not modelled	97.7	17	**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
65	c1wao4_	Alignment	not modelled	97.5	16	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
66	c3floG_	Alignment	not modelled	97.1	18	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase alpha subunit b; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
67	c2e76D_	Alignment		80.1	23	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
68	c2fynO_	Alignment	not modelled	56.5	22	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
69	d3clsc1	Alignment	not modelled	56.4	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
70	c1p84E_	Alignment	not modelled	54.9	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
71	c3ih5A_	Alignment	not modelled	50.5	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
72	d1efva1	Alignment	not modelled	48.5	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
73	c1t9gR_	Alignment	not modelled	41.8	21	**PDB header:**oxidoreductase, electron transport **Chain:** R: **PDB Molecule:**electron transfer flavoprotein alpha-subunit, **PDBTitle:** structure of the human mcad:etf complex
74	c2ebjB_	Alignment	not modelled	37.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrrolidone carboxyl peptidase; **PDBTitle:** crystal structure of pyrrolidone carboxyl peptidase from thermus2 thermophilus
75	c2fyuE_	Alignment	not modelled	35.0	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
76	d3bzka5	Alignment	not modelled	28.1	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
77	d1kbia1	Alignment	not modelled	28.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
78	d1o94c_	Alignment	not modelled	27.2	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits

79	c2ei9A_	Alignment	not modelled	27.0	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein; **PDBTitle:** crystal structure of r1bm endonuclease domain
80	d1duvg2	Alignment	not modelled	26.2	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
81	d1a2za_	Alignment	not modelled	21.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
82	c3k2qA_	Alignment	not modelled	20.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
83	d1uuya_	Alignment	not modelled	19.9	28	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
84	c3rfqC_	Alignment	not modelled	19.6	20	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
85	d2f48a1	Alignment	not modelled	19.5	16	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
86	d1auga_	Alignment	not modelled	18.8	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) **Family:**Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
87	d1zl0a1	Alignment	not modelled	18.5	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LD-carboxypeptidase A C-terminal domain-like **Family:**LD-carboxypeptidase A C-terminal domain-like
88	c3tebA_	Alignment	not modelled	18.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase; **PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
89	d1dxha2	Alignment	not modelled	18.2	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
90	c3qi7A_	Alignment	not modelled	17.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
91	c3n0vD_	Alignment	not modelled	17.3	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
92	c3obiC_	Alignment	not modelled	16.9	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
93	c3p9xB_	Alignment	not modelled	16.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
94	c2higA_	Alignment	not modelled	16.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
95	c1cr6A_	Alignment	not modelled	16.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
96	c2yxbA_	Alignment	not modelled	16.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
97	d1fh9a_	Alignment	not modelled	15.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
98	d1ua4a_	Alignment	not modelled	15.1	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
99	c3lacA_	Alignment	not modelled	14.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrrolidone-carboxylate peptidase; **PDBTitle:** crystal structure of bacillus anthracis pyrrolidone-carboxylate2 peptidase, pcp