Phyre^2

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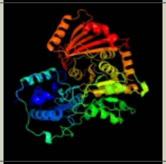
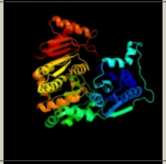
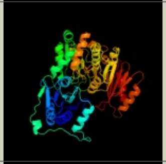
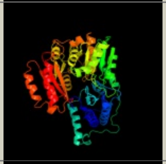
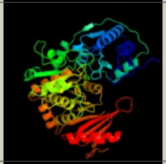
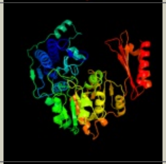
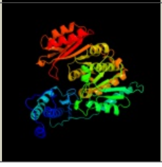
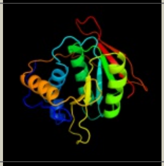
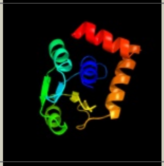
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fuvB_	Alignment		100.0	96	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
2	c2z0fA_	Alignment		100.0	54	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphoglucomutase; **PDBTitle:** crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
3	c1kfiA_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoglucomutase 1; **PDBTitle:** crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
4	c1c4gB_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
5	c1wqaB_	Alignment		100.0	27	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phospho-sugar mutase; **PDBTitle:** crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
6	c2f7lA_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
7	c3c04A_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphomannomutase/phosphoglucomutase; **PDBTitle:** structure of the p368g mutant of pmm/pgm from p. aeruginosa
8	c3pdkB_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** crystal structure of phosphoglucosamine mutase from b. anthracis
9	c1tuoA_	Alignment		100.0	29	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative phosphomannomutase; **PDBTitle:** crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
10	c3i3wB_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
11	c2dkdA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoacetylglucosamine mutase; **PDBTitle:** crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex

12	d1kfia1	Alignment		100.0	24	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
13	d3pmga1	Alignment		100.0	30	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
14	d1p5dx1	Alignment		100.0	25	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
15	d3pmga3	Alignment		99.9	23	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
16	d1kfia3	Alignment		99.9	29	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
17	d1p5dx3	Alignment		99.9	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
18	d1p5dx2	Alignment		99.9	22	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
19	d1kfia2	Alignment		99.9	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
20	d3pmga2	Alignment		99.8	25	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
21	d1p5dx4	Alignment	not modelled	99.8	20	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
22	d1wjwa_	Alignment	not modelled	99.3	21	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
23	d3pmga4	Alignment	not modelled	98.1	17	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
24	d1kfia4	Alignment	not modelled	97.9	17	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
25	c3s5pA_	Alignment	not modelled	84.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
26	c3qayC_	Alignment	not modelled	82.3	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
27	c3he8A_	Alignment	not modelled	80.1	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
28	d1nn4a_	Alignment	not modelled	80.0	22	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
						Fold: Ribose/Galactose isomerase RpiB/AlsB

29	d2vvpa1	Alignment	not modelled	79.7	28	**Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
30	c2ppwA_	Alignment	not modelled	78.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
31	c3c5yD_	Alignment	not modelled	76.0	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
32	d3bula2	Alignment	not modelled	73.9	19	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
33	c3ne8A_	Alignment	not modelled	73.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
34	c3k7pA_	Alignment	not modelled	70.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
35	c3m1pA_	Alignment	not modelled	70.0	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
36	c1k98A_	Alignment	not modelled	65.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
37	d1o1xa_	Alignment	not modelled	59.5	18	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
38	c3k6qB_	Alignment	not modelled	53.1	9	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
39	d1e5da1	Alignment	not modelled	49.0	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
40	d2bl5a1	Alignment	not modelled	44.9	24	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
41	c3onoA_	Alignment	not modelled	44.3	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
42	c2q9uB_	Alignment	not modelled	44.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
43	d1x74a1	Alignment	not modelled	42.1	10	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
44	d1ccwa_	Alignment	not modelled	42.0	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
45	c3op1A_	Alignment	not modelled	41.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
46	c2zkiH_	Alignment	not modelled	41.2	12	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
47	d1gvfa_	Alignment	not modelled	40.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
48	c3nvtA_	Alignment	not modelled	40.4	14	**PDB header:**transferase/isomerase **Chain:** A: **PDB Molecule:**3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; **PDBTitle:** 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
49	c2i2xD_	Alignment	not modelled	38.1	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**methyltransferase 1; **PDBTitle:** crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
50	c3a9rA_	Alignment	not modelled	37.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-arabinose isomerase; **PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
51	c3pm6B_	Alignment	not modelled	36.9	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
52	d1yt8a4	Alignment	not modelled	34.6	8	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
53	c1bmtB_	Alignment	not modelled	33.9	18	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
54	c2ql5A_	Alignment	not modelled	33.6	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7;

						PDBTitle: crystal structure of caspase-7 with inhibitor ac-dmqd-cho
55	d1t6t1_	Alignment	not modelled	33.5	19	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
56	c3qd5B_	Alignment	not modelled	33.1	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of a putative ribose-5-phosphate isomerase from2 coccidioides immitis solved by combined iodide ion sad and mr
57	c1y80A_	Alignment	not modelled	32.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
58	c2plqA_	Alignment	not modelled	32.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aliphatic amidase; **PDBTitle:** crystal structure of the amidase from geobacillus pallidus rapc8
59	c2iswB_	Alignment	not modelled	32.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
60	d1b0aa2	Alignment	not modelled	30.7	18	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
61	d1ykga1	Alignment	not modelled	30.0	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
62	d3eeqa2	Alignment	not modelled	29.8	12	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
63	c1pyoA_	Alignment	not modelled	29.8	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-2; **PDBTitle:** crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho
64	d1jwqa_	Alignment	not modelled	27.9	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
65	d1a4ia2	Alignment	not modelled	26.9	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
66	d7reqa2	Alignment	not modelled	26.8	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
67	d1vmea1	Alignment	not modelled	25.6	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
68	c3qqzA_	Alignment	not modelled	25.4	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein yjik; **PDBTitle:** crystal structure of the c-terminal domain of the yjik protein from2 escherichia coli cft073
69	c1pyaD_	Alignment	not modelled	25.2	19	**PDB header:**carboxy-lyase **Chain:** D: **PDB Molecule:**pyruvoyl-dependent histidine decarboxylase (l- **PDBTitle:** refined structure of the pyruvoyl-dependent histidine2 decarboxylase from lactobacillus 30a
70	c3hlyA_	Alignment	not modelled	25.0	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
71	c3sz8D_	Alignment	not modelled	24.1	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
72	c1i51A_	Alignment	not modelled	23.5	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7 subunit p20; **PDBTitle:** crystal structure of caspase-7 complexed with xiap
73	d1jf8a_	Alignment	not modelled	23.5	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
74	c3f93D_	Alignment	not modelled	23.1	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
75	d2nmla1	Alignment	not modelled	22.8	13	**Fold:**ERH-like **Superfamily:**ERH-like **Family:**ERH-like
76	c2nn3D_	Alignment	not modelled	22.3	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-1; **PDBTitle:** structure of pro-sf-caspase-1
77	d1rvga_	Alignment	not modelled	22.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
78	c3tqkA_	Alignment	not modelled	22.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
79	d2aeea1	Alignment	not modelled	21.5	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

80	c2w37A_	Alignment	not modelled	21.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
81	d1m72a_	Alignment	not modelled	20.6	17	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
82	c3nolA_	Alignment	not modelled	20.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine cyclotransferase; **PDBTitle:** crystal structure of zymomonas mobilis glutaminyl cyclase (trigonal2 form)
83	c3q94B_	Alignment	not modelled	19.9	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
84	d1dxha2	Alignment	not modelled	19.7	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
85	c2if2C_	Alignment	not modelled	19.0	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of the putative dephospho-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.
86	c3mw8A_	Alignment	not modelled	19.0	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
87	d1ycga1	Alignment	not modelled	18.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
88	c1qdul_	Alignment	not modelled	18.7	5	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**caspase-8 alpha-chain; **PDBTitle:** crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk
89	c2wnsB_	Alignment	not modelled	18.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
90	d1tubb1	Alignment	not modelled	18.4	16	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
91	d1k1ga_	Alignment	not modelled	18.4	30	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
92	c2au3A_	Alignment	not modelled	18.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
93	c1a1sA_	Alignment	not modelled	18.3	19	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
94	c3chgB_	Alignment	not modelled	17.7	16	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
95	c3edqC_	Alignment	not modelled	17.6	7	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**caspase-3; **PDBTitle:** crystal structure of caspase-3 with inhibitor ac-ldesd-cho
96	c3hdtB_	Alignment	not modelled	17.2	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
97	c3c52B_	Alignment	not modelled	16.9	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
98	c2p2gD_	Alignment	not modelled	16.2	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
99	c1tvmA_	Alignment	not modelled	16.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system