Phyre2

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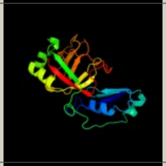
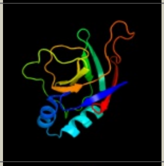
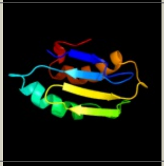
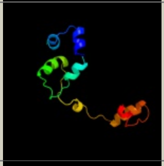
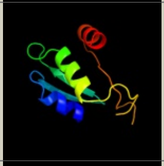
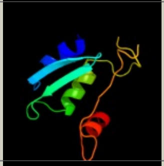
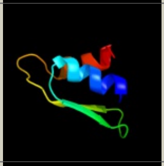
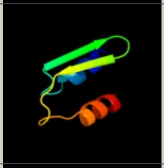
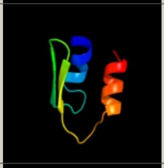
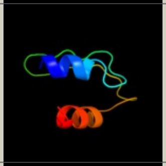
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2phcB_	Alignment		100.0	39	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
2	c3oepA_	Alignment		100.0	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0988; **PDBTitle:** crystal structure of ttha0988 in space group p43212
3	c3mmlD_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
4	d2phcb1	Alignment		100.0	54	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
5	c2zp2B_	Alignment		100.0	57	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
6	c2kwaA_	Alignment		99.5	17	**PDB header:**transferase inhibitor **Chain:** A: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** 1h, 13c and 15n backbone and side chain resonance assignments of the2 n-terminal domain of the histidine kinase inhibitor kipi from3 bacillus subtilis
7	d2phcb2	Alignment		99.5	17	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
8	c2qf7A_	Alignment		94.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
9	c2j89A_	Alignment		88.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine sulfoxide reductase a; **PDBTitle:** functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
10	c1nwaA_	Alignment		86.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
11	d1nwaa_	Alignment		86.9	17	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase

12	c3mmlE_	Alignment		83.3	24	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**allophanate hydrolase subunit 2; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
13	c3e0mB_	Alignment		78.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
14	c2ropA_	Alignment		76.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of domains 3 and 4 of human atp7b
15	c3bqhA_	Alignment		73.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb; **PDBTitle:** structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
16	d1afia_	Alignment		72.7	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
17	c2ew9A_	Alignment		72.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** solution structure of apowln5-6
18	c2rmlA_	Alignment		71.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
19	d1p6ta2	Alignment		69.6	22	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	d1s6ua_	Alignment		69.2	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
21	d1q8la_	Alignment	not modelled	68.1	4	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
22	c3dxsX_	Alignment	not modelled	63.6	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
23	d1kvja_	Alignment	not modelled	63.5	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	c2kkhA_	Alignment	not modelled	62.3	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
25	d2qifa1	Alignment	not modelled	61.6	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
26	d1whza_	Alignment	not modelled	61.6	20	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
27	d1ff3a_	Alignment	not modelled	61.6	10	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
28	c2ldiA_	Alignment	not modelled	61.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
29	c2qa7A	Alignment	not modelled	61.0	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1;

29	c2ga7A_	Alignment	not modelled	61.0	7	**PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
30	d1ff3c_	Alignment	not modelled	60.6	10	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
31	c1yjrA_	Alignment	not modelled	60.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
32	c2l3mA_	Alignment	not modelled	60.1	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
33	c1fvaA_	Alignment	not modelled	59.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of bovine methionine sulfoxide reductase
34	d1osda_	Alignment	not modelled	59.7	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
35	c3pilA_	Alignment	not modelled	58.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
36	c2ofhX_	Alignment	not modelled	57.6	16	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
37	c1y3kA_	Alignment	not modelled	55.8	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
38	d1cpza_	Alignment	not modelled	53.6	11	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
39	c2dy3B_	Alignment	not modelled	51.4	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
40	d1fvga_	Alignment	not modelled	49.9	10	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
41	c1l0oC_	Alignment	not modelled	46.6	35	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
42	d1l0oc_	Alignment	not modelled	46.6	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
43	d2cbpa_	Alignment	not modelled	41.7	27	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
44	d1rp3a1	Alignment	not modelled	39.1	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
45	c3j09A_	Alignment	not modelled	37.9	4	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
46	c3gwqB_	Alignment	not modelled	37.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-serine deaminase; **PDBTitle:** crystal structure of a putative d-serine deaminase (bxe_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
47	d1mdah_	Alignment	not modelled	37.2	25	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Methylamine dehydrogenase, H-chain
48	d3cnxa1	Alignment	not modelled	36.5	38	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SAV4671-like
49	c2k6zA_	Alignment	not modelled	34.9	36	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1943; **PDBTitle:** solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
50	d1pina2	Alignment	not modelled	32.1	36	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
51	c1yw5A_	Alignment	not modelled	31.5	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans
52	d1m5ya3	Alignment	not modelled	29.9	45	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
53	d1eq3a_	Alignment	not modelled	29.4	36	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
54	d1mv8a1	Alignment	not modelled	29.1	20	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
						Fold: Ferredoxin-like

55	d2aw0a_	Alignment	not modelled	28.9	9	**Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
56	d1ku2a1	Alignment	not modelled	27.4	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
57	c1zeqX_	Alignment	not modelled	27.0	33	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
58	d1p6ta1	Alignment	not modelled	26.7	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
59	d1dlja1	Alignment	not modelled	26.5	25	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
60	c3h87D_	Alignment	not modelled	26.4	26	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
61	c3h25A_	Alignment	not modelled	26.2	12	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein b; **PDBTitle:** crystal structure of the catalytic domain of primase repb' in complex2 with initiator dna
62	d1z67a1	Alignment	not modelled	25.4	13	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
63	c2q3eH_	Alignment	not modelled	24.2	8	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
64	c2rqsA_	Alignment	not modelled	24.1	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
65	c3m9yB_	Alignment	not modelled	23.4	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
66	c1f8aB_	Alignment	not modelled	23.0	36	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
67	c2l55A_	Alignment	not modelled	22.7	50	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
68	c1zk6A_	Alignment	not modelled	22.5	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
69	c2jzvA_	Alignment	not modelled	22.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
70	d1wi9a_	Alignment	not modelled	21.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
71	d1x9la_	Alignment	not modelled	21.5	28	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**DR1885-like metal-binding protein **Family:**DR1885-like metal-binding protein
72	d1xnea_	Alignment	not modelled	21.2	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
73	c1kzlA_	Alignment	not modelled	20.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** riboflavin synthase from s.pombe bound to2 carboxyethyllumazine
74	c2odoC_	Alignment	not modelled	19.9	26	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of pseudomonas fluorescens alanine racemase
75	d1r2ra_	Alignment	not modelled	19.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
76	d2ggpb1	Alignment	not modelled	19.5	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
77	d1m6ja_	Alignment	not modelled	19.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
78	d2pv2a1	Alignment	not modelled	19.2	18	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
79	c3s6dA_	Alignment	not modelled	19.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative triosephosphate isomerase; **PDBTitle:** crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
80	d1n7va_	Alignment	not modelled	18.3	40	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
						Fold:FKBP-like

81	d1j6ya_	Alignment	not modelled	18.2	27	**Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
82	c2k53A_	Alignment	not modelled	18.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
83	c3a35B_	Alignment	not modelled	18.1	14	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**lumazine protein; **PDBTitle:** crystal structure of lump complexed with riboflavin
84	d2btma_	Alignment	not modelled	18.1	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
85	c3gpkA_	Alignment	not modelled	17.5	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
86	c3jt0B_	Alignment	not modelled	16.9	21	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a
87	c2kqaA_	Alignment	not modelled	16.8	58	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cerato-platanin; **PDBTitle:** the solution structure of the fungal elicitor cerato-platanin
88	d2rcda1	Alignment	not modelled	16.8	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BxeB1374-like
89	d1ndsa2	Alignment	not modelled	16.6	19	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
90	c3kspA_	Alignment	not modelled	16.5	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**calcium/calmodulin-dependent kinase ii association domain; **PDBTitle:** crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution
91	c2kt2A_	Alignment	not modelled	16.4	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
92	c2pv3B_	Alignment	not modelled	16.4	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**chaperone sura; **PDBTitle:** crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
93	c3cieC_	Alignment	not modelled	16.4	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
94	d1jnsa_	Alignment	not modelled	16.0	45	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
95	d1o7ia_	Alignment	not modelled	16.0	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
96	c3krsB_	Alignment	not modelled	15.9	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
97	c2kgjA_	Alignment	not modelled	15.6	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase d; **PDBTitle:** solution structure of parvulin domain of ppid from e.coli
98	c2becA_	Alignment	not modelled	15.6	29	**PDB header:**metal binding protein/transport protein **Chain:** A: **PDB Molecule:**calcineurin b homologous protein 2; **PDBTitle:** crystal structure of chp2 in complex with its binding2 region in nhe1 and insights into the mechanism of ph3 regulation
99	c3th6B_	Alignment	not modelled	15.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.