Phyre^2

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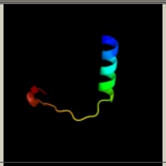
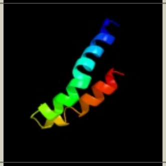
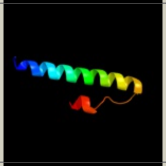
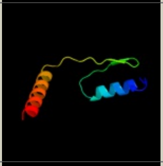
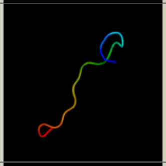
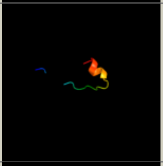
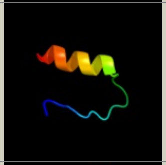
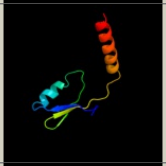
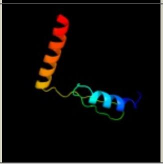
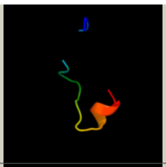
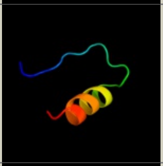
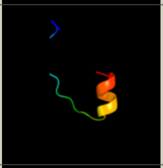
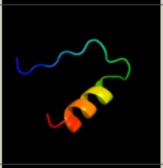
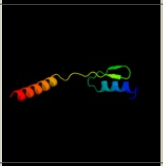
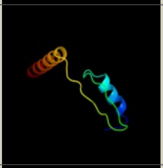
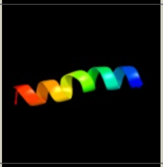
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mxnA_	Alignment		62.6	17	**PDB header:**replication **Chain:** A: **PDB Molecule:**recq-mediated genome instability protein 1; **PDBTitle:** crystal structure of the rmi core complex
2	c2ke4A_	Alignment		52.2	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cdc42-interacting protein 4; **PDBTitle:** the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
3	d2ca5a1	Alignment		48.9	14	**Fold:**Long alpha-hairpin **Superfamily:**MxiH-like **Family:**MxiH-like
4	c3dxsX_	Alignment		44.9	36	**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
5	d1is1a_	Alignment		43.9	23	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
6	d1ge9a_	Alignment		39.4	19	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
7	d1bcoa1	Alignment		35.3	29	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
8	c3kwmC_	Alignment		34.7	30	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
9	d1osda_	Alignment		33.7	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
10	d1eh1a_	Alignment		33.4	22	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
11	d1dd5a_	Alignment		32.7	16	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF

12	d1m0sa2	Alignment		32.5	35	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
13	d2aw0a_	Alignment		32.4	24	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
14	c2pjmA_	Alignment		32.0	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
15	c1yjrA_	Alignment		30.4	16	**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
16	d1ek8a_	Alignment		29.9	25	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
17	d1wqga1	Alignment		28.8	25	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
18	c1nu5A_	Alignment		28.8	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
19	c1nhlA_	Alignment		28.2	37	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**synaptosomal-associated protein 23; **PDBTitle:** snap-23n structure
20	c2rogA_	Alignment		27.4	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
21	d1uj4a2	Alignment	not modelled	26.7	35	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
22	d1spia_	Alignment	not modelled	26.0	50	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
23	c3l7oB_	Alignment	not modelled	25.2	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
24	c3cqxD_	Alignment	not modelled	25.1	19	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**bag family molecular chaperone regulator 2; **PDBTitle:** chaperone complex
25	c3u7jA_	Alignment	not modelled	24.8	45	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
26	c1lkzB_	Alignment	not modelled	23.9	50	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
27	d1o8ba2	Alignment	not modelled	23.6	50	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
28	c1m0sA_	Alignment	not modelled	23.2	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
						PDB header:metal binding protein

29	c2l3mA_	Alignment	not modelled	22.3	20	**Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
30	d1ftaa_	Alignment	not modelled	22.3	50	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
31	d1p6ta1	Alignment	not modelled	22.2	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
32	d1q8la_	Alignment	not modelled	22.1	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
33	d1mwza_	Alignment	not modelled	22.0	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c3tj4B_	Alignment	not modelled	21.8	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
35	c1xtzA_	Alignment	not modelled	21.8	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
36	c2qv5A_	Alignment	not modelled	21.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
37	c2ofhX_	Alignment	not modelled	21.5	22	**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
38	d1r6wa1	Alignment	not modelled	21.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
39	c1uj6A_	Alignment	not modelled	21.2	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
40	c2kt2A_	Alignment	not modelled	19.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
41	c3czqA_	Alignment	not modelled	19.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
42	c1lk5C_	Alignment	not modelled	19.5	35	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
43	c2kkhA_	Alignment	not modelled	19.2	27	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
44	c2fhyL_	Alignment	not modelled	18.5	50	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**fructose-1,6-bisphosphatase 1; **PDBTitle:** structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
45	c1svfC_	Alignment	not modelled	18.3	35	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**protein (fusion glycoprotein); **PDBTitle:** paramyxovirus sv5 fusion protein core
46	d1p6ta2	Alignment	not modelled	18.0	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
47	c1y3kA_	Alignment	not modelled	18.0	30	**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
48	c2qgyA_	Alignment	not modelled	17.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**enolase from the environmental genome shotgun **PDBTitle:** crystal structure of an enolase from the environmental2 genome shotgun sequencing of the sargasso sea
49	c2gq1A_	Alignment	not modelled	17.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphatase; **PDBTitle:** crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
50	c2jvrA_	Alignment	not modelled	17.7	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** segmental isotope labeling of npl3p
51	d1nuwa_	Alignment	not modelled	17.3	50	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
52	d1afia_	Alignment	not modelled	17.0	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
53	c1bm4A_	Alignment	not modelled	17.0	38	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
54	d1w55a2	Alignment	not modelled	16.9	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like

55	c2v6lI_	Alignment	not modelled	16.8	14	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**mxih; **PDBTitle:** molecular model of a type iii secretion system needle
56	d2fiqa1	Alignment	not modelled	16.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
57	c3h2zA_	Alignment	not modelled	16.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
58	c2pmpA_	Alignment	not modelled	16.1	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
59	c3ugvE_	Alignment	not modelled	15.9	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of an enolase from alpha pretobacterium bal199 (efi2 target efi-501650) with bound mg
60	d1bk4a_	Alignment	not modelled	15.4	50	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
61	d1lk5a2	Alignment	not modelled	15.1	35	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
62	c2d7dB_	Alignment	not modelled	14.8	23	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**40-mer from uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
63	c3ce2A_	Alignment	not modelled	14.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase from chlamydophila abortus
64	d2qifa1	Alignment	not modelled	14.2	36	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
65	c2qnfB_	Alignment	not modelled	14.1	12	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**recombination endonuclease vii; **PDBTitle:** crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
66	c2o012_	Alignment	not modelled	14.0	55	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
67	c1yg0A_	Alignment	not modelled	13.9	32	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
68	c2gcfA_	Alignment	not modelled	13.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
69	c3hheA_	Alignment	not modelled	13.6	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
70	c2jowA_	Alignment	not modelled	12.9	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein prgi; **PDBTitle:** differences in the electrostatic surfaces of the type iii2 secretion needle proteins
71	d1gx1a_	Alignment	not modelled	12.8	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
72	c2ldiA_	Alignment	not modelled	12.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
73	c2oz8B_	Alignment	not modelled	11.6	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mll7089 protein; **PDBTitle:** crystal structure of putative mandelate racemase from mesorhizobium2 loti
74	c2kyzA_	Alignment	not modelled	11.6	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
75	d1wi6a1	Alignment	not modelled	11.3	22	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
76	c3q45E_	Alignment	not modelled	11.1	19	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family; **PDBTitle:** crystal structure of dipeptide epimerase from cytophaga hutchinsonii2 complexed with mg and dipeptide d-ala-l-val
77	c3g65A_	Alignment	not modelled	10.9	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell cycle checkpoint control protein rad9a; **PDBTitle:** crystal structure of the human rad9-rad1-hus1 dna damage2 checkpoint complex
78	c3ohwB_	Alignment	not modelled	10.8	44	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**phycobilisome lcm core-membrane linker polypeptide; **PDBTitle:** x-ray structure of phycobilisome lcm core-membrane linker polypeptide2 (fragment 721-860) from synechocystis sp. pcc 6803, northeast3 structural genomics consortium target sgr209e
79	c3kmlB_	Alignment	not modelled	10.4	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** circular permutant of the tobacco mosaic virus

80	d1rwta_	Alignment	not modelled	10.4	21	**Fold:**Chlorophyll a-b binding protein **Superfamily:**Chlorophyll a-b binding protein **Family:**Chlorophyll a-b binding protein
81	c2f8mB_	Alignment	not modelled	10.1	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
82	c2ky4A_	Alignment	not modelled	9.9	29	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
83	d1s6ua_	Alignment	not modelled	9.8	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
84	d1brwa1	Alignment	not modelled	9.6	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
85	c3l9vE_	Alignment	not modelled	9.3	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
86	d1kvja_	Alignment	not modelled	8.8	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
87	d1d9qa_	Alignment	not modelled	8.8	53	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
88	c2bezC_	Alignment	not modelled	8.8	22	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** structure of a proteolitically resistant core from the2 severe acute respiratory syndrome coronavirus s2 fusion3 protein
89	c1ybxA_	Alignment	not modelled	8.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
90	c2x5kO_	Alignment	not modelled	8.7	16	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**d-erythrose-4-phosphate dehydrogenase; **PDBTitle:** structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
91	c2osrA_	Alignment	not modelled	8.3	35	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** nmr structure of rrm-2 of yeast npl3 protein
92	d1jjcb6	Alignment	not modelled	8.2	21	**Fold:**PheT/TilS domain **Superfamily:**PheT/TilS domain **Family:**B3/B4 domain of PheRS, PheT
93	d2phcb2	Alignment	not modelled	8.1	16	**Fold:**DCoH-like **Superfamily:**PH0987 N-terminal domain-like **Family:**PH0987 N-terminal domain-like
94	c3uksB_	Alignment	not modelled	7.9	40	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sedoheptulose-1,7 bisphosphatase, putative; **PDBTitle:** 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
95	d1hdgo2	Alignment	not modelled	7.8	26	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
96	c3tr9A_	Alignment	not modelled	7.8	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
97	d2tpta1	Alignment	not modelled	7.7	7	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
98	d1e52a_	Alignment	not modelled	7.6	20	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
99	d2ggpb1	Alignment	not modelled	7.5	19	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain