Phyre^2

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Description	P0A9I3
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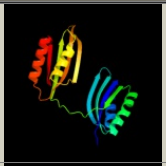
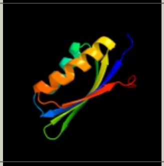
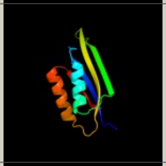
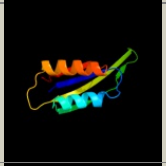
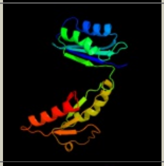
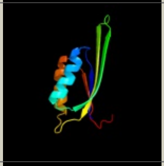
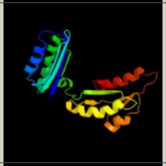
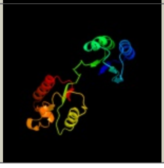
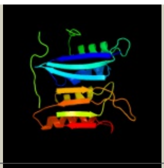
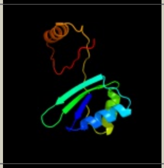
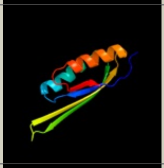
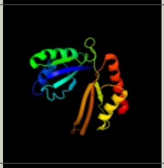
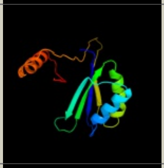
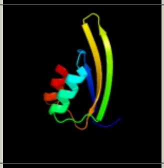
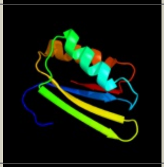
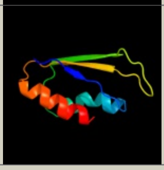
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u8sB_	Alignment		100.0	44	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
2	c2nyiB_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
3	c3p96A_	Alignment		99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
4	d1u8sa1	Alignment		99.8	55	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
5	c3nrbD_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
6	d1u8sa2	Alignment		99.7	34	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
7	d1zpva1	Alignment		99.7	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
8	c3obiC_	Alignment		99.6	15	**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
9	c3n0vD_	Alignment		99.6	12	**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
10	c3louB_	Alignment		99.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
11	c3o1lB_	Alignment		99.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution

12	c3l76B_	Alignment		99.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
13	c2f06B_	Alignment		99.0	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
14	c3ibwA_	Alignment		98.4	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
15	c2dtjA_	Alignment		98.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
16	c2zhoB_	Alignment		98.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
17	c2re1A_	Alignment		98.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
18	d1ygya3	Alignment		97.9	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
19	d1sc6a3	Alignment		97.8	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
20	d2fgca2	Alignment		97.8	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
21	c3c1nA_	Alignment	not modelled	97.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
22	d2f06a2	Alignment	not modelled	97.7	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
23	c2fgcA_	Alignment	not modelled	97.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
24	d2pc6a2	Alignment	not modelled	97.7	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
25	d2f1fa1	Alignment	not modelled	97.7	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
26	c2pc6C_	Alignment	not modelled	97.6	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
27	c3mwbA_	Alignment	not modelled	97.5	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
28	c3ab4K_	Alignment	not modelled	97.3	15	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant

						of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
29	c2f1fA_	Alignment	not modelled	97.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
30	c2cdqB_	Alignment	not modelled	97.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
31	d2f06a1	Alignment	not modelled	97.2	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
32	d2qmwa2	Alignment	not modelled	97.1	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
33	c2qmxB_	Alignment	not modelled	97.0	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
34	c1ygyA_	Alignment	not modelled	97.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
35	c2qmwA_	Alignment	not modelled	96.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
36	c3luyA_	Alignment	not modelled	96.7	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
37	d1phza1	Alignment	not modelled	96.6	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
38	c3mtjA_	Alignment	not modelled	96.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
39	c3mahA_	Alignment	not modelled	96.0	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
40	d2hmfa3	Alignment	not modelled	95.6	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
41	c1y7pB_	Alignment	not modelled	94.8	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
42	c3k5pA_	Alignment	not modelled	94.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
43	d2hmfa2	Alignment	not modelled	94.1	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
44	c1ybaC_	Alignment	not modelled	93.6	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
45	c2j0wA_	Alignment	not modelled	92.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
46	d2cdqa2	Alignment	not modelled	92.3	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
47	d2cdqa3	Alignment	not modelled	86.4	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
48	d2j0wa2	Alignment	not modelled	86.4	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
49	c1tdjA_	Alignment	not modelled	79.7	9	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
50	c2phmA_	Alignment	not modelled	73.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
51	d1vgya2	Alignment	not modelled	60.0	14	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
52	c2jheB_	Alignment	not modelled	59.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription regulator tyrr; **PDBTitle:** n-terminal domain of tyrr transcription factor (residues 1 -2 190)
53	d2j0wa3	Alignment	not modelled	56.4	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
						Fold: Ferredoxin-like

54	d1zhva2	Alignment	not modelled	52.3	7	**Superfamily:**ACT-like **Family:**Atu0741-like
55	d1rwua_	Alignment	not modelled	51.7	14	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
56	c1rwuA_	Alignment	not modelled	51.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
57	d3ceda1	Alignment	not modelled	49.4	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
58	c1zhvA_	Alignment	not modelled	46.9	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
59	d1geea_	Alignment	not modelled	43.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
60	d1zvpa2	Alignment	not modelled	38.6	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
61	d1gtda_	Alignment	not modelled	36.3	8	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
62	c2qc8J_	Alignment	not modelled	34.6	19	**PDB header:**ligase **Chain:** J: **PDB Molecule:**glutamine synthetase; **PDBTitle:** crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
63	c2yvqA_	Alignment	not modelled	33.6	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
64	d1v5va2	Alignment	not modelled	32.0	12	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
65	c1zvpB_	Alignment	not modelled	31.8	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein vc0802; **PDBTitle:** crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein
66	c2uygF_	Alignment	not modelled	30.8	19	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
67	d3bypa1	Alignment	not modelled	29.9	15	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
68	d1gqoa_	Alignment	not modelled	28.7	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
69	c3n8kG_	Alignment	not modelled	25.6	6	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
70	d1wosa2	Alignment	not modelled	25.1	9	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
71	d1uqra_	Alignment	not modelled	23.6	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
72	c3lwzC_	Alignment	not modelled	23.1	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
73	d1u5ta1	Alignment	not modelled	22.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
74	c1x31A_	Alignment	not modelled	22.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
75	d1lfpa_	Alignment	not modelled	22.4	14	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
76	c1worA_	Alignment	not modelled	21.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of t-protein of the glycine cleavage2 system
77	d1fc4a_	Alignment	not modelled	20.9	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
78	c2k4mA_	Alignment	not modelled	19.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
79	d1zcza1	Alignment	not modelled	19.4	17	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
80	d1xq1a_	Alignment	not modelled	17.6	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

81	d1gtza_	Alignment	not modelled	17.3	13	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
82	c3u80A_	Alignment	not modelled	16.7	4	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase, type ii; **PDBTitle:** 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
83	c2oz5A_	Alignment	not modelled	14.7	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphotyrosine protein phosphatase ptpb; **PDBTitle:** crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
84	d1ulua_	Alignment	not modelled	14.5	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
85	d1pj5a4	Alignment	not modelled	14.5	13	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**Aminomethyltransferase folate-binding domain
86	c2ptgA_	Alignment	not modelled	14.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
87	d1h05a_	Alignment	not modelled	13.9	7	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
88	d1nxia_	Alignment	not modelled	13.1	11	**Fold:**Ferredoxin-like **Superfamily:**Hypothetical protein VC0424 **Family:**Hypothetical protein VC0424
89	c2d1uA_	Alignment	not modelled	12.4	7	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**iron(iii) dicitrate transport protein feca; **PDBTitle:** solution strcuture of the periplasmic signaling domain of2 feca from escherichia coli
90	d1tdja2	Alignment	not modelled	11.6	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
91	d2joqa1	Alignment	not modelled	11.5	3	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**HP0495-like
92	c2zw2B_	Alignment	not modelled	11.2	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
93	c3jrnA_	Alignment	not modelled	11.1	9	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**at1g72930 protein; **PDBTitle:** crystal structure of tir domain from arabidopsis thaliana
94	c3oziB_	Alignment	not modelled	11.0	9	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**l6tr; **PDBTitle:** crystal structure of the tir domain from the flax disease resistance2 protein l6
95	d1d7oa_	Alignment	not modelled	10.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	c2zmeA_	Alignment	not modelled	10.7	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
97	d1a9xa2	Alignment	not modelled	10.6	11	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
98	d1ywfa1	Alignment	not modelled	10.2	33	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
99	c2w8wA_	Alignment	not modelled	9.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine palmitoyltransferase; **PDBTitle:** n100y spt with plp-ser