Phyre^2

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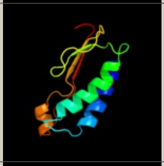
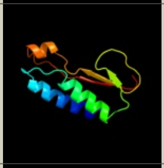
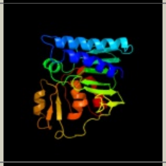
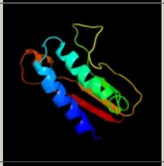
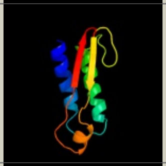
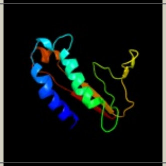
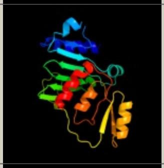
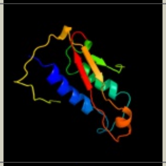
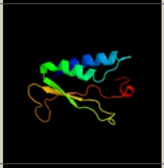
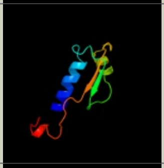
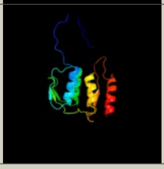
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ni9a_	Alignment		100.0	56	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
2	c3luzA_	Alignment		97.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extragenic suppressor protein suhb; **PDBTitle:** crystal structure of extragenic suppressor protein suhb from2 bartonella henselae, via combined iodide sad molecular replacement
3	c2qflA_	Alignment		96.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** structure of suhb: inositol monophosphatase and extragenic2 suppressor from e. coli
4	d1lbva_	Alignment		96.8	21	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
5	c2czhB_	Alignment		96.8	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
6	c2fvzB_	Alignment		96.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** human inositol monophosphosphatase 2
7	c2p3nB_	Alignment		96.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** thermotoga maritima impase tm1415
8	d1g0ha_	Alignment		96.6	17	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
9	c2pcrA_	Alignment		96.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** crystal structure of myo-inositol-1(or 4)-monophosphatase (aq_1983)2 from aquifex aeolicus vf5
10	d1xi6a_	Alignment		96.3	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
11	c2q74B_	Alignment		96.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol-1-monophosphatase; **PDBTitle:** mycobacterium tuberculosis suhb

12	d2hhma_	Alignment		95.6	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
13	c3b8bA_	Alignment		95.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysq, sulfite synthesis pathway protein; **PDBTitle:** crystal structure of cysq from bacteroides thetaiotaomicron, a2 bacterial member of the inositol monophosphatase family
14	d1vdwa_	Alignment		94.9	19	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
15	d1inpa_	Alignment		94.2	21	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
16	d1jp4a_	Alignment		94.1	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
17	d1d9qa_	Alignment		89.1	14	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
18	c3uksB_	Alignment		85.1	15	**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
19	d1ka1a_	Alignment		81.6	28	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
20	d1g6sa_	Alignment		81.3	16	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
21	d1j5ta_	Alignment	not modelled	75.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
22	c2yvkA_	Alignment	not modelled	67.6	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
23	c3a11D_	Alignment	not modelled	60.7	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
24	d1cjca2	Alignment	not modelled	59.6	14	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
25	c3aerC_	Alignment	not modelled	57.7	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
26	c3j08A_	Alignment	not modelled	54.3	14	**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
27	d1t5oa_	Alignment	not modelled	53.9	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
28	d2aeea1	Alignment	not modelled	52.7	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

29	c3ecsD_	Alignment	not modelled	52.6	25	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
30	c3j09A_	Alignment	not modelled	49.0	14	**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
31	d2a0ua1	Alignment	not modelled	47.6	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
32	d1spia_	Alignment	not modelled	44.4	18	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
33	d1t9ka_	Alignment	not modelled	44.1	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
34	c3n91A_	Alignment	not modelled	43.7	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a structural genomics, unknown function2 (bacova_03430) from bacteroides ovatus at 2.40 a resolution
35	c3pajA_	Alignment	not modelled	40.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
36	c3rf7A_	Alignment	not modelled	39.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
37	c2kg4A_	Alignment	not modelled	39.2	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**growth arrest and dna-damage-inducible protein **PDBTitle:** three-dimensional structure of human gadd45alpha in2 solution by nmr
38	d1vb5a_	Alignment	not modelled	37.2	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
39	c3gwpA_	Alignment	not modelled	36.4	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbon-sulfur lyase involved in aluminum resistance; **PDBTitle:** crystal structure of carbon-sulfur lyase involved in aluminum2 resistance (yp_878183.1) from clostridium novyi nt at 2.90 a3 resolution
40	c2xdqA_	Alignment	not modelled	35.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
41	d1lmb3_	Alignment	not modelled	33.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
42	c3pdiB_	Alignment	not modelled	33.0	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
43	d1u7pa_	Alignment	not modelled	32.7	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Magnesium-dependent phosphatase-1, Mdp1
44	c2ejaB_	Alignment	not modelled	31.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
45	d1m1nb_	Alignment	not modelled	30.5	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
46	c3roiA_	Alignment	not modelled	30.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii
47	d1i4na_	Alignment	not modelled	29.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
48	c2k2wA_	Alignment	not modelled	28.2	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**recombination and dna repair protein; **PDBTitle:** second brct domain of nbs1
49	c2ewtA_	Alignment	not modelled	27.9	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
50	d7reqa2	Alignment	not modelled	27.7	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
51	d1vlja_	Alignment	not modelled	27.4	7	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
52	c2decA_	Alignment	not modelled	25.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
						PDB header:oxidoreductase

53	c3bfjK_	Alignment	not modelled	25.4	18	**Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
54	c3ox4D_	Alignment	not modelled	24.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
55	c1w2wJ_	Alignment	not modelled	23.4	17	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
56	c3e59A_	Alignment	not modelled	23.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyoverdine biosynthesis protein pvca; **PDBTitle:** crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
57	c3t76A_	Alignment	not modelled	23.3	8	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
58	d1wpga2	Alignment	not modelled	23.2	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
59	c3knzA_	Alignment	not modelled	23.0	6	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
60	c2infB_	Alignment	not modelled	22.9	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
61	c2fhyL_	Alignment	not modelled	22.0	25	**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
62	d1uc8a1	Alignment	not modelled	21.2	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
63	d1uj4a1	Alignment	not modelled	20.5	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
64	d3by5a1	Alignment	not modelled	20.5	18	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
65	c3by5A_	Alignment	not modelled	20.5	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
66	c1oi7A_	Alignment	not modelled	20.5	17	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
67	c2gq1A_	Alignment	not modelled	20.4	20	**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
68	d1llib_	Alignment	not modelled	19.4	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
69	c3r38A_	Alignment	not modelled	19.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; **PDBTitle:** 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
70	c3ht4B_	Alignment	not modelled	19.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aluminum resistance protein; **PDBTitle:** crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213
71	c2b8eB_	Alignment	not modelled	18.7	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain
72	c2z01A_	Alignment	not modelled	18.7	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus
73	c2duwA_	Alignment	not modelled	18.1	16	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
74	d1v8ba2	Alignment	not modelled	18.1	17	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
75	d1m1na_	Alignment	not modelled	17.8	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
76	c1x1oC_	Alignment	not modelled	17.3	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
77	c3mwdB_	Alignment	not modelled	16.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound

78	d2ofya1	Alignment	not modelled	16.6	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
79	d1miob_	Alignment	not modelled	16.3	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
80	d1mioa_	Alignment	not modelled	16.2	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
81	d1utxa_	Alignment	not modelled	16.1	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
82	c3bs3A_	Alignment	not modelled	15.9	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
83	c3b7hA_	Alignment	not modelled	15.7	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
84	d1ccwa_	Alignment	not modelled	15.3	23	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
85	c3fd0B_	Alignment	not modelled	15.3	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative cystathionine beta-lyase involved in aluminum **PDBTitle:** crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
86	c3ff4A_	Alignment	not modelled	14.8	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
87	c3lisB_	Alignment	not modelled	14.7	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
88	c3nklA_	Alignment	not modelled	14.5	18	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
89	c3cnhA_	Alignment	not modelled	14.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase family protein; **PDBTitle:** crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
90	c3ej6D_	Alignment	not modelled	14.5	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
91	d2vgna3	Alignment	not modelled	14.3	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
92	c2jtvA_	Alignment	not modelled	14.3	8	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
93	c3fkjA_	Alignment	not modelled	14.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
94	c3clhA_	Alignment	not modelled	13.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
95	d1x52a1	Alignment	not modelled	13.5	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
96	d1ejda_	Alignment	not modelled	13.4	22	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
97	d1ri9a_	Alignment	not modelled	13.1	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
98	c1ri9A_	Alignment	not modelled	13.1	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fyn-binding protein; **PDBTitle:** structure of a helically extended sh3 domain of the t cell2 adapter protein adap
99	d2cyga1	Alignment	not modelled	13.0	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases