



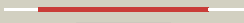


















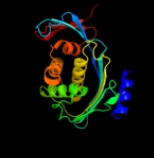




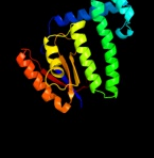

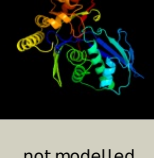


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1pieA_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> galactokinase; <b>PDBTitle:</b> crystal structure of lactococcus lactis galactokinase2 complexed with galactose
2	<a href="#">c2aj4B_</a>	 Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> galactokinase; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae galactokinase2 in complex with galactose and mg:amppnp
3	<a href="#">c1wuua_</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> galactokinase; <b>PDBTitle:</b> crystal structure of human galactokinase complexed with2 mgamppnp and galactose
4	<a href="#">c2a2cA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylgalactosamine kinase; <b>PDBTitle:</b> x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-adp and n-acetyl galactosamine 1-3 phosphate
5	<a href="#">c2cz9A_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable galactokinase; <b>PDBTitle:</b> crystal structure of galactokinase from pyrococcus horikoshi
6	<a href="#">c2r42A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate kinase; <b>PDBTitle:</b> the biochemical and structural basis for feedback2 inhibition of mevalonate kinase and isoprenoid metabolism
7	<a href="#">c3k17A_</a>	 Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lin0012 protein; <b>PDBTitle:</b> crystal structure of a lin0012 protein from listeria innocua
8	<a href="#">c2hfuB_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> mevalonate kinase, putative; <b>PDBTitle:</b> crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
9	<a href="#">c1k47F_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> phosphomevalonate kinase; <b>PDBTitle:</b> crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
10	<a href="#">c1kkhA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate kinase; <b>PDBTitle:</b> crystal structure of the methanococcus jannaschii2 mevalonate kinase
11	<a href="#">c2x7iA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate kinase; <b>PDBTitle:</b> crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252

12	<a href="#">c2oi2A_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate kinase; <b>PDBTitle:</b> streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
13	<a href="#">dlpiea1</a>	Alignment		100.0	33	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
14	<a href="#">c3k85B_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> d-glycero-d-manno-heptose 1-phosphate kinase; <b>PDBTitle:</b> crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
15	<a href="#">dlwuua1</a>	Alignment		100.0	43	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
16	<a href="#">c1fwlD_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> crystal structure of homoserine kinase
17	<a href="#">dlpiea2</a>	Alignment		100.0	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
18	<a href="#">dls4ea2</a>	Alignment		100.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
19	<a href="#">c2gs8A_</a>	Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate pyrophosphate decarboxylase; <b>PDBTitle:</b> structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
20	<a href="#">c3hulA_</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> structure of putative homoserine kinase thrb from listeria2 monocytogenes
21	<a href="#">dlwuua2</a>	Alignment	not modelled	100.0	42	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
22	<a href="#">dls4ea1</a>	Alignment	not modelled	100.0	44	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
23	<a href="#">c2hk3A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphomevalonate decarboxylase; <b>PDBTitle:</b> crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
24	<a href="#">dlkha1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
25	<a href="#">c2v34B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-diphosphocytidyl-2c-methyl-d-erythritol kinase; <b>PDBTitle:</b> ispe in complex with cytidine and ligand
26	<a href="#">dlkva1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
27	<a href="#">cluekA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-(cytidine 5'-diphospho)-2c-methyl-d-erythritol <b>PDBTitle:</b> crystal structure of 4-(cytidine 5'-diphospho)-2c-methyl-d-2 erythritol kinase
28	<a href="#">cloj4B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-diphosphocytidyl-2-c-methyl-d-erythritol <b>PDBTitle:</b> ternary complex of2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase

29	<a href="#">d1k47a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
30	<a href="#">c3ltoB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mevalonate diphosphate decarboxylase; <b>PDBTitle:</b> crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila
31	<a href="#">d1h72c1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
32	<a href="#">d1oj4a1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
33	<a href="#">d1k47a2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Phosphomevalonate kinase (PMK)
34	<a href="#">d1kvka2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Mevalonate kinase
35	<a href="#">c2hkeB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diphosphomevalonate decarboxylase, putative; <b>PDBTitle:</b> mevalonate diphosphate decarboxylase from trypanosoma brucei
36	<a href="#">d1kkha2</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Mevalonate kinase
37	<a href="#">d1ueka1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
38	<a href="#">c1fi4A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate 5-diphosphate decarboxylase; <b>PDBTitle:</b> the x-ray crystal structure of mevalonate 5-di-phosphate decarboxylase2 at 2.3 angstrom resolution.
39	<a href="#">d1fi4a1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
40	<a href="#">c3f0nB_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mevalonate pyrophosphate decarboxylase; <b>PDBTitle:</b> mus musculus mevalonate pyrophosphate decarboxylase
41	<a href="#">d1h72c2</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Homoserine kinase
42	<a href="#">d1ueka2</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
43	<a href="#">d1oj4a2</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
44	<a href="#">d1fi4a2</a>	Alignment	not modelled	96.0	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Mevalonate 5-di-phosphate decarboxylase
45	<a href="#">c3c7bA_</a>	Alignment	not modelled	79.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
46	<a href="#">c2v4jA_</a>	Alignment	not modelled	68.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
47	<a href="#">d3c7bb2</a>	Alignment	not modelled	60.3	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
48	<a href="#">d1lb2b_</a>	Alignment	not modelled	39.2	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
49	<a href="#">d2v4jb2</a>	Alignment	not modelled	35.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
50	<a href="#">d1doqa_</a>	Alignment	not modelled	34.1	13	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
51	<a href="#">c2v4jE_</a>	Alignment	not modelled	31.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
52	<a href="#">d1z3eb1</a>	Alignment	not modelled	30.8	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
53	<a href="#">c3c7bE_</a>	Alignment	not modelled	30.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from

						archaeoglobus2 fulgidus
54	<a href="#">d2cz4a1</a>	Alignment	not modelled	26.0	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GlnB-like <b>Family:</b> Prokaryotic signal transducing protein
55	<a href="#">dlzj8a1</a>	Alignment	not modelled	25.5	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> Duplicated SiR/NiR-like domains 1 and 3
56	<a href="#">d2pv7a1</a>	Alignment	not modelled	23.9	15	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> TyrA dimerization domain-like
57	<a href="#">dlcooa_</a>	Alignment	not modelled	23.6	14	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> C-terminal domain of RNA polymerase alpha subunit <b>Family:</b> C-terminal domain of RNA polymerase alpha subunit
58	<a href="#">d2z15a1</a>	Alignment	not modelled	21.8	23	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
59	<a href="#">c3mnfA_</a>	Alignment	not modelled	20.5	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pac2 family protein; <b>PDBTitle:</b> crystal structure of pac2 family protein from streptomyces avermitilis2 ma
60	<a href="#">d3e9va1</a>	Alignment	not modelled	19.0	26	<b>Fold:</b> BTG domain-like <b>Superfamily:</b> BTG domain-like <b>Family:</b> BTG domain-like
61	<a href="#">dlihwa_</a>	Alignment	not modelled	19.0	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
62	<a href="#">c3sftA_</a>	Alignment	not modelled	18.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator protein-glutamate <b>PDBTitle:</b> crystal structure of thermotoga maritima cheb methyltransferase catalytic2 domain
63	<a href="#">dlex4a1</a>	Alignment	not modelled	18.7	14	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
64	<a href="#">c3gaaB_</a>	Alignment	not modelled	17.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein ta1441; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 thermoplasma acidophilum
65	<a href="#">c2dztA_</a>	Alignment	not modelled	16.3	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
66	<a href="#">d1chda_</a>	Alignment	not modelled	15.9	32	<b>Fold:</b> Methylesterase CheB, C-terminal domain <b>Superfamily:</b> Methylesterase CheB, C-terminal domain <b>Family:</b> Methylesterase CheB, C-terminal domain
67	<a href="#">c2p90B_</a>	Alignment	not modelled	15.7	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein cgl1923; <b>PDBTitle:</b> the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
68	<a href="#">d2bv3a3</a>	Alignment	not modelled	15.6	12	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components
69	<a href="#">c2d99A_</a>	Alignment	not modelled	15.5	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
70	<a href="#">d3c7ba2</a>	Alignment	not modelled	14.0	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nitrite/Sulfite reductase N-terminal domain-like <b>Family:</b> DsrA/DsrB N-terminal-domain-like
71	<a href="#">c2y9jt_</a>	Alignment	not modelled	13.7	10	<b>PDB header:</b> protein transport <b>Chain:</b> T: <b>PDB Molecule:</b> protein prgh; <b>PDBTitle:</b> three-dimensional model of salmonella's needle complex at2 subnanometer resolution
72	<a href="#">c2e3lA_</a>	Alignment	not modelled	13.7	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor gtf2ird2 beta; <b>PDBTitle:</b> solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
73	<a href="#">c1vkrA_</a>	Alignment	not modelled	13.6	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mannitol-specific pts system enzyme iia bc components; <b>PDBTitle:</b> structure of iib domain of the mannitol-specific permease enzyme ii
74	<a href="#">d1vkra_</a>	Alignment	not modelled	13.6	29	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellulose specific IIB subunit
75	<a href="#">c3m05A_</a>	Alignment	not modelled	13.4	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pepe_1480; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
76	<a href="#">d1a6qa1</a>	Alignment	not modelled	12.4	30	<b>Fold:</b> Another 3-helical bundle <b>Superfamily:</b> Protein serine/threonine phosphatase 2C, C-terminal domain <b>Family:</b> Protein serine/threonine phosphatase 2C, C-terminal domain
77	<a href="#">d1mg7a2</a>	Alignment	not modelled	12.3	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Early switch protein XOL-1
78	<a href="#">c2dn5A_</a>	Alignment	not modelled	12.2	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna

79	<a href="#">c3u4gA</a>	Alignment	not modelled	11.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> namn:dmb phosphoribosyltransferase; <b>PDBTitle:</b> the structure of cobt from pyrococcus horikoshii
80	<a href="#">c3ff2A</a>	Alignment	not modelled	11.6	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized cystatin fold protein (yp_497570.1) from <b>PDBTitle:</b> crystal structure of an uncharacterized cystatin fold protein2 (saro_2299) from novosphingobium aromaticivorans dsm at 1.90 a3 resolution
81	<a href="#">d1q60a</a>	Alignment	not modelled	10.4	43	<b>Fold:</b> GTF2I-like repeat <b>Superfamily:</b> GTF2I-like repeat <b>Family:</b> GTF2I-like repeat
82	<a href="#">d1ri9a</a>	Alignment	not modelled	10.3	26	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> SH3-domain <b>Family:</b> SH3-domain
83	<a href="#">c1ri9A</a>	Alignment	not modelled	10.3	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> fyn-binding protein; <b>PDBTitle:</b> structure of a helically extended sh3 domain of the t cell12 adapter protein adap
84	<a href="#">d1szpb1</a>	Alignment	not modelled	10.1	11	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
85	<a href="#">d2axtj1</a>	Alignment	not modelled	10.1	83	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, PsbJ <b>Family:</b> PsbJ-like
86	<a href="#">c3e0dA</a>	Alignment	not modelled	10.1	25	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
87	<a href="#">d1c6vx</a>	Alignment	not modelled	9.8	18	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
88	<a href="#">c1c6vX</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> protein (siu89134); <b>PDBTitle:</b> siv integrase (catalytic domain + dna biding domain2 comprising residues 50-293) mutant with phe 185 replaced3 by his (f185h)
89	<a href="#">d2hmfa2</a>	Alignment	not modelled	9.8	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Aspartokinase allosteric domain-like
90	<a href="#">c2dn4A</a>	Alignment	not modelled	9.8	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
91	<a href="#">d2gexa1</a>	Alignment	not modelled	9.7	16	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-like polyketide cyclase
92	<a href="#">c2ed2A</a>	Alignment	not modelled	9.4	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
93	<a href="#">c2dzqA</a>	Alignment	not modelled	9.2	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i repeat domain- <b>PDBTitle:</b> solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
94	<a href="#">c2ejeA</a>	Alignment	not modelled	9.2	43	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general transcription factor ii-i; <b>PDBTitle:</b> solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
95	<a href="#">c2akjA</a>	Alignment	not modelled	9.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nitrite reductase, chloroplast; <b>PDBTitle:</b> structure of spinach nitrite reductase
96	<a href="#">d1vola2</a>	Alignment	not modelled	9.1	16	<b>Fold:</b> Cyclin-like <b>Superfamily:</b> Cyclin-like <b>Family:</b> Transcription factor IIB (TFIIB), core domain
97	<a href="#">d2i1qa1</a>	Alignment	not modelled	9.0	9	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Rad51 N-terminal domain-like <b>Family:</b> DNA repair protein Rad51, N-terminal domain
98	<a href="#">c5aopA</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase hemoprotein; <b>PDBTitle:</b> sulfite reductase structure reduced with crii edta, 5-coordinate2 siroheme, siroheme feii, [4fe-4s] +1
99	<a href="#">d3ec9a1</a>	Alignment	not modelled	8.5	12	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> PhzA/PhzB-like