Phyre²

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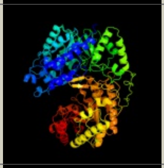
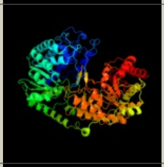
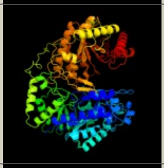
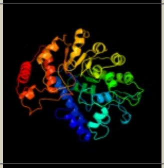
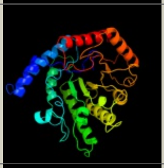
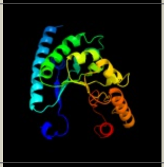
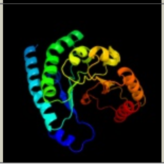
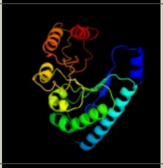
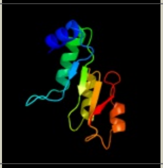
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t7lA_	Alignment		100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of cobalamin-independent methionine2 synthase from t. maritima
2	c3l7sA_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate--homocysteine **PDBTitle:** crystal structure of mete coordinated with zinc from streptococcus2 mutans
3	c1u22A_	Alignment		100.0	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** a. thaliana cobalamine independent methionine synthase
4	c2nq5A_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** crystal structure of methyltransferase from streptococcus2 mutans
5	d1u1ha1	Alignment		100.0	41	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
6	d1u1ha2	Alignment		100.0	58	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
7	c3rpdB_	Alignment		100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methionine synthase (b12-independent); **PDBTitle:** the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
8	c1ypxA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative vitamin-b12 independent methionine synthase family **PDBTitle:** crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
9	d1j93a_	Alignment		99.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
10	c3cyvA_	Alignment		99.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
11	c1jpkA_	Alignment		99.5	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase

12	d1r3sa_	Alignment		99.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
13	c2infB_	Alignment		99.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 bacillus subtilis
14	c2ejaB_	Alignment		99.4	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
15	c3qc3B_	Alignment		93.7	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
16	d1rpxa_	Alignment		93.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
17	d1h1ya_	Alignment		91.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
18	c3inpA_	Alignment		91.7	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
19	d1tqja_	Alignment		91.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
20	c1yadD_	Alignment		90.4	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
21	c3nm3D_	Alignment	not modelled	90.3	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes
22	c3ceuA_	Alignment	not modelled	90.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
23	d1tqxa_	Alignment	not modelled	88.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
24	d2tpsa_	Alignment	not modelled	87.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
25	c3bolB_	Alignment	not modelled	84.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
26	c3cu2A_	Alignment	not modelled	80.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
27	c3lrmB_	Alignment	not modelled	80.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
						Fold:TIM beta/alpha-barrel

28	d1xi3a_	Alignment	not modelled	79.4	13	**Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
29	c3ipwA_	Alignment	not modelled	76.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
30	d1ojxa_	Alignment	not modelled	75.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
31	c3a23A_	Alignment	not modelled	75.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
32	c2ze3A_	Alignment	not modelled	71.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
33	c2bmbA_	Alignment	not modelled	70.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
34	d3bofa2	Alignment	not modelled	69.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
35	c2h90A_	Alignment	not modelled	69.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
36	d1ur4a_	Alignment	not modelled	63.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
37	d1r46a2	Alignment	not modelled	60.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
38	d2flia1	Alignment	not modelled	60.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
39	d1uasa2	Alignment	not modelled	58.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
40	d1qapa1	Alignment	not modelled	57.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
41	c1tx2A_	Alignment	not modelled	57.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
42	d1tx2a_	Alignment	not modelled	57.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
43	c3ct7E_	Alignment	not modelled	56.6	10	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
44	c2qjhH_	Alignment	not modelled	56.1	17	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
45	c3tr9A_	Alignment	not modelled	56.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
46	d1ps9a1	Alignment	not modelled	55.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
47	c2jbmA_	Alignment	not modelled	54.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
48	c1j0yD_	Alignment	not modelled	53.6	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-amylase; **PDBTitle:** beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
49	c1qapA_	Alignment	not modelled	53.6	20	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
50	c3l2iB_	Alignment	not modelled	53.5	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
51	c1ps9A_	Alignment	not modelled	52.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
52	c3a5vA_	Alignment	not modelled	52.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea
53	d1vema2	Alignment	not modelled	51.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

54	c2gl0A_	Alignment	not modelled	51.5	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of pae2307 in complex with adenosine
55	c3hf3A_	Alignment	not modelled	50.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
56	c1o4uA_	Alignment	not modelled	47.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
57	c3e2vA_	Alignment	not modelled	45.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
58	c2y5sA_	Alignment	not modelled	44.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
59	c2d16B_	Alignment	not modelled	43.4	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph1918; **PDBTitle:** crystal structure of ph1918 protein from pyrococcus horikoshii ot3
60	c1x1oC_	Alignment	not modelled	42.7	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
61	d1e0ta2	Alignment	not modelled	42.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
62	d1o4ua1	Alignment	not modelled	41.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
63	d1vgga_	Alignment	not modelled	41.0	22	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
64	c3f41B_	Alignment	not modelled	40.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phytase; **PDBTitle:** structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
65	d1rd5a_	Alignment	not modelled	40.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
66	c1djnB_	Alignment	not modelled	40.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase; **PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
67	c2jvfA_	Alignment	not modelled	39.8	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
68	d1qopa_	Alignment	not modelled	39.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
69	c3bg3B_	Alignment	not modelled	37.9	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
70	d1xcfa_	Alignment	not modelled	37.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
71	c3thaB_	Alignment	not modelled	35.1	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
72	c3l0gD_	Alignment	not modelled	35.1	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
73	d1ad1a_	Alignment	not modelled	34.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
74	c3labA_	Alignment	not modelled	34.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
75	d1luca_	Alignment	not modelled	34.3	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
76	c2b7pA_	Alignment	not modelled	34.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
77	d1umya_	Alignment	not modelled	33.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
78	c2xioA_	Alignment	not modelled	32.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a

79	c2fcdA_	Alignment	not modelled	31.0	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
80	c3pajA_	Alignment	not modelled	30.7	20	**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
81	c1mh3A_	Alignment	not modelled	29.8	12	**PDB header:**sugar binding, dna binding protein **Chain:** A: **PDB Molecule:**maltose binding-a1 homeodomain protein chimera; **PDBTitle:** maltose binding-a1 homeodomain protein chimera, crystal2 form i
82	c3js3C_	Alignment	not modelled	28.8	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
83	d3bofa1	Alignment	not modelled	28.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
84	c3o63B_	Alignment	not modelled	27.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
85	c3fpjA_	Alignment	not modelled	27.4	16	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
86	c2wdfA_	Alignment	not modelled	26.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
87	d1gqna_	Alignment	not modelled	26.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
88	d1wa3a1	Alignment	not modelled	26.5	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
89	c1qysA_	Alignment	not modelled	24.4	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
90	c3l5aA_	Alignment	not modelled	24.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
91	c3rhgA_	Alignment	not modelled	23.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
92	c2v82A_	Alignment	not modelled	23.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
93	c2ekcA_	Alignment	not modelled	23.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
94	c3a98A_	Alignment	not modelled	23.3	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dedicator of cytokinesis protein 2; **PDBTitle:** crystal structure of the complex of the interacting regions of dock22 and elmo1
95	d1pkla2	Alignment	not modelled	23.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
96	c2yr1B_	Alignment	not modelled	23.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
97	d1vjia_	Alignment	not modelled	22.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
98	d1piia1	Alignment	not modelled	22.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
99	d1ajza_	Alignment	not modelled	21.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
100	c3gndC_	Alignment	not modelled	21.7	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
101	d1qpoa1	Alignment	not modelled	21.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
102	c2vefB_	Alignment	not modelled	21.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae