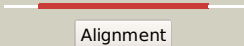

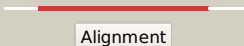

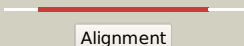







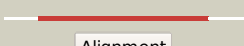











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1296_(thrB)_1452003_1452953
Date	Wed Jul 31 22:05:39 BST 2019
Unique Job ID	6e54de5348aaf18a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6cyzA_</a>	 Alignment		100.0	60	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> mycobacterial homoserine kinase thrb in complex with amppnp
2	<a href="#">c5watB_</a>	 Alignment		100.0	51	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> corynebacterium glutamicum full length homoserine kinase
3	<a href="#">c4p52A_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> crystal structure of homoserine kinase from cytophaga hutchinsonii2 atcc 33406, nysgrc target 032717.
4	<a href="#">c4rpfA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> crystal structure of homoserine kinase from yersinia pestis nepal516,2 nysgrc target 032715
5	<a href="#">c1fwlD_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> crystal structure of homoserine kinase
6	<a href="#">c3pygA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase; <b>PDBTitle:</b> mycobacterium tuberculosis 4-diphosphocytidyl-2-c-methyl-d-erythritol2 kinase (ispe) in complex with adp
7	<a href="#">c3hulA_</a>	 Alignment		100.0	30	<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
8	<a href="#">c2v34B_</a>	 Alignment		100.0	21	<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
9	<a href="#">c1uekA_</a>	 Alignment		100.0	25	<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
10	<a href="#">c1oj4B_</a>	 Alignment		100.0	19	<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 of f2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase
11	<a href="#">c4z7cA_</a>	 Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphomevalonate decarboxylase; <b>PDBTitle:</b> diphosphomevalonate decarboxylase from the sulfobolbus solfataricus,2 space group h32

12	<a href="#">c2cz9A_</a>	Alignment		100.0	20	<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
13	<a href="#">c2hk3A_</a>	Alignment		100.0	17	<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)
14	<a href="#">c6n0yB_</a>	Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diphosphomevalonate decarboxylase; <b>PDBTitle:</b> crystal structure of anaerolinea thermophila mevalonate 5-phosphate2 decarboxylase complexed with (r)-mvapp
15	<a href="#">c5v2IA_</a>	Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate diphosphate decarboxylase; <b>PDBTitle:</b> mevalonate diphosphate mediated atp binding mechanism of the2 mevalonate diphosphate decarboxylase from enterococcus faecalis
16	<a href="#">c2qs8A_</a>	Alignment		100.0	16	<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
17	<a href="#">c4hacA_</a>	Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mevalonate kinase; <b>PDBTitle:</b> crystal structure of the mevalonate kinase from an archaeon2 methanosarcina mazei
18	<a href="#">c2x7iA_</a>	Alignment		100.0	18	<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
19	<a href="#">c2hfuB_</a>	Alignment		100.0	18	<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
20	<a href="#">c3k17A_</a>	Alignment		100.0	18	<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
21	<a href="#">c4ut4B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar kinase; <b>PDBTitle:</b> burkholderia pseudomallei heptokinase wcbl, d-mannose complex.
22	<a href="#">c1kkhA_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">c4n3oB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative d-glycero-d-manno-heptose 7-phosphate kinase; <b>PDBTitle:</b> 2.4 angstrom resolution crystal structure of putative sugar kinase2 from campylobacter jejuni.
24	<a href="#">c2oi2A_</a>	Alignment	not modelled	100.0	18	<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
25	<a href="#">c3ltoB_</a>	Alignment	not modelled	100.0	17	<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
26	<a href="#">d1h72c1</a>	Alignment	not modelled	100.0	26	<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="#">c1k47F_</a>	Alignment	not modelled	100.0	16	<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)
28	<a href="#">c3k85B_</a>	Alignment	not modelled	100.0	18	<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
29	<a href="#">c1pieA_</a>	Alignment	not modelled	100.0	16	<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
30	<a href="#">c2r42A_</a>	Alignment	not modelled	100.0	18	<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
31	<a href="#">c5yysC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> l-fucokinase, l-fucose-1-p guanylyltransferase; <b>PDBTitle:</b> cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacterioides fragilis
32	<a href="#">c1wuua_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> galactokinase; <b>PDBTitle:</b> crystal structure of human galactokinase complexed with2 mgampnp and galactose
33	<a href="#">c2a2cA_</a>	Alignment	not modelled	100.0	16	<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- <i>adp</i> and n-acetyl galactosamine 1-3 phosphate
34	<a href="#">c2aj4B_</a>	Alignment	not modelled	100.0	19	<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: <i>ampnp</i>
35	<a href="#">d1ueka1</a>	Alignment	not modelled	99.9	30	<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
36	<a href="#">d1oj4a1</a>	Alignment	not modelled	99.9	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
37	<a href="#">c3v2uC_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> protein gal3; <b>PDBTitle:</b> crystal structure of the yeast gal regulon complex of the repressor,2 gal80p, and the transducer, gal3p, with galactose and atp
38	<a href="#">d1h72c2</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Homoserine kinase
39	<a href="#">d1fi4a1</a>	Alignment	not modelled	99.9	26	<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="#">d1k47a1</a>	Alignment	not modelled	99.9	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
41	<a href="#">c2hkeB_</a>	Alignment	not modelled	99.9	20	<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
42	<a href="#">d1kkha1</a>	Alignment	not modelled	99.9	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
43	<a href="#">d1ueka2</a>	Alignment	not modelled	99.7	17	<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="#">c6n10A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diphosphomevalonate decarboxylase mvd1, peroxisomal; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase 1 complexed with (r)-mvapp
45	<a href="#">c1fi4A_</a>	Alignment	not modelled	99.7	20	<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-diphosphate decarboxylase2 at 2.3 angstrom resolution.
46	<a href="#">d1s4ea1</a>	Alignment	not modelled	99.7	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
47	<a href="#">d1kvka1</a>	Alignment	not modelled	99.6	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
48	<a href="#">d1piea1</a>	Alignment	not modelled	99.6	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
49	<a href="#">d1oj4a2</a>	Alignment	not modelled	99.6	17	<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
50	<a href="#">c4rksB_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ta1305; <b>PDBTitle:</b> crystal structure of mevalonate-3-kinase from thermoplasma acidophilum2 (mevalonate bound)
51	<a href="#">d1wuua1</a>	Alignment	not modelled	99.5	17	<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
52	<a href="#">d1kvka2</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Mevalonate kinase
53	<a href="#">d1k47a2</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Phosphomevalonate kinase (PMK)
54	<a href="#">c3f0nB_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mevalonate pyrophosphate

54	<a href="#">c3vnb_</a>	Alignment	not modelled	99.2	13	decarboxylase; <b>PDBTitle:</b> mus musculus mevalonate pyrophosphate decarboxylase
55	<a href="#">d1kkha2</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Mevalonate kinase
56	<a href="#">d1s4ea2</a>	Alignment	not modelled	98.8	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
57	<a href="#">d1wuua2</a>	Alignment	not modelled	98.6	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
58	<a href="#">d1piea2</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> Galactokinase
59	<a href="#">c5wasB_</a>	Alignment	not modelled	97.0	67	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine kinase; <b>PDBTitle:</b> corynebacterium glutamicum hydrolyzed homoserine kinase
60	<a href="#">c3u88M_</a>	Alignment	not modelled	66.0	44	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> histone-lysine n-methyltransferase 2a; <b>PDBTitle:</b> crystal structure of human menin in complex with ml1 and ledgf
61	<a href="#">d1rjda_</a>	Alignment	not modelled	20.0	38	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Leucine carboxy methyltransferase Ppm1
62	<a href="#">c3ieiD_</a>	Alignment	not modelled	19.8	38	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
63	<a href="#">c4iaoB_</a>	Alignment	not modelled	18.9	20	<b>PDB header:</b> hydrolase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent histone deacetylase sir2; <b>PDBTitle:</b> crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4
64	<a href="#">c3mntA_</a>	Alignment	not modelled	16.3	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 1; <b>PDBTitle:</b> crystal structure of human leucine carboxyl methyltransferase 1
65	<a href="#">c2zwaA_</a>	Alignment	not modelled	16.0	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> leucine carboxyl methyltransferase 2; <b>PDBTitle:</b> crystal structure of trna wybutosine synthesizing enzyme2 tyw4
66	<a href="#">c2jyaA_</a>	Alignment	not modelled	15.5	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1810; <b>PDBTitle:</b> nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
67	<a href="#">d1kbia1</a>	Alignment	not modelled	14.2	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
68	<a href="#">c5jvoA_</a>	Alignment	not modelled	13.8	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor from the pathogenic2 bacterium corynebacterium pseudotuberculosis
69	<a href="#">c2rdaA_</a>	Alignment	not modelled	11.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyacid oxidase 1; <b>PDBTitle:</b> crystal structure of human glycolate oxidase (go) in complex with cdst
70	<a href="#">c3dclC_</a>	Alignment	not modelled	10.0	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> tm1086; <b>PDBTitle:</b> crystal structure of tm1086
71	<a href="#">c4rwwB_</a>	Alignment	not modelled	10.0	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2692 protein; <b>PDBTitle:</b> crystal structure of l. monocytogenes psta in complex with cyclic-di-2 amp
72	<a href="#">c6d7yA_</a>	Alignment	not modelled	9.6	22	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> 1.75 angstrom resolution crystal structure of the toxic c-terminal tip2 of cdia from pseudomonas aeruginosa in complex with immune protein
73	<a href="#">d1wb9a2</a>	Alignment	not modelled	9.6	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
74	<a href="#">c4rleA_</a>	Alignment	not modelled	9.1	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yaaq; <b>PDBTitle:</b> crystal structure of the c-di-amp binding pii-like protein dara
75	<a href="#">d1ub4c_</a>	Alignment	not modelled	9.1	19	<b>Fold:</b> Double-split beta-barrel <b>Superfamily:</b> AbrB/MazE/MraZ-like <b>Family:</b> Kis/PemI addiction antidote
76	<a href="#">d1tb3a1</a>	Alignment	not modelled	8.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
77	<a href="#">d1jdqa_</a>	Alignment	not modelled	7.9	17	<b>Fold:</b> IF3-like <b>Superfamily:</b> SirA-like <b>Family:</b> SirA-like
78	<a href="#">c2e77B_</a>	Alignment	not modelled	7.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate oxidase; <b>PDBTitle:</b> crystal structure of l-lactate oxidase with pyruvate complex
79	<a href="#">c4wk1A_</a>	Alignment	not modelled	7.5	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> psta; <b>PDBTitle:</b> crystal structure of staphylococcus aureus psta in complex with c-di-2 amp

80	<a href="#">c1fcbA</a>	Alignment	not modelled	7.4	16	<b>PDB header:</b> oxidoreductase (ch-oh(d)-cytochrome(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome b2; <b>PDBTitle:</b> molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
81	<a href="#">c5fkvA</a>	Alignment	not modelled	7.4	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
82	<a href="#">d1oe1a2</a>	Alignment	not modelled	7.2	23	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
83	<a href="#">c3ucOB</a>	Alignment	not modelled	7.2	14	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope protein; <b>PDBTitle:</b> crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
84	<a href="#">d1zq1a1</a>	Alignment	not modelled	7.0	18	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> GatD N-terminal domain-like <b>Family:</b> GatD N-terminal domain-like
85	<a href="#">c4hhuA</a>	Alignment	not modelled	7.0	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> or280; <b>PDBTitle:</b> crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
86	<a href="#">d2auna2</a>	Alignment	not modelled	6.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> LD-carboxypeptidase A N-terminal domain-like
87	<a href="#">d2dfaa1</a>	Alignment	not modelled	6.6	64	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
88	<a href="#">d1v6ta</a>	Alignment	not modelled	6.5	36	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
89	<a href="#">c5uscB</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
90	<a href="#">c2x5eA</a>	Alignment	not modelled	6.4	45	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0271 protein pa4511; <b>PDBTitle:</b> crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
91	<a href="#">c6i9bA</a>	Alignment	not modelled	6.3	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> la-related protein 4; <b>PDBTitle:</b> nmr structure of the la module from human larp4a
92	<a href="#">c5ireA</a>	Alignment	not modelled	6.0	27	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> the cryo-em structure of zika virus
93	<a href="#">d1xw8a</a>	Alignment	not modelled	5.9	55	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
94	<a href="#">d2p5ma1</a>	Alignment	not modelled	5.9	5	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
95	<a href="#">c3m05A</a>	Alignment	not modelled	5.5	13	<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 protein pepe_1480 from2 pediococcus pentosaceus atcc 25745
96	<a href="#">c2qx2A</a>	Alignment	not modelled	5.4	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sex pheromone staph-cam373; <b>PDBTitle:</b> structure of the c-terminal domain of sex pheromone staph-cam3732 precursor from staphylococcus aureus
97	<a href="#">d1xxaa</a>	Alignment	not modelled	5.4	10	<b>Fold:</b> DCoH-like <b>Superfamily:</b> C-terminal domain of arginine repressor <b>Family:</b> C-terminal domain of arginine repressor
98	<a href="#">d1wh9a</a>	Alignment	not modelled	5.3	16	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
99	<a href="#">c1zrsB</a>	Alignment	not modelled	5.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> wild-type ld-carboxypeptidase