

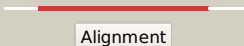

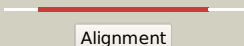







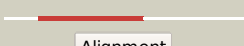











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1133c_(metE)_1259072_1261351
Date	Wed Jul 31 22:05:21 BST 2019
Unique Job ID	2e7534f6cb532bb3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ztxA_</a>	 Alignment		100.0	46	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin-independent methionine synthase; <b>PDBTitle:</b> neurospora crassa cobalamin-independent methionine synthase complexed2 with zn2+
2	<a href="#">c1t7IA_</a>	 Alignment		100.0	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of cobalamin-independent methionine synthase from t.2 maritima
3	<a href="#">c3l7sA_</a>	 Alignment		100.0	46	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of mete coordinated with zinc from streptococcus2 mutans
4	<a href="#">c1u22A_</a>	 Alignment		100.0	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> a. thaliana cobalamine independent methionine synthase
5	<a href="#">c2nq5A_</a>	 Alignment		100.0	47	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of methyltransferase from streptococcus mutans
6	<a href="#">c3ppgA_</a>	 Alignment		100.0	47	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of the candida albicans methionine synthase by2 surface entropy reduction, alanine variant with zinc
7	<a href="#">d1u1ha1</a>	 Alignment		100.0	45	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Cobalamin-independent methionine synthase
8	<a href="#">d1u1ha2</a>	 Alignment		100.0	57	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Cobalamin-independent methionine synthase
9	<a href="#">c3rpdB_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase (b12-independent); <b>PDBTitle:</b> the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
10	<a href="#">c1ypxA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative vitamin-b12 independent methionine synthase family <b>PDBTitle:</b> crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
11	<a href="#">c4ay8B_</a>	 Alignment		99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methylcobalamin): coenzyme m methyltransferase; <b>PDBTitle:</b> semet-derivative of a methyltransferase from m. mazei

12	<a href="#">c3cyvA_</a>	Alignment		99.5	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
13	<a href="#">d1j93a_</a>	Alignment		99.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
14	<a href="#">c1jpkA_</a>	Alignment		99.5	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
15	<a href="#">c2ejaB_</a>	Alignment		99.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
16	<a href="#">c2infB_</a>	Alignment		99.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
17	<a href="#">c4exqA_</a>	Alignment		99.4	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
18	<a href="#">c4zr8B_</a>	Alignment		99.3	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
19	<a href="#">d1r3sa_</a>	Alignment		99.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
20	<a href="#">c3qc3B_</a>	Alignment		93.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> d-ribulose-5-phosphate-3-epimerase; <b>PDBTitle:</b> crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
21	<a href="#">d1h1ya_</a>	Alignment	not modelled	91.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
22	<a href="#">d1ur4a_</a>	Alignment	not modelled	91.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
23	<a href="#">c4nu7C_</a>	Alignment	not modelled	88.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
24	<a href="#">c3ceuA_</a>	Alignment	not modelled	87.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine phosphate pyrophosphorylase; <b>PDBTitle:</b> crystal structure of thiamine phosphate pyrophosphorylase (bt_0647)2 from bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr268
25	<a href="#">c3ct7E_</a>	Alignment	not modelled	87.7	15	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> d-allulose-6-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
26	<a href="#">d1rpxa_</a>	Alignment	not modelled	87.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
27	<a href="#">c4dnhA_</a>	Alignment	not modelled	85.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of hypothetical protein smc04132 from sinorhizobium2 meliloti 1021
28	<a href="#">d1tqxa_</a>	Alignment	not modelled	85.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase

29	<a href="#">c3inpA</a>	Alignment	not modelled	85.2	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
30	<a href="#">d1tqja</a>	Alignment	not modelled	84.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
31	<a href="#">c3ipwA</a>	Alignment	not modelled	84.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase tatd family protein; <b>PDBTitle:</b> crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
32	<a href="#">c5umfB</a>	Alignment	not modelled	83.7	25	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
33	<a href="#">c3l2iB</a>	Alignment	not modelled	81.9	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
34	<a href="#">c2jbmA</a>	Alignment	not modelled	80.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human
35	<a href="#">d2tpsa</a>	Alignment	not modelled	78.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
36	<a href="#">c2bmbA</a>	Alignment	not modelled	74.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> folic acid synthesis protein fol1; <b>PDBTitle:</b> x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase from3 saccharomyces cerevisiae
37	<a href="#">c3nm3D</a>	Alignment	not modelled	73.6	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thiamine biosynthetic bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
38	<a href="#">c3cu2A</a>	Alignment	not modelled	72.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose-5-phosphate 3-epimerase; <b>PDBTitle:</b> crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
39	<a href="#">c5n2pA</a>	Alignment	not modelled	72.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> sulfobolus solfataricus tryptophan synthase a
40	<a href="#">d1umya</a>	Alignment	not modelled	72.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
41	<a href="#">c2h90A</a>	Alignment	not modelled	72.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
42	<a href="#">c5kzmA</a>	Alignment	not modelled	70.6	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
43	<a href="#">d1xcfa</a>	Alignment	not modelled	69.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
44	<a href="#">c3rhgA</a>	Alignment	not modelled	69.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphotriesterase; <b>PDBTitle:</b> crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
45	<a href="#">c3bolB</a>	Alignment	not modelled	67.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate s-homocysteine <b>PDBTitle:</b> cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
46	<a href="#">c5k9xA</a>	Alignment	not modelled	67.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
47	<a href="#">c2ze3A</a>	Alignment	not modelled	66.9	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
48	<a href="#">c2ekcA</a>	Alignment	not modelled	65.5	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
49	<a href="#">c3lrmB</a>	Alignment	not modelled	65.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosidase 1; <b>PDBTitle:</b> structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
50	<a href="#">d2flia1</a>	Alignment	not modelled	64.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
51	<a href="#">d1qopa</a>	Alignment	not modelled	64.2	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
52	<a href="#">c4mwaA</a>	Alignment	not modelled	63.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
53	<a href="#">c5ey5A</a>	Alignment	not modelled	62.7	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
54	<a href="#">c2h7nA</a>	Alignment	not modelled	62.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide pyrophosphorylase;

54	<a href="#">c207pA</a>	Alignment	not modelled	62.1	21	<b>PDBTitle:</b> crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
55	<a href="#">c2d16B</a>	Alignment	not modelled	60.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph1918; <b>PDBTitle:</b> crystal structure of ph1918 protein from pyrococcus horikoshii ot3
56	<a href="#">d1vema2</a>	Alignment	not modelled	57.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
57	<a href="#">c1j0yD</a>	Alignment	not modelled	57.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-amylase; <b>PDBTitle:</b> beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
58	<a href="#">c3navB</a>	Alignment	not modelled	57.3	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
59	<a href="#">d1ps9a1</a>	Alignment	not modelled	57.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
60	<a href="#">c1ps9A</a>	Alignment	not modelled	56.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
61	<a href="#">c3vndD</a>	Alignment	not modelled	56.5	16	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
62	<a href="#">c3a23A</a>	Alignment	not modelled	55.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted alpha-galactosidase; <b>PDBTitle:</b> crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
63	<a href="#">c3e2vA</a>	Alignment	not modelled	55.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3'-5'-exonuclease; <b>PDBTitle:</b> crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
64	<a href="#">d1xi3a</a>	Alignment	not modelled	54.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Thiamin phosphate synthase <b>Family:</b> Thiamin phosphate synthase
65	<a href="#">c4i6kA</a>	Alignment	not modelled	53.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase family protein; <b>PDBTitle:</b> crystal structure of probable 2-pyrone-4,6-dicarboxylic acid hydrolase2 abaye1769 (target efi-505029) from acinetobacter baumannii with3 citric acid bound
66	<a href="#">c1yadD</a>	Alignment	not modelled	53.7	6	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> regulatory protein teni; <b>PDBTitle:</b> structure of teni from bacillus subtilis
67	<a href="#">c3f41B</a>	Alignment	not modelled	53.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
68	<a href="#">c4ap6C</a>	Alignment	not modelled	51.5	34	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-fucose protein o-fucosyltransferase 2; <b>PDBTitle:</b> crystal structure of human pofut2 e54a mutant in complex with gdp-2 fucose
69	<a href="#">c6gpaA</a>	Alignment	not modelled	50.9	17	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> arabinogalactan endo-beta-1,4-galactanase; <b>PDBTitle:</b> beta-1,4-galactanase from bacteroides thetaiotaomicron with galactose
70	<a href="#">c4mozC</a>	Alignment	not modelled	50.5	22	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> fructose-bisphosphate aldolase from slackia heliotrinireducens dsm2 20476
71	<a href="#">d3bofa1</a>	Alignment	not modelled	50.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
72	<a href="#">c1o4uA</a>	Alignment	not modelled	49.1	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinolinic acid phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
73	<a href="#">d1o4ua1</a>	Alignment	not modelled	48.5	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
74	<a href="#">c3a5vA</a>	Alignment	not modelled	48.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of alpha-galactosidase i from mortierella vinacea
75	<a href="#">c3js3C</a>	Alignment	not modelled	47.7	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase; <b>PDBTitle:</b> crystal structure of type i 3-dehydroquinatase dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
76	<a href="#">d1r46a2</a>	Alignment	not modelled	47.5	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
77	<a href="#">d1qapa1</a>	Alignment	not modelled	47.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
78	<a href="#">c5eu0B</a>	Alignment	not modelled	46.9	24	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin 1; <b>PDBTitle:</b> fic domain of bep1 from bartonella rochalimae in complex with biao
79	<a href="#">d1uasa2</a>	Alignment	not modelled	46.5	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases

						<b>Family:</b> Amylase, catalytic domain
80	<a href="#">c2y5sA_</a>	Alignment	not modelled	44.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
81	<a href="#">c1djnB_</a>	Alignment	not modelled	44.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
82	<a href="#">d1liua2</a>	Alignment	not modelled	43.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
83	<a href="#">c2jvfA_</a>	Alignment	not modelled	43.0	28	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo protein m7; <b>PDBTitle:</b> solution structure of m7, a computationally-designed2 artificial protein
84	<a href="#">c2ekmC_</a>	Alignment	not modelled	42.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein st1511; <b>PDBTitle:</b> structure of st1219 protein from sulfolobus tokodaii
85	<a href="#">c2yciX_</a>	Alignment	not modelled	42.5	12	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
86	<a href="#">c5kinC_</a>	Alignment	not modelled	42.5	25	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
87	<a href="#">c5foeA_</a>	Alignment	not modelled	41.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-fucose protein o-fucosyltransferase 2,thrombospondin-1; <b>PDBTitle:</b> crystal structure of the c. elegans protein o-fucosyltransferase 22 (cepofut2) double mutant (r298k-r299k) in complex with gdp and the3 human tsr1 from thrombospondin 1
88	<a href="#">d1gqna_</a>	Alignment	not modelled	41.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
89	<a href="#">c2xioA_</a>	Alignment	not modelled	40.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative deoxyribonuclease tatdn1; <b>PDBTitle:</b> structure of putative deoxyribonuclease tatdn1 isoform a
90	<a href="#">c3vocA_</a>	Alignment	not modelled	40.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta/alpha-amylase; <b>PDBTitle:</b> crystal structure of the catalytic domain of beta-amylase from2 paenibacillus polymyxa
91	<a href="#">d1vgga_</a>	Alignment	not modelled	40.1	21	<b>Fold:</b> Ta1353-like <b>Superfamily:</b> Ta1353-like <b>Family:</b> Ta1353-like
92	<a href="#">c2gl0A_</a>	Alignment	not modelled	39.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> structure of pae2307 in complex with adenosine
93	<a href="#">c2vefB_</a>	Alignment	not modelled	38.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
94	<a href="#">c4nziA_</a>	Alignment	not modelled	38.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha-galactosidase; <b>PDBTitle:</b> crystal structure of a putative alpha-galactosidase (bf1418) from2 bacteroides fragilis nctc 9343 at 1.57 a resolution
95	<a href="#">d1qpoa1</a>	Alignment	not modelled	37.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
96	<a href="#">c3hf3A_</a>	Alignment	not modelled	37.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
97	<a href="#">c4cczA_</a>	Alignment	not modelled	36.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase; <b>PDBTitle:</b> crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
98	<a href="#">d1ojxa_</a>	Alignment	not modelled	36.2	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
99	<a href="#">c1qpoA_</a>	Alignment	not modelled	35.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolate acid phosphoribosyl transferase; <b>PDBTitle:</b> quinolate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
100	<a href="#">c3fokH_</a>	Alignment	not modelled	35.5	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> uncharacterized protein cgl0159; <b>PDBTitle:</b> crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
101	<a href="#">d1ajza_</a>	Alignment	not modelled	35.2	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
102	<a href="#">c2o1eB_</a>	Alignment	not modelled	34.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ycdh; <b>PDBTitle:</b> crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
103	<a href="#">c3thaB_</a>	Alignment	not modelled	34.8	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> tryptophan synthase subunit alpha from campylobacter jejuni.
						<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-dependent flavin



104	<a href="#">c5ocsB_</a>	Alignment	not modelled	34.6	9	oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
105	<a href="#">d1luca_</a>	Alignment	not modelled	34.4	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
106	<a href="#">c4xrvB_</a>	Alignment	not modelled	33.9	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic solute binding protein; <b>PDBTitle:</b> structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
107	<a href="#">c5d4yA_</a>	Alignment	not modelled	32.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylanase; <b>PDBTitle:</b> a psychrophilic glycoside hydrolase family 10 endo-beta-1,4-xylanase
108	<a href="#">c2yr1B_</a>	Alignment	not modelled	31.9	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
109	<a href="#">c3ih1A_</a>	Alignment	not modelled	31.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
110	<a href="#">d1e0ta2</a>	Alignment	not modelled	31.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
111	<a href="#">c3l0gD_</a>	Alignment	not modelled	31.5	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
112	<a href="#">c5ze4A_</a>	Alignment	not modelled	30.7	7	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxy-acid dehydratase, chloroplastic; <b>PDBTitle:</b> the structure of holo- structure of dhad complex with [2fe-2s] cluster
113	<a href="#">c5suswD_</a>	Alignment	not modelled	30.5	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> the crystal structure of 7,8-dihydropteroate synthase from vibrio2 fischeri es114
114	<a href="#">c3tqvA_</a>	Alignment	not modelled	30.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
115	<a href="#">d1bf6a_</a>	Alignment	not modelled	28.9	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> Phosphotriesterase-like
116	<a href="#">c1x1oC_</a>	Alignment	not modelled	28.8	26	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0268 from thermus thermophilus hb8
117	<a href="#">c6cluC_</a>	Alignment	not modelled	28.3	20	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> C: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
118	<a href="#">d1to3a_</a>	Alignment	not modelled	28.2	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
119	<a href="#">d1lt7a_</a>	Alignment	not modelled	27.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
120	<a href="#">c3k2gA_</a>	Alignment	not modelled	27.9	19	<b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase- <b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides