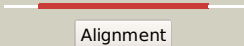

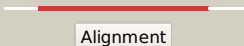

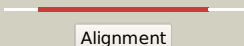







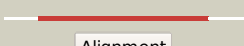









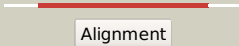

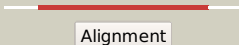

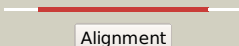



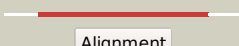

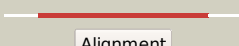

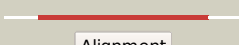






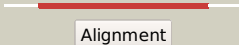
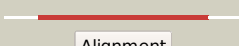

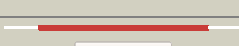




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0498 (- )_588328_589170
Date	Fri Jul 26 01:50:04 BST 2019
Unique Job ID	1f7d20b7e0762585

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1i60a_</a>			100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
2	<a href="#">c5zfsA_</a>			100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allulose-3-epimerase; <b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
3	<a href="#">c3vylB_</a>			100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose 3-epimerase; <b>PDBTitle:</b> structure of l-ribulose 3-epimerase
4	<a href="#">c3kwsB_</a>			100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
5	<a href="#">c5hmqE_</a>			100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
6	<a href="#">c3vniC_</a>			100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
7	<a href="#">c2hk1D_</a>			100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
8	<a href="#">c3cnyA_</a>			100.0	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> inositol catabolism protein iole; <b>PDBTitle:</b> crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
9	<a href="#">c3wqoB_</a>			100.0	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mj1311; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase-like protein
10	<a href="#">d2g0wa1</a>			100.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
11	<a href="#">c2ou4C_</a>			100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> d-tagatose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii

12	<a href="#">c3dx5A_</a>	 Alignment		100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
13	<a href="#">c2zdsB_</a>	 Alignment		100.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of sco6571 from streptomyces coelicolor a3(2)
14	<a href="#">c5tnvA_</a>	 Alignment		100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family protein 2; <b>PDBTitle:</b> crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
15	<a href="#">c3ju2A_</a>	 Alignment		100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein smc04130; <b>PDBTitle:</b> crystal structure of protein smc04130 from sinorhizobium melliloti 1021
16	<a href="#">c3cqkB_</a>	 Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose-5-phosphate 3-epimerase ulae; <b>PDBTitle:</b> crystal structure of l-xyulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
17	<a href="#">c3obeB_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distansonis atcc 8503 at 1.70 a resolution
18	<a href="#">d1k77a_</a>	 Alignment		100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Hypothetical protein YgbM (EC1530)
19	<a href="#">c2zvrA_</a>	 Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm_0416; <b>PDBTitle:</b> crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
20	<a href="#">c4ovxA_</a>	 Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
21	<a href="#">c3lmzA_</a>	 Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distansonis atcc 8503 at 1.44 a resolution
22	<a href="#">c3qxbB_</a>	 Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative xylose isomerase; <b>PDBTitle:</b> crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
23	<a href="#">c3ktcB_</a>	 Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
24	<a href="#">c3l23A_</a>	 Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distansonis atcc 8503 at 1.70 a3 resolution
25	<a href="#">d1xp3a1</a>	 Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
26	<a href="#">c2qw5B_</a>	 Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase-like tim barrel; <b>PDBTitle:</b> crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
27	<a href="#">c4k3zA_</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-erythrose 4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythrose 4-phosphate

					dehydrogenase from2 brucella melitensis, solved by iodide sad
28	<a href="#">d2q02a1</a>	Alignment	not modelled	100.0	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
29	<a href="#">c3p6A</a>	Alignment	not modelled	100.0	14 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distansoni atcc 8503 at 1.85 a resolution
30	<a href="#">c3ngfA</a>	Alignment	not modelled	100.0	15 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family 2; <b>PDBTitle:</b> crystal structure of ap endonuclease, family 2 from brucella2 melitensis
31	<a href="#">d1yx1a1</a>	Alignment	not modelled	100.0	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> KguE-like
32	<a href="#">c2x7vA</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
33	<a href="#">d1qtwa</a>	Alignment	not modelled	100.0	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
34	<a href="#">c4kw2A</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative uncharacterized protein (bdi_1873)2 from parabacteroides distansoni atcc 8503 at 2.32 a resolution
35	<a href="#">c3aamA</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease iv; <b>PDBTitle:</b> crystal structure of endonuclease iv from thermus thermophilus hb8
36	<a href="#">c5zhzA</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of the apurinic/aprimidinic endonuclease iv from2 mycobacterium tuberculosis
37	<a href="#">d1muwa</a>	Alignment	not modelled	100.0	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
38	<a href="#">d1qt1a</a>	Alignment	not modelled	100.0	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
39	<a href="#">d1bxba</a>	Alignment	not modelled	100.0	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
40	<a href="#">d1tz9a</a>	Alignment	not modelled	100.0	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> UxuA-like
41	<a href="#">d1bxca</a>	Alignment	not modelled	100.0	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
42	<a href="#">d2glka1</a>	Alignment	not modelled	100.0	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
43	<a href="#">d1xima</a>	Alignment	not modelled	100.0	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
44	<a href="#">c3aytA</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein tthb071; <b>PDBTitle:</b> tthb071 protein from thermus thermophilus hb8
45	<a href="#">c3bdkB</a>	Alignment	not modelled	99.9	12 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase; <b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
46	<a href="#">d1xlma</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
47	<a href="#">c4eacC</a>	Alignment	not modelled	99.9	19 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> mannonate dehydratase; <b>PDBTitle:</b> crystal structure of mannonate dehydratase from escherichia coli2 strain k12
48	<a href="#">c2i56A</a>	Alignment	not modelled	99.7	12 <b>PDB header:</b> isomerase, metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose isomerase; <b>PDBTitle:</b> crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
49	<a href="#">d1a0da</a>	Alignment	not modelled	99.7	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
50	<a href="#">d1a0ea</a>	Alignment	not modelled	99.7	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
51	<a href="#">d1a0ca</a>	Alignment	not modelled	99.6	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
52	<a href="#">c4xkmB</a>	Alignment	not modelled	99.6	11 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase; <b>PDBTitle:</b> crystal structure of xylose isomerase from an human intestinal tract2 microbe bacteroides thetaiotaomicron
53	<a href="#">c3bzjA</a>	Alignment	not modelled	99.5	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uv endonuclease; <b>PDBTitle:</b> uvde k229l

54	<a href="#">c3tc3B_</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uv damage endonuclease; <b>PDBTitle:</b> crystal structure of sacuvde
55	<a href="#">c3bwwA_</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function duf692/cog3220; <b>PDBTitle:</b> crystal structure of a duf692 family protein (hs_1138) from <i>Haemophilus somnus</i> 129pt at 2.20 Å resolution
56	<a href="#">c3p14C_</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> l-rhamnose isomerase; <b>PDBTitle:</b> crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from <i>Bacillus halodurans</i>
57	<a href="#">d1d8wa_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> L-rhamnose isomerase
58	<a href="#">d1qwga_</a>	Alignment	not modelled	95.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
59	<a href="#">c5ks8D_</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate carboxylase subunit beta; <b>PDBTitle:</b> crystal structure of two-subunit pyruvate carboxylase from <i>Methylobacillus flagellatus</i>
60	<a href="#">d2flia1</a>	Alignment	not modelled	94.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
61	<a href="#">c2qjhH_</a>	Alignment	not modelled	93.5	20	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400; <b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to 2-dihydroxyacetone phosphate
62	<a href="#">c3ivuB_</a>	Alignment	not modelled	92.5	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homocitrate synthase, mitochondrial; <b>PDBTitle:</b> homocitrate synthase lys4 bound to 2-og
63	<a href="#">d1h1ya_</a>	Alignment	not modelled	92.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
64	<a href="#">d1x7fa2</a>	Alignment	not modelled	92.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Outer surface protein, N-terminal domain
65	<a href="#">c1rr2A_</a>	Alignment	not modelled	92.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
66	<a href="#">c1x7fA_</a>	Alignment	not modelled	91.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> outer surface protein; <b>PDBTitle:</b> crystal structure of an uncharacterized <i>B. cereus</i> protein
67	<a href="#">c4qnwA_</a>	Alignment	not modelled	91.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chanoclavine-i aldehyde reductase; <b>PDBTitle:</b> crystal structure of easa, an old yellow enzyme from <i>Aspergillus fumigatus</i>
68	<a href="#">c4ot7A_</a>	Alignment	not modelled	90.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of a variant of ncr from <i>Zymomonas mobilis</i>
69	<a href="#">c3w9zA_</a>	Alignment	not modelled	90.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
70	<a href="#">c6ei9A_</a>	Alignment	not modelled	89.8	16	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase b; <b>PDBTitle:</b> crystal structure of <i>E. coli</i> trna-dihydrouridine synthase b (dusb)
71	<a href="#">c1sr9A_</a>	Alignment	not modelled	89.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of leua from <i>Mycobacterium tuberculosis</i>
72	<a href="#">c3hpxB_</a>	Alignment	not modelled	89.1	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase; <b>PDBTitle:</b> crystal structure of <i>Mycobacterium tuberculosis</i> leua active site2 domain 1-425 (truncation mutant delta:426-644)
73	<a href="#">c2ftpA_</a>	Alignment	not modelled	88.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of hydroxymethylglutaryl-coa lyase from <i>Pseudomonas aeruginosa</i>
74	<a href="#">c3inpA_</a>	Alignment	not modelled	88.7	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-ribulose-phosphate 3-epimerase; <b>PDBTitle:</b> 2.05 Å resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from <i>Francisella tularensis</i> .
75	<a href="#">d1vyra_</a>	Alignment	not modelled	88.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
76	<a href="#">c2vncB_</a>	Alignment	not modelled	88.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen operon protein glgx; <b>PDBTitle:</b> crystal structure of glycogen debranching enzyme trex from <i>Sulfolobus solfataricus</i>
77	<a href="#">c2nx9B_</a>	Alignment	not modelled	87.9	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the 2-oxaloacetate decarboxylase na+ pump from <i>Vibrio cholerae</i>
78	<a href="#">d1u83a_</a>	Alignment	not modelled	87.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (2r)-phospho-3-sulfolactate synthase ComA <b>Family:</b> (2r)-phospho-3-sulfolactate synthase ComA
79	<a href="#">c1u83A_</a>	Alignment	not modelled	87.6	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphosulfolactate synthase; <b>PDBTitle:</b> psl synthase from <i>Bacillus subtilis</i>
						<b>PDB header:</b> plant protein

80	<a href="#">c6e1jB_</a>	Alignment	not modelled	87.5	8	<b>Chain:</b> B: <b>PDB Molecule:</b> 2-isopropylmalate synthase, a genome specific 1; <b>PDBTitle:</b> crystal structure of methylthioalkylmalate synthase (bjumam1.1) from <i>Brassica juncea</i>
81	<a href="#">c5ey5A_</a>	Alignment	not modelled	87.5	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lbcats-a; <b>PDBTitle:</b> lbcats
82	<a href="#">c4nu7C_</a>	Alignment	not modelled	87.1	13	<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 from <i>Toxoplasma gondii</i> .
83	<a href="#">c2cw6B_</a>	Alignment	not modelled	87.1	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase, mitochondrial; <b>PDBTitle:</b> crystal structure of human hmg-coa lyase: insights into 2 catalysis and the molecular basis for 3 hydroxymethylglutaric aciduria
84	<a href="#">c4xp7A_</a>	Alignment	not modelled	86.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine(20) synthase [nad(p)+]-like; <b>PDBTitle:</b> crystal structure of human trna dihydrouridine synthase 2
85	<a href="#">d2zdra2</a>	Alignment	not modelled	86.9	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
86	<a href="#">c2wskA_</a>	Alignment	not modelled	86.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen debranching enzyme; <b>PDBTitle:</b> crystal structure of glycogen debranching enzyme glgx from <i>Escherichia coli</i> k-12
87	<a href="#">c3ct7E_</a>	Alignment	not modelled	86.6	14	<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-epimerase 2 from <i>Escherichia coli</i> k-12
88	<a href="#">d1tqja_</a>	Alignment	not modelled	85.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
89	<a href="#">c3vocA_</a>	Alignment	not modelled	85.4	9	<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 from <i>Paenibacillus polymyxa</i>
90	<a href="#">c4ml9A_</a>	Alignment	not modelled	85.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized tim barrel protein with the 2 conserved phosphate binding site from <i>Sebaldeella termitidis</i>
91	<a href="#">c1ehaA_</a>	Alignment	not modelled	85.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltrehalose trehalohydrolase; <b>PDBTitle:</b> crystal structure of glycosyltrehalose trehalohydrolase from <i>Sulfolobus solfataricus</i>
92	<a href="#">d1rpxa_</a>	Alignment	not modelled	84.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
93	<a href="#">c6gvbC_</a>	Alignment	not modelled	84.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> exo-beta-1,4-mannosidase; <b>PDBTitle:</b> crystal structure of <i>Cutibacterium acnes</i> exo-beta-1,4-mannosidase
94	<a href="#">c3am1A_</a>	Alignment	not modelled	84.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> os06g0726400 protein; <b>PDBTitle:</b> structure of the starch branching enzyme i (bei) from <i>Oryza sativa</i> l
95	<a href="#">c1bf2A_</a>	Alignment	not modelled	84.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of <i>Pseudomonas</i> isoamylase
96	<a href="#">c517jA_</a>	Alignment	not modelled	84.7	17	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elp3 family; <b>PDBTitle:</b> crystal structure of elp3 from <i>Dehalococcoides mccartyi</i>
97	<a href="#">d1gcya2</a>	Alignment	not modelled	84.6	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
98	<a href="#">c5tchG_</a>	Alignment	not modelled	84.5	17	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from <i>M. tuberculosis</i> -2 ligand-free form, trpa-g66v mutant
99	<a href="#">c3thaB_</a>	Alignment	not modelled	84.4	16	<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 <i>Campylobacter jejuni</i> .
100	<a href="#">c1jdaA_</a>	Alignment	not modelled	84.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha maltotetrahydrolase; <b>PDBTitle:</b> maltotetraose-forming exo-amylase
101	<a href="#">c5umfB_</a>	Alignment	not modelled	84.2	18	<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 <i>Neisseria</i> 2 gonorrhoeae with bound phosphate
102	<a href="#">c1ydoC_</a>	Alignment	not modelled	84.2	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> hmg-coa lyase; <b>PDBTitle:</b> crystal structure of the <i>Bacillus subtilis</i> hmg-coa lyase, northeast 2 structural genomics target sr181.
103	<a href="#">c2x4bA_</a>	Alignment	not modelled	84.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> limit dextrinase; <b>PDBTitle:</b> barley limit dextrinase in complex with beta-cyclodextrin
104	<a href="#">c5k9xA_</a>	Alignment	not modelled	83.7	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 <i>Legionella</i> 2 pneumophila subsp. pneumophila
105	<a href="#">c5gquA_</a>	Alignment	not modelled	83.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha-glucan branching enzyme glgb; <b>PDBTitle:</b> crystal structure of branching enzyme from <i>Cyanospora</i> sp. atcc 51142



106	<a href="#">c4mozC_</a>	Alignment	not modelled	83.5	16	<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
107	<a href="#">d1vema2</a>	Alignment	not modelled	83.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
108	<a href="#">c6mywA_</a>	Alignment	not modelled	83.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> gluconobacter ene-reductase (gluer) mutant - t36a
109	<a href="#">c4u5iB_</a>	Alignment	not modelled	83.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase h; <b>PDBTitle:</b> complex structure of mutant ctcel5e (e314a) with xylobiose
110	<a href="#">c2vg2C_</a>	Alignment	not modelled	82.8	7	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> undecaprenyl pyrophosphate synthetase; <b>PDBTitle:</b> rv2361 with ipp
111	<a href="#">c3navB_</a>	Alignment	not modelled	82.1	12	<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
112	<a href="#">c5kzmA_</a>	Alignment	not modelled	81.9	19	<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
113	<a href="#">d1ujpa_</a>	Alignment	not modelled	81.7	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
114	<a href="#">c2ekcA_</a>	Alignment	not modelled	81.6	17	<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
115	<a href="#">c4a3uB_</a>	Alignment	not modelled	81.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh\;flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
116	<a href="#">c1ydnA_</a>	Alignment	not modelled	81.2	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
117	<a href="#">c5ocsB_</a>	Alignment	not modelled	80.6	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-depndent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
118	<a href="#">c6mp2B_</a>	Alignment	not modelled	79.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> blman5b; <b>PDBTitle:</b> crystal structure of blman5b solved by siras
119	<a href="#">d1nvma2</a>	Alignment	not modelled	79.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
120	<a href="#">c4ov9A_</a>	Alignment	not modelled	79.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> isopropylmalate synthase; <b>PDBTitle:</b> structure of isopropylmalate synthase binding with alpha-2 isopropylmalate