Phyre2

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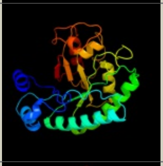
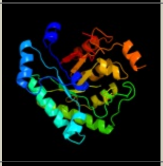
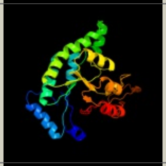
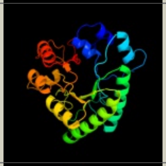
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bdkB_	Alignment		100.0	45	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
2	d1tz9a_	Alignment		100.0	41	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
3	c2hk1D_	Alignment		99.9	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
4	d1i60a_	Alignment		99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
5	c3kwsB_	Alignment		99.9	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
6	c2ou4C_	Alignment		99.9	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
7	c3qxbB_	Alignment		99.9	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative xylose isomerase; **PDBTitle:** crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
8	c3cnyA_	Alignment		99.9	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
9	d1k77a_	Alignment		99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
10	c3obeB_	Alignment		99.9	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
11	c3lmzA_	Alignment		99.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution

12	c3dx5A_	Alignment		99.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
13	c3ju2A_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
14	c2zdsB_	Alignment		99.9	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
15	c3l23A_	Alignment		99.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
16	c3ngfA_	Alignment		99.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
17	c3p6lA_	Alignment		99.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
18	c2qw5B_	Alignment		99.8	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
19	c3ktcB_	Alignment		99.8	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
20	c2zvrA_	Alignment		99.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416; **PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
21	d2g0wa1	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
22	c3cqkB_	Alignment	not modelled	99.8	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-ribulose-5-phosphate 3-epimerase ulae; **PDBTitle:** crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
23	d1xp3a1	Alignment	not modelled	99.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
24	d2q02a1	Alignment	not modelled	99.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
25	d1yx1a1	Alignment	not modelled	99.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
26	d1qtwa_	Alignment	not modelled	99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
27	d1bxca_	Alignment	not modelled	99.7	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
28	d2glka1	Alignment	not modelled	99.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
29	d1muwa_	Alignment	not modelled	99.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like

						Family: Xylose isomerase
30	d1bxba_	Alignment	not modelled	99.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
31	c2x7vA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
32	d1qt1a_	Alignment	not modelled	99.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
33	d1xima_	Alignment	not modelled	99.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
34	c3aamA_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease iv; **PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8
35	d1xlma_	Alignment	not modelled	99.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
36	c2i56A_	Alignment	not modelled	98.7	16	**PDB header:**isomerase, metal-binding protein **Chain:** A: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
37	c3bzjA_	Alignment	not modelled	97.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
38	d1a0ea_	Alignment	not modelled	96.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
39	d1a0da_	Alignment	not modelled	96.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
40	d1a0ca_	Alignment	not modelled	95.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
41	c3p14C_	Alignment	not modelled	94.8	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
42	c3bwwA_	Alignment	not modelled	92.3	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein of unknown function duf692/cog3220; **PDBTitle:** crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
43	d1ob0a2	Alignment	not modelled	86.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
44	c1sr9A_	Alignment	not modelled	83.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of leua from mycobacterium tuberculosis
45	c3atyA_	Alignment	not modelled	83.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prostaglandin f2a synthase; **PDBTitle:** crystal structure of tcoye
46	d1vgga_	Alignment	not modelled	81.7	25	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
47	c2ekmC_	Alignment	not modelled	80.1	22	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein st1511; **PDBTitle:** structure of st1219 protein from sulfolobus tokodaii
48	c3hpxB_	Alignment	not modelled	78.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of mycobacterium tuberculosis leua active site2 domain 1-425 (truncation mutant delta:426-644)
49	c2p10D_	Alignment	not modelled	77.8	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
50	c2gl0A_	Alignment	not modelled	77.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of pae2307 in complex with adenosine
51	c2xfyA_	Alignment	not modelled	77.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-amylase; **PDBTitle:** crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
52	d1olta_	Alignment	not modelled	77.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
53	d1fa2a_	Alignment	not modelled	77.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
54	c2c3zA_	Alignment	not modelled	77.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
55	d1wdpa1	Alignment	not modelled	77.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

56	d1mxga2	Alignment	not modelled	76.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
57	d1to3a_	Alignment	not modelled	75.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
58	c3iacA_	Alignment	not modelled	74.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucuronate isomerase; **PDBTitle:** 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
59	d1b1ya_	Alignment	not modelled	73.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	d2p10a1	Alignment	not modelled	72.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
61	d1avaa2	Alignment	not modelled	71.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
62	d1r30a_	Alignment	not modelled	71.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
63	c1r30A_	Alignment	not modelled	71.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
64	d1rlha_	Alignment	not modelled	70.9	25	**Fold:**Ta1353-like **Superfamily:**Ta1353-like **Family:**Ta1353-like
65	d1hvxa2	Alignment	not modelled	70.5	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	c2vg2C_	Alignment	not modelled	65.4	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
67	d1hx0a2	Alignment	not modelled	63.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	d2gjpa2	Alignment	not modelled	63.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	c3eb2A_	Alignment	not modelled	62.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
70	d1x7fa2	Alignment	not modelled	62.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
71	d1tj1a2	Alignment	not modelled	59.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Proline dehydrohenase domain of bifunctional PutA protein
72	d1vema2	Alignment	not modelled	59.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	d3dhpa2	Alignment	not modelled	58.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	c2vc7A_	Alignment	not modelled	57.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aryldialkylphosphatase; **PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
75	d1i4na_	Alignment	not modelled	55.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
76	c3blpX_	Alignment	not modelled	55.5	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
77	c2yusA_	Alignment	not modelled	55.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
78	d1ud2a2	Alignment	not modelled	53.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
79	c3cixA_	Alignment	not modelled	52.6	19	**PDB header:**adomet binding protein **Chain:** A: **PDB Molecule:**fefe-hydrogenase maturase; **PDBTitle:** x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
80	d1eg7a_	Alignment	not modelled	51.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
81	c1tdjA_	Alignment	not modelled	51.0	13	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
82	d2cu7a1	Alignment	not modelled	49.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain

83	d1g5aa2	Alignment	not modelled	48.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	c2ehhE_	Alignment	not modelled	47.8	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
85	c2yumA_	Alignment	not modelled	47.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger zz-type-containing protein 3; **PDBTitle:** solution structure of the myb-like dna-binding domain of2 human zzz3 protein
86	c3dhuC_	Alignment	not modelled	46.8	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
87	d1phza1	Alignment	not modelled	46.8	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
88	c2d16B_	Alignment	not modelled	45.8	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph1918; **PDBTitle:** crystal structure of ph1918 protein from pyrococcus horikoshii ot3
89	d1e9yb2	Alignment	not modelled	45.7	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
90	d1d8wa_	Alignment	not modelled	45.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**L-rhamnose isomerase
91	c1x7fA_	Alignment	not modelled	45.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
92	d1ujpa_	Alignment	not modelled	43.7	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
93	d1ejxc2	Alignment	not modelled	43.3	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
94	c3pnuA_	Alignment	not modelled	42.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dihydroorotase; **PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni.
95	d1ht6a2	Alignment	not modelled	41.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	c1rr2A_	Alignment	not modelled	41.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
97	c3f6tA_	Alignment	not modelled	41.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
98	d2cbia2	Alignment	not modelled	40.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
99	c1ud8A_	Alignment	not modelled	40.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
100	d1e43a2	Alignment	not modelled	40.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
101	d1foba_	Alignment	not modelled	40.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
102	d1hjqa_	Alignment	not modelled	40.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
103	c2o8vA_	Alignment	not modelled	39.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
104	d2aaaa2	Alignment	not modelled	39.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
105	c2zy3A_	Alignment	not modelled	39.6	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
106	c2yxgD_	Alignment	not modelled	39.5	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
107	d1m7xa3	Alignment	not modelled	39.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
108	c2p0oA_	Alignment	not modelled	39.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf871; **PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
109	d1piia2	Alignment	not modelled	39.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel

						Family: Tryptophan biosynthesis enzymes
110	c3k13A_	Alignment	not modelled	39.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
111	c3t7vA_	Alignment	not modelled	39.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylornithine synthase pylb; **PDBTitle:** crystal structure of methylornithine synthase (pylb)
112	d1j5ta_	Alignment	not modelled	39.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
113	d1vr3a1	Alignment	not modelled	38.2	24	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
114	c2wcsA_	Alignment	not modelled	38.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
115	d2bhua3	Alignment	not modelled	37.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c3amlA_	Alignment	not modelled	37.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
117	d1j5sa_	Alignment	not modelled	37.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Uronate isomerase-like
118	c2e8yA_	Alignment	not modelled	36.8	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
119	d1jaea2	Alignment	not modelled	36.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
120	c1zlpA_	Alignment	not modelled	36.4	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct