Phyre2

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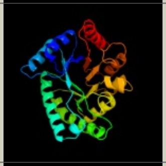
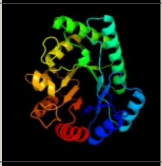
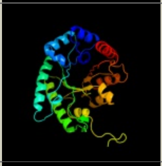
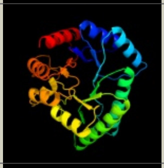
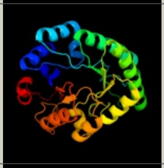
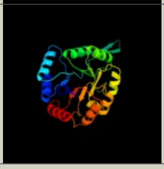
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kwsB_	Alignment		100.0	25	**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
2	c2hk1D_	Alignment		100.0	24	**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
3	c2ou4C_	Alignment		100.0	26	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
4	c2zvrA_	Alignment		100.0	24	**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
5	c2qw5B_	Alignment		100.0	17	**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
6	d1i60a_	Alignment		100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
7	c2zdsB_	Alignment		100.0	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
8	c3obeB_	Alignment		100.0	18	**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
9	c3cnyA_	Alignment		100.0	21	**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
10	c3ktcB_	Alignment		100.0	18	**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
11	c3l23A_	Alignment		100.0	18	**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

12	c3dx5A_	Alignment		100.0	18	**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	d1k77a_	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
14	c3ju2A_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
15	c3cqkB_	Alignment		100.0	22	**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
16	c3lmzA_	Alignment		100.0	17	**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
17	c3ngfA_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
18	c3qxbB_	Alignment		100.0	14	**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
19	d2g0wa1	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
20	c3p6lA_	Alignment		100.0	17	**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
21	d1xp3a1	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
22	d2q02a1	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
23	c2x7vA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
24	d1yx1a1	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
25	d1qtwa_	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
26	d1muwa_	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
27	d1qt1a_	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
28	d2glka1	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
29	c3aamA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease iv;

29	c3aamA_	Alignment	not modelled	100.0	19	**PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8
30	d1bxba_	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
31	d1tz9a_	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
32	d1bxca_	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
33	d1xima_	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
34	c3bdkB_	Alignment	not modelled	99.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
35	d1xlma_	Alignment	not modelled	99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
36	c2i56A_	Alignment	not modelled	99.8	13	**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	d1a0ea_	Alignment	not modelled	99.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
38	d1a0ca_	Alignment	not modelled	99.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
39	d1a0da_	Alignment	not modelled	99.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
40	c3bzjA_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
41	c3bwwA_	Alignment	not modelled	98.8	10	**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
42	c3p14C_	Alignment	not modelled	98.4	12	**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
43	d1d8wa_	Alignment	not modelled	98.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**L-rhamnose isomerase
44	c1rr2A_	Alignment	not modelled	97.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
45	c2nx9B_	Alignment	not modelled	97.6	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**oxaloacetate decarboxylase 2, subunit alpha; **PDBTitle:** crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
46	c3ivuB_	Alignment	not modelled	97.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
47	d1nvma2	Alignment	not modelled	97.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
48	d1h1ya_	Alignment	not modelled	97.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
49	c2ftpA_	Alignment	not modelled	97.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
50	d2flia1	Alignment	not modelled	97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
51	c1sr9A_	Alignment	not modelled	97.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of leua from mycobacterium tuberculosis
52	c3ct7E_	Alignment	not modelled	97.0	19	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
53	c1ydnA_	Alignment	not modelled	96.9	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
54	c3inpA_	Alignment	not modelled	96.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
55	c1nvmG_	Alignment	not modelled	96.7	13	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-

						dehydrogenase :2 sequestering a reactive and volatile intermediate
56	c3ewbX_	Alignment	not modelled	96.7	19	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
57	d1rpxa_	Alignment	not modelled	96.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
58	d1tqja_	Alignment	not modelled	96.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
59	c3qc3B_	Alignment	not modelled	96.5	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
60	c3hpxB_	Alignment	not modelled	96.5	13	**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)
61	c3eegB_	Alignment	not modelled	96.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
62	d1qwga_	Alignment	not modelled	96.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
63	c3bg3B_	Alignment	not modelled	95.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase, mitochondrial; **PDBTitle:** crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
64	c2zyfA_	Alignment	not modelled	95.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homocitrate synthase; **PDBTitle:** crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
65	c2bdqA_	Alignment	not modelled	95.4	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
66	c3a24A_	Alignment	not modelled	95.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of bt1871 retaining glycosidase
67	c3bleA_	Alignment	not modelled	95.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
68	c2cw6B_	Alignment	not modelled	95.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hydroxymethylglutaryl-coa lyase, mitochondrial; **PDBTitle:** crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
69	d1m5wa_	Alignment	not modelled	95.1	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
70	c3iwpK_	Alignment	not modelled	94.9	13	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
71	d1sr9a2	Alignment	not modelled	94.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
72	d1i4na_	Alignment	not modelled	94.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
73	c3l55B_	Alignment	not modelled	94.1	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**b-1,4-endoglucanase/cellulase; **PDBTitle:** crystal structure of a putative beta-1,4-endoglucanase /2 cellulase from prevotella bryantii
74	d1x7fa2	Alignment	not modelled	93.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Outer surface protein, N-terminal domain
75	c3gk0H_	Alignment	not modelled	93.4	19	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
76	c1uz4A_	Alignment	not modelled	93.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
77	d1uuqa_	Alignment	not modelled	93.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
78	c1x7fA_	Alignment	not modelled	92.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**outer surface protein; **PDBTitle:** crystal structure of an uncharacterized b. cereus protein
79	c1ydoC_	Alignment	not modelled	92.8	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
						PDB header:hydrolase

80	c2vhiG_	Alignment	not modelled	92.3	16	**Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
81	d1twda_	Alignment	not modelled	91.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
82	c2h90A_	Alignment	not modelled	91.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
83	d1tqxa_	Alignment	not modelled	91.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
84	c2dzaA_	Alignment	not modelled	91.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
85	d1olta_	Alignment	not modelled	91.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
86	c3bg5C_	Alignment	not modelled	90.8	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
87	d1vc4a_	Alignment	not modelled	90.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
88	c3ogrA_	Alignment	not modelled	90.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
89	d1vlia2	Alignment	not modelled	90.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
90	c2y8kA_	Alignment	not modelled	90.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbohydrate binding family 6; **PDBTitle:** structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
91	c2xioA_	Alignment	not modelled	89.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
92	c3dxiB_	Alignment	not modelled	89.5	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
93	d1egza_	Alignment	not modelled	88.4	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
94	c3mmwB_	Alignment	not modelled	88.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
95	c3f4wA_	Alignment	not modelled	88.0	18	**PDB header:**synthase, lyase **Chain:** A: **PDB Molecule:**putative hexulose 6 phosphate synthase; **PDBTitle:** the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
96	d1u83a_	Alignment	not modelled	87.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
97	c1u83A_	Alignment	not modelled	87.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
98	d1vjza_	Alignment	not modelled	87.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
99	d1tvna1	Alignment	not modelled	87.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
100	c3muxB_	Alignment	not modelled	87.4	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
101	c3qjaA_	Alignment	not modelled	87.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
102	c2vg2C_	Alignment	not modelled	87.2	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
103	c3pzqA_	Alignment	not modelled	87.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family **PDBTitle:** structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
104	c3m6yA_	Alignment	not modelled	87.2	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
105	d1ujpa_	Alignment	not modelled	86.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
						PDB header:resiniferatoxin binding protein

106	c3k2gA_	Alignment	not modelled	86.8	14	**Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
107	d1j5ta_	Alignment	not modelled	86.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
108	d2c0ha1	Alignment	not modelled	86.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
109	c3noyA_	Alignment	not modelled	86.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
110	c1piiA_	Alignment	not modelled	86.0	19	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
111	d1rqba2	Alignment	not modelled	85.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
112	c3gzaB_	Alignment	not modelled	85.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
113	c2zunB_	Alignment	not modelled	85.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**458aa long hypothetical endo-1,4-beta-glucanase; **PDBTitle:** functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
114	c2yfnA_	Alignment	not modelled	85.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
115	c3ndyA_	Alignment	not modelled	85.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase d; **PDBTitle:** the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
116	c3navB_	Alignment	not modelled	84.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
117	c3eypB_	Alignment	not modelled	84.7	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
118	c3jugA_	Alignment	not modelled	84.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-mannanase; **PDBTitle:** crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
119	c2zq0B_	Alignment	not modelled	84.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
120	c3aysA_	Alignment	not modelled	84.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** gh5 endoglucanase from a ruminal fungus in complex with cellotriose