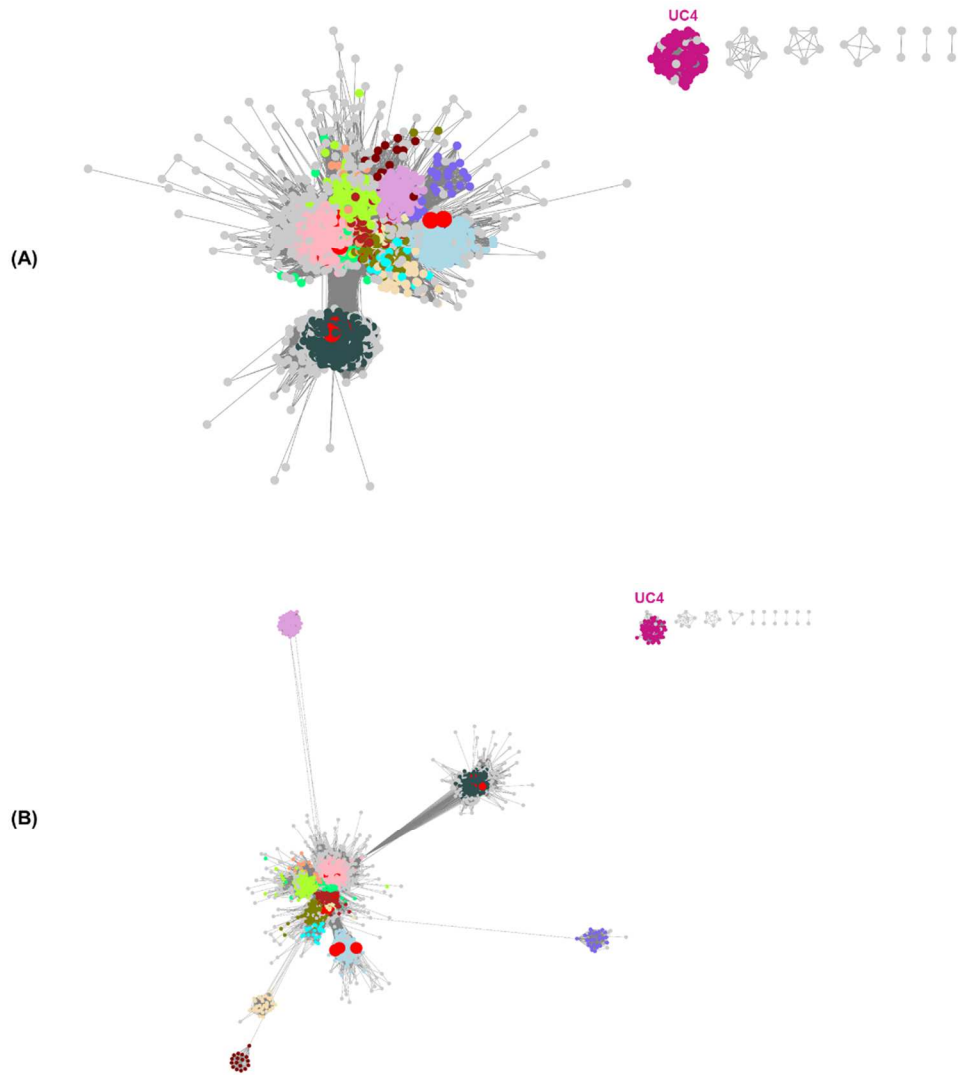
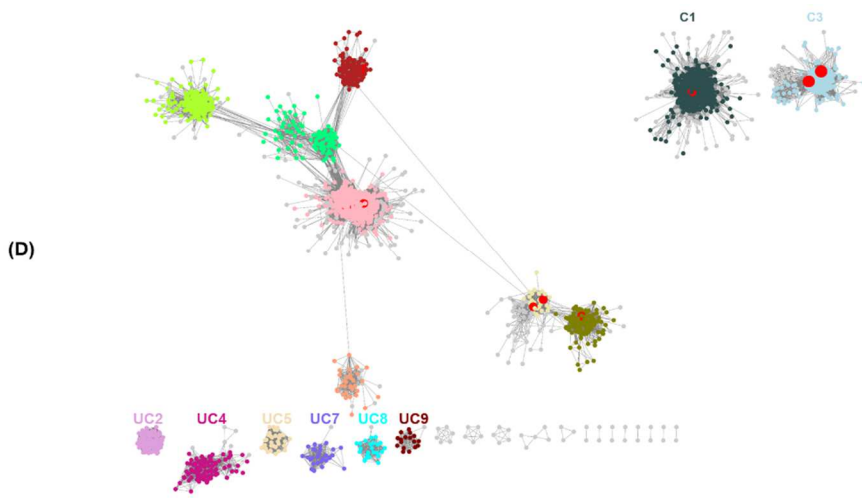


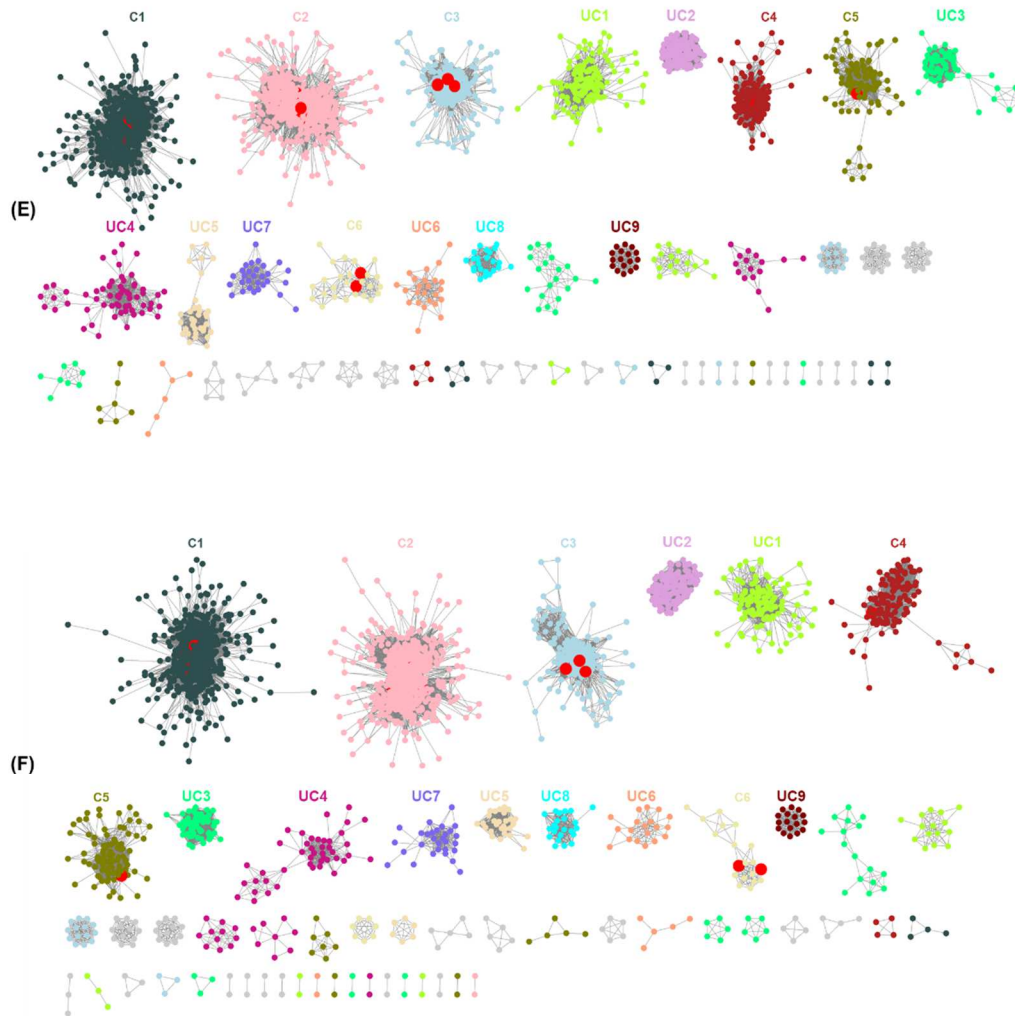
## Supplementary Figures and Tables

<b>Figure S1</b> .....	2
<b>Figure S2</b> .....	5
<b>Figure S3</b> .....	7
<b>Figure S4</b> .....	8
<b>Figure S5</b> .....	9
<b>Figure S6</b> .....	10
<b>Table S1</b> .....	11
<b>C1</b> .....	11
<b>C2</b> .....	56
<b>C3</b> .....	96
<b>C4</b> .....	105
<b>C5</b> .....	114
<b>C6</b> .....	118
<b>UC1</b> .....	120
<b>UC2</b> .....	125
<b>UC3</b> .....	130
<b>UC4</b> .....	134
<b>UC5</b> .....	136
<b>UC6</b> .....	138
<b>UC7</b> .....	139
<b>UC8</b> .....	139
<b>UC9</b> .....	140
<b>Small meta-nodes</b> .....	141
<b>Singletons</b> .....	144
<b>Table S2</b> .....	161
<b>Table S3</b> .....	162
<b>Table S4</b> .....	163

Figure S1







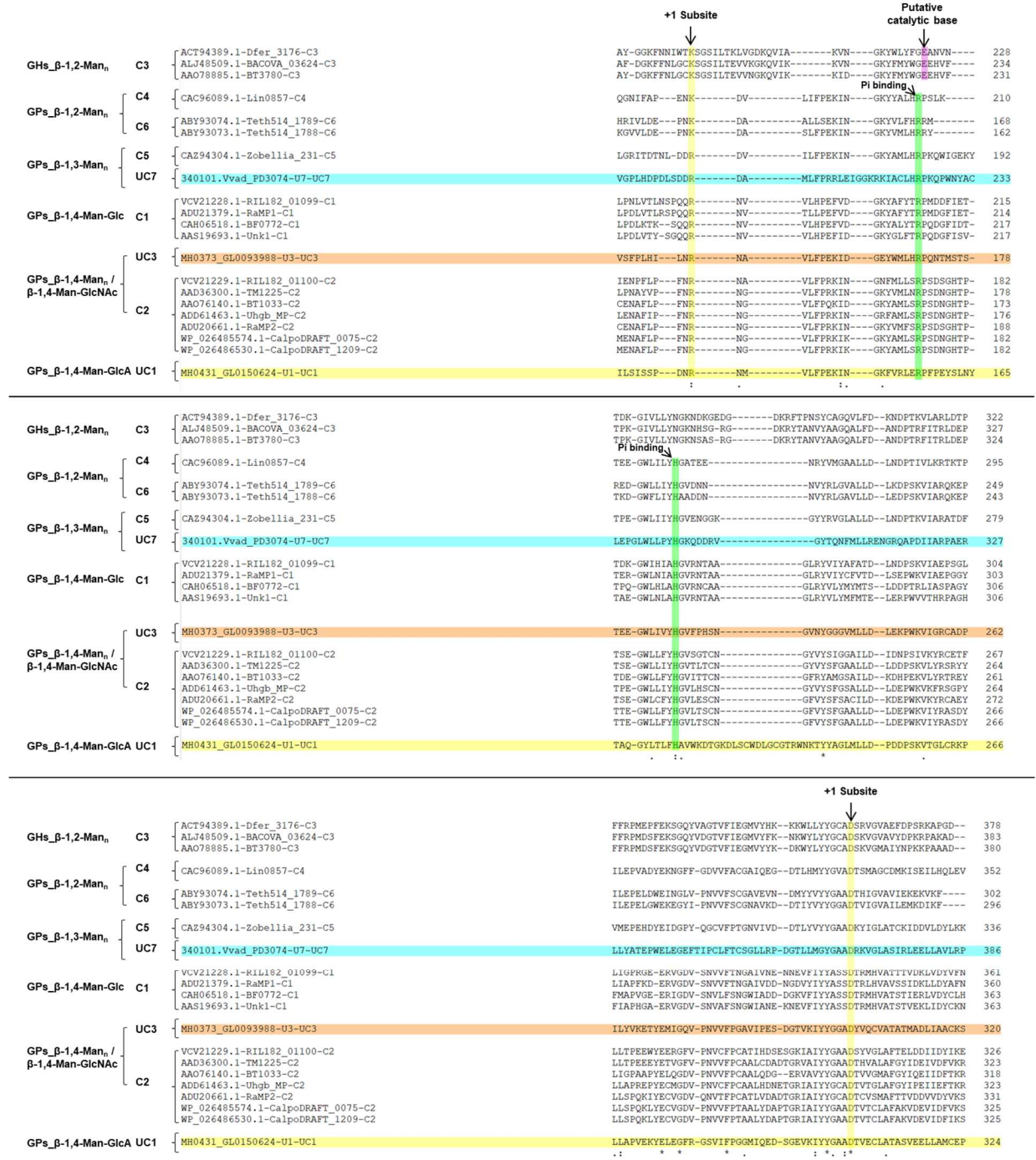
**Figure S1:** Protein sequence similarity networks (SSNs) of the 6,308 GH130 sequences from the CAZy database and from gut metagenomes, with various E-value thresholds. The 3,637 nodes contain sequences with more than 70% identity. Red nodes correspond to biochemically characterized members of the GH130 family. Other nodes are colored according to the meta-node they belong to in the optimal SSN, obtained with the E-value threshold  $10^{-70}$ . (A), E-value threshold  $10^{-30}$ , corresponding to 32% sequence identity; the 79 sequences appearing in 78 singletons have been omitted from the figure. (B), E-value threshold  $10^{-40}$ , corresponding to 41% sequence identity; the 189 sequences appearing in 177 singletons have been omitted from the figure. (C), E-value threshold  $10^{-50}$ , corresponding to 53% sequence identity; the 333 sequences appearing in 315 singletons have been omitted from the figure. (D), E-value threshold  $10^{-60}$ , corresponding to 61% sequence identity; the 491 sequences appearing in 457 singletons have been omitted from the figure. (E), E-value threshold  $10^{-80}$ , corresponding to 64% sequence identity; the 896 sequences appearing in 826 singletons have been omitted from the figure. (F), E-value threshold  $10^{-90}$ , corresponding to 65% sequence identity; the 1130 sequences appearing in 1027 singletons have been omitted from the figure.

Figure S2

		+1 Subsite	
		↓	
GHs $_{\beta}$ -1,2-Man $_n$	C3	ACT94389.1-Dfer_3176-C3	GVPVPSVSDSTTRFFCFPMKREVWESNDTFNPAATMKN---GKIVLVLYAEDKAGK--- 93
		ALJ48509.1-BACOVA_03624-C3	NVNPVISPIENTKFCYFLTKDSIAWESNDTFNPAATLYN---GEIVLVLYAEDKSGV--- 99
		AAO78885.1-BT3780-C3	GANPVISPIENTKFCYFMTQDYVAWESNDTFNPAATLHD---GKIVLVLYAEDKSGV--- 96
GPs $_{\beta}$ -1,2-Man $_n$	C4	CAC96089.1-Lin0857-C4	EENPLITFLDVK-----PIHEGFEVIGAFNGGVAEYN---GEVLLLRVAEKPVSEDP 56
		ABY93074.1-Teth514_1789-C6	SNKPILSPKEH-----EWEKEAVFNAAVIYEG---NKPHLFYFASNNKF---- 49
GPs $_{\beta}$ -1,2-Man $_n$	C6	ABY93073.1-Teth514_1788-C6	SKPVLMKPAEN-----EWEAAVFNAAIYDN---GLPHLIYFATDIGP---- 49
		CAZ94304.1-Zobellia_231-C5	FNNPILKPHPTN-----YWENLVVNCVGFEN---GKTMFLYFAAGDD---- 47
GPs $_{\beta}$ -1,3-Man $_n$	UC7	340101.Vvad_PD3074-U7-UC7	EKRCILSPVPGS-----FWAGKMLNFMADIADPEKIHMLFRATGFQFQAR-- 52
		VCV21228.1-RIL182_01099-C1	DLNPETNPFYME-----RLGINAVMNSGAIELN---GKYLVARIEG----- 89
GPs $_{\beta}$ -1,4-Man-Glc	C1	ADU21379.1-RAMP1-C1	DLNKEETNPFQE-----RLGINAVFNAGAIKLN---DRYCLVARVEG----- 89
		CAH06518.1-BF0772-C1	DLNEETNPFLE-----RIGMNATLNAGAIKWD---GKYLMLVRVEG----- 91
		AAS19693.1-Unk1-C1	DLNEKTNPHLME-----RQGINAAFNAGAMYWN---GKYLVARVEG----- 91
GPs $_{\beta}$ -1,4-Man $_n$ / $\beta$ -1,4-Man-GlcNAc	UC3	MH0373_GL0093988-U3-UC3	ENNPILKPELMP-----APCCAVYNSGVVKT---DDGEYIMMSRFEZ----- 49
		VCV21229.1-RIL182_01100-C2	NENPIIGRNVPK-----GV-ARIFNSAVMPYE---DGFVGVFRGEQ----- 68
GPs $_{\beta}$ -1,4-Man $_n$ / $\beta$ -1,4-Man-GlcNAc	C2	AAD36300.1-TM1225-C2	SNKPIIGRNVPV-----KG-ARVFN SAVVFN---GEFVGVFRIDH----- 64
		AAO76140.1-BT1033-C2	SQNPVIGRYHIP-----SS-NSIFNSAVVFEK---DGFAGVFRCDN----- 59
		ADD61463.1-Uhgb_MP-C2	VANPIIPRDLIP-----TS-NSIFNSAVVFG---DGFAGVFRCDN----- 62
		ADU20661.1-RAMP2-C2	DANPIIPRDLIP-----TS-NSIFNSAVVFESEKGFAGVFRVDD----- 70
		WF_026485574.1-CalpoDRAFT_0075-C2	QQNPVIPRDLIP-----SS-NSIFNSAVVFN---GEFAGVFRCDT----- 67
WF_026486530.1-CalpoDRAFT_1209-C2	QQNPVIPRDLIP-----SS-NSIFNSAVVFN---GEFAGVFRCDT----- 67		
GPs $_{\beta}$ -1,4-Man-GlcA UC1	MH0431_GL0150624-U1-UC1	ENNPVLSADLS-----YPSLNVFNAGVAKYR---NQYVMVFNVDVGFAPD-- 49	

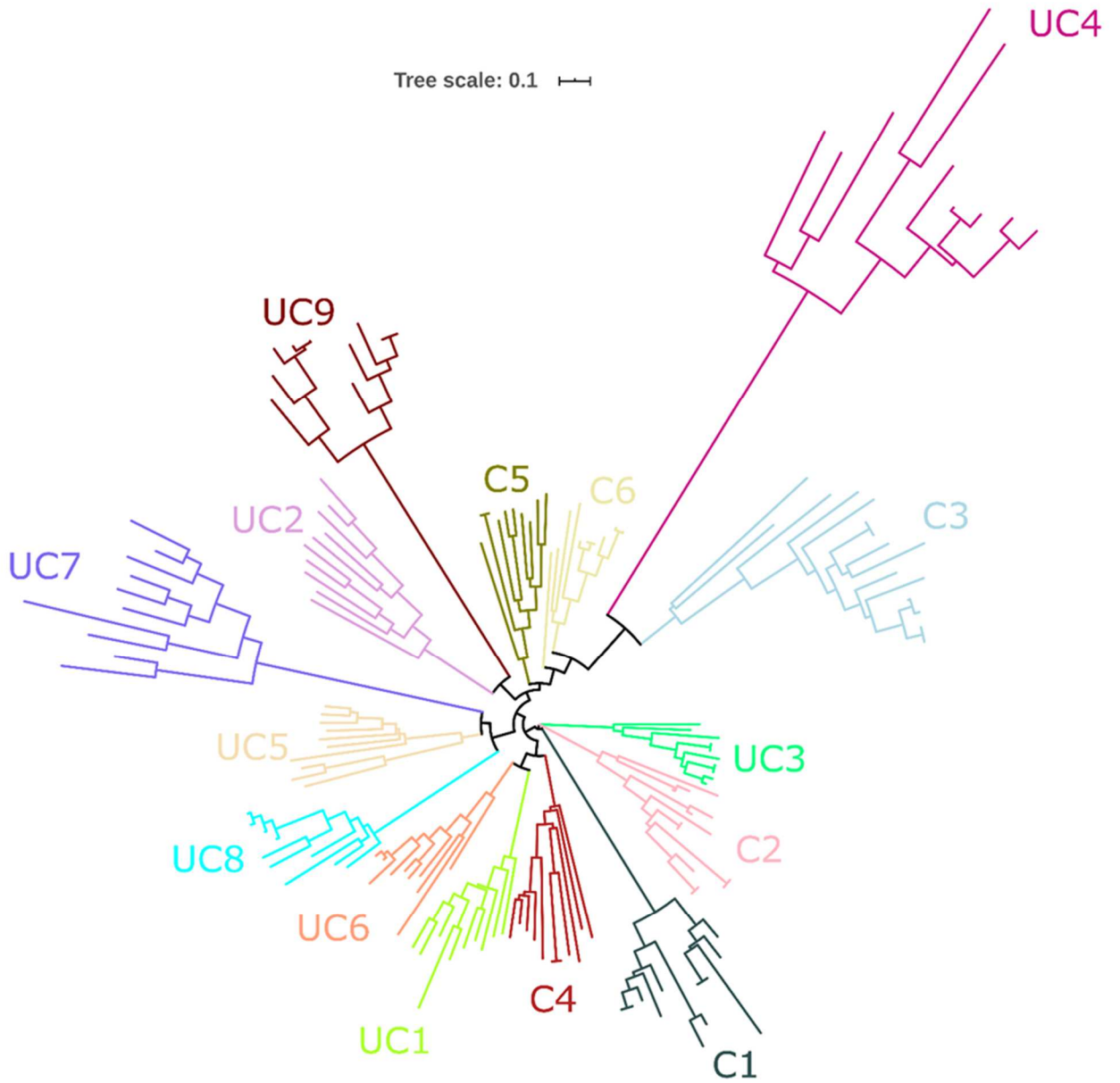
---

		+1 Subsite Proton donor	
		↓	
GHs $_{\beta}$ -1,2-Man $_n$	C3	ACT94389.1-Dfer_3176-C3	G-IHFKRKKE-PVLFPAEDSQ--K-----ANEWPGGCEPRVAVTEDGL-YVVI 153
		ALJ48509.1-BACOVA_03624-C3	G-THFOREKT-PVFPDNDQ--K-----ELEWPGGCEPRVAVTEDGL-YVVI 159
		AAO78885.1-BT3780-C3	G-IHFKRKKT-PVFPDNDQ--K-----KLEWPGGCEPRVAVTEDGL-YVVI 156
GPs $_{\beta}$ -1,2-Man $_n$	C4	CAC96089.1-Lin0857-C4	G-HHFTLDEK-PFL-YFF-----NEYQTFGIEDARVTIQIDTY-HVNF 155
		ABY93074.1-Teth514_1789-C6	G-INFERFDK-PVL-VGE-----IQEAWGVDEPRITKIDNKY-YMLY 112
GPs $_{\beta}$ -1,2-Man $_n$	C6	ABY93073.1-Teth514_1788-C6	G-INFMRLDK-PVM-SNE-----TEQELRGLDEPRIVKIDGIY-YMY 106
		CAZ94304.1-Zobellia_231-C5	G-IHFNRCSEPAFEPST-----DGPDKGGIEDPRIVKFGEEF-YVY 102
GPs $_{\beta}$ -1,3-Man $_n$	UC7	340101.Vvad_PD3074-U7-UC7	GGADWQFDLSRPMAMPFLFDRDRFLARGMRDGMFDYANGCIEDPRLFYFEEQL-YLSV 130
		VCV21228.1-RIL182_01099-C1	G-IDGFRFDWYPIILLPTCPEETN-----VYDMRLTKHEDGVIYGVF 144
GPs $_{\beta}$ -1,4-Man-Glc	C1	ADU21379.1-RAMP1-C1	G-TEGFRFRQYVVLPAITDDETN-----VYDMRLTKHEDGVIYGVF 144
		CAH06518.1-BF0772-C1	G-IDNFRFEWYPIITPEVVPATN-----VYDMRLTKHEDGVIYGVF 146
		AAS19693.1-Unk1-C1	G-IDNFRFDWYPIITPEVVPATN-----VYDMRLTKHEDGVIYGVF 146
GPs $_{\beta}$ -1,4-Man $_n$ / $\beta$ -1,4-Man-GlcNAc	UC3	MH0373_GL0093988-U3-UC3	G-FHFTPDSE-PVSVFCAPEEEEEYNETVYLNQ-QKALIGSWDPRINPVEGEY-YITY 119
		VCV21229.1-RIL182_01100-C2	A-IHWNFDEN-KINFVDE--EGKPFMPRY-----AYDPRLVKVEDTY-YIIW 124
GPs $_{\beta}$ -1,4-Man $_n$ / $\beta$ -1,4-Man-GlcNAc	C2	AAD36300.1-TM1225-C2	G-INWIEPE-EIQWVDV--NGEPFQPSY-----AYDPRVVKIEDTY-YITF 120
		AAO76140.1-BT1033-C2	G-IHWDISHE-PIQFKAG--NTEIESEY-----KYDPRVTWIEDRY-WVTW 115
		ADD61463.1-Uhgb_MP-C2	A-INWNKKEE-PLKFCQD--DEEIGTWVY-----GYDPRVCFIEDRY-YVTW 118
		ADU20661.1-RAMP2-C2	G-IHWINDFP-RIVEQAESTEEVNWQGY-----GYDPRVCFIEDRF-WVTW 129
		WF_026485574.1-CalpoDRAFT_0075-C2	G-LNWDIHE-RIKFICD--DEEVSFRVY-----AYDPRVCKIEDRY-YITW 123
WF_026486530.1-CalpoDRAFT_1209-C2	G-LNWDIHE-RIKFICD--DEEVSFRVY-----AYDPRVCKIEDRY-YITW 123		
GPs $_{\beta}$ -1,4-Man-GlcA UC1	MH0431_GL0150624-U1-UC1	G-KQWKPAHP-PWLETAG-----RHPELEIYDPRLVIEDRC-YICF 105	



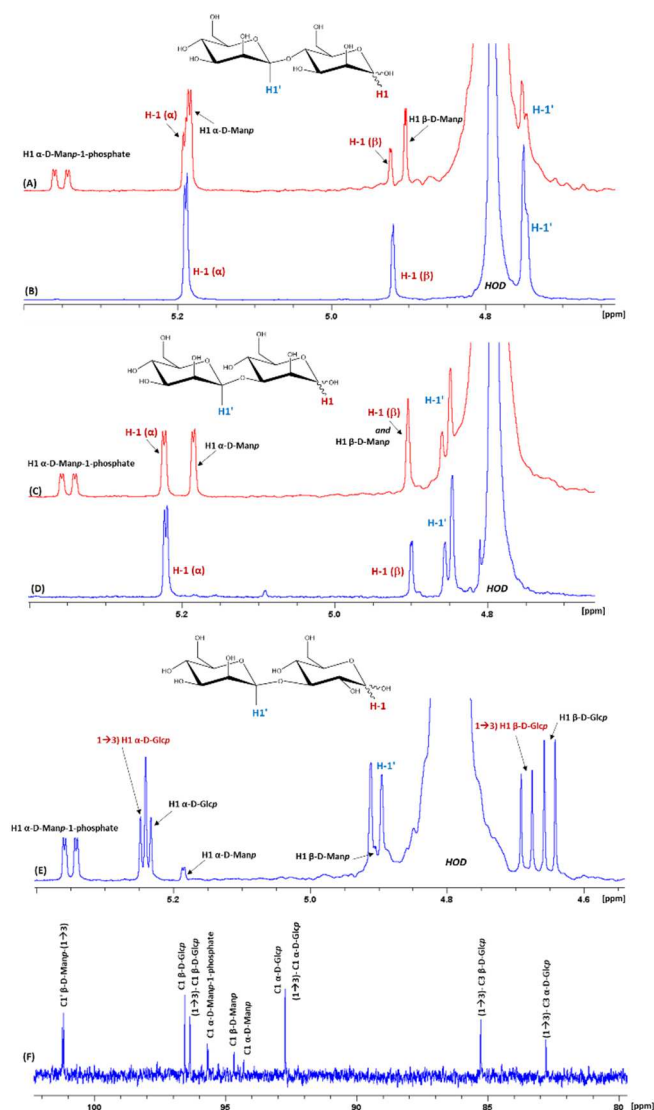
**Figure S2:** Multiple sequence alignment of all the characterized GH130 enzymes, including U1, U3 and U7.

Figure S3



**Figure S3:** Maximum-likelihood phylogenetic tree, generated using 10 representative sequences for each SSN meta-node, defined with an E-value threshold of  $10^{-70}$ .

**Figure S4**



**Figure S4:** NMR analysis of the reverse-phosphorolysis reactional mixtures incubation for 24hrs with U3 and U7. The reactions were performed in the presence of 10 mM of  $\alpha$ Man1P (glycosyl donor) and 10 mM Glc or Man (acceptors). (A, B, C, D, E) 500 MHz <sup>1</sup>H NMR spectra of the anomeric region (5.5-4.5 ppm) and (F) <sup>13</sup>C NMR spectra region (102-80 ppm). (A), U3 reaction medium: at 5.19 ppm (H1 $\alpha$ ), 4.92 ppm (H1 $\beta$ ), 4.74 ppm (H1'). (B),  $\beta$ -1,4-mannobiose standard (Megazyme). (C), U7 reaction medium performed with Man as acceptor: at 5.22 ppm (H1 $\alpha$ ), 4.90 ppm (H1 $\beta$ ), 4.85 ppm (H1'). (D),  $\beta$ -1,3-mannobiose standard (Carbosynth). (E, F), U7 reaction medium performed with Glc as acceptor: at 5.24 ppm (H1 $\alpha$ ), 4.68 ppm (H1 $\beta$ ), 4.90 ppm (H1') and 85.2 ppm (1 $\rightarrow$ 3)- C3  $\beta$ -D-Glcp, 82,7 ppm (1 $\rightarrow$ 3)- C3  $\alpha$ -D-Glcp.



Figure S5

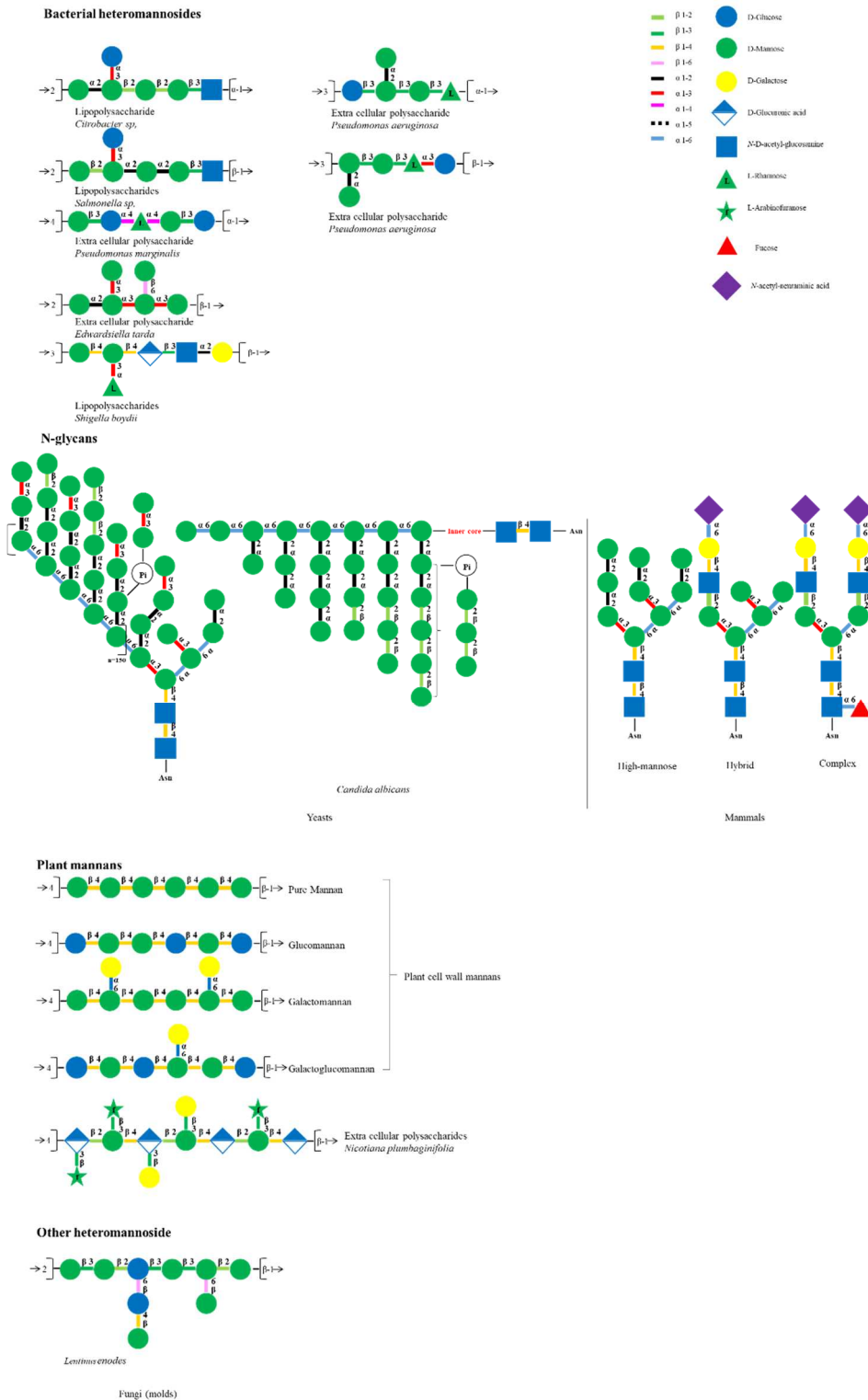
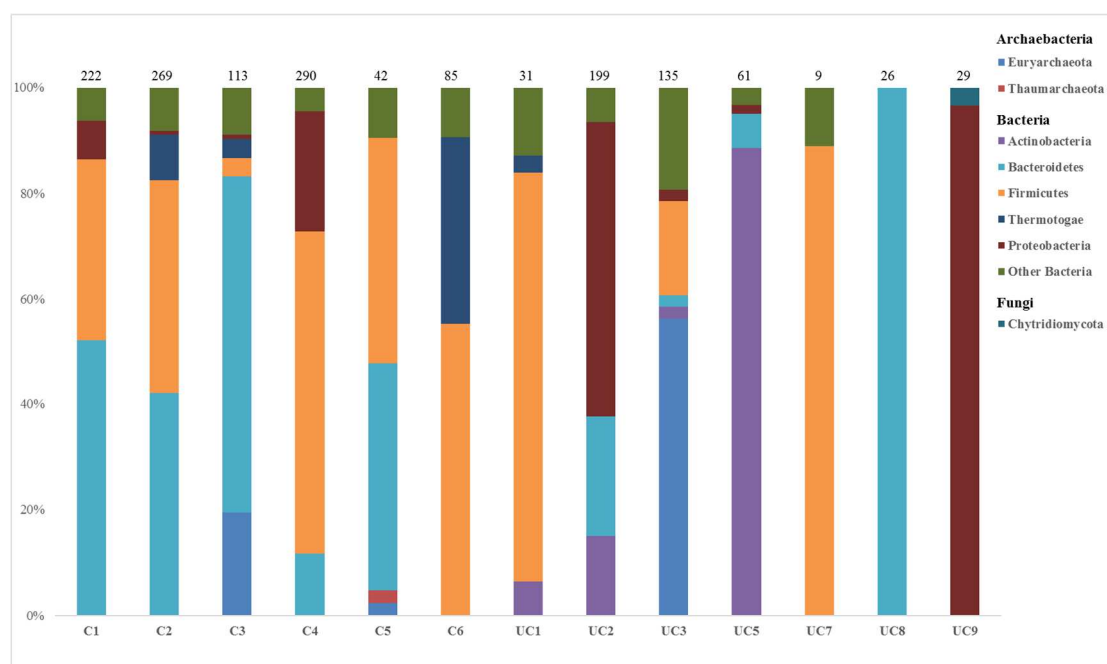


Figure S5: Examples of mannoside and heteromannoside structures containing the motifs targeted by GH130 enzymes.

**Figure S6**



**Figure S6:** Taxonomical origin of the GH130 sequences listed in the CAZy database, for each SSN meta-node.

**Table S1**

Accession numbers of all the GH130 sequences used in this study, classified by meta-node. Each line corresponds to one node, which might contain several sequences. The accession numbers of the characterized enzymes are highlighted in green.

**C1**

<p>["Ncazy AOC95706.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Flavobacterium anhuiense]", "cazy AWK07196.1 glycosidase [Flavobacterium sp. HYN0056]", "cazy AXB58825.1 glycosidase [Flavobacterium sp. HYN0086]", "cazy 146157100 gb ABQ07954.1  protein of unknown function [Flavobacterium johnsoniae UW101]"]</p>
<p>["cazy CCgij 315447815 gb ADU21379.1 β-1", "4-mannosylglucose phosphorylase_glycosidase related protein [Ruminococcus albus 7 = DSM 20455]", "rumen552_GL1509507_1 [gene] locus=scaffold458827_1:1426:2586:+[Complete]"]</p>
<p>["cazy CCgij 42556009 gb AAS19693.1 β-1", "4-mannosylglucose phosphorylase_Unk1 [Cellvibrio mixtus]", "cazy AQT61561.1 glycosidase [Cellvibrio sp. PSBB023]", "cazy ARU28674.1 glycosidase [Cellvibrio sp. PSBB006]", "cazy 190688591 gb ACE86269.1  conserved domain protein [Cellvibrio japonicus Ueda107]", "cazy 189949756 gb ABD79771.1  glycosidase", "PH1107-related [Saccharophagus degradans 2-40]"]</p>
<p>["cazy CCgij 60491760 emb CAH06518.1 β-1", "4-mannosylglucose phosphorylase_conserved hypothetical protein [Bacteroides fragilis NCTC 9343]", "cazy AST52477.1 glycosidase [Parabacteroides sp. CT06]", "cazy AUJ45342.1 glycosidase [Bacteroides fragilis]", "cazy AVM47144.1 glycosidase [Victivallales bacterium CCUG 44730]", "cazy SCV06945.1 conserved hypothetical protein [Bacteroides ovatus V975]", "humangutMH0002_GL0047733 [gene] locus=scaffold13171_4:7351:8523:- [Complete] codon-table.11", "humangutMH0030_GL0024174 [gene] locus=scaffold3427_5:970:2142:+ [Complete] codon-table.11", "humangutMH0031_GL0013281 [gene] locus=scaffold17867_1:3054:4226:- [Complete] codon-table.11", "humangutMH0046_GL0000475 [gene] locus=scaffold34128_5:3085:4257:- [Complete] codon-table.11", "humangutMH0047_GL0030846 [gene] locus=scaffold14012_1:552:1724:+ [Complete] codon-table.11", "humangutMH0057_GL0015944 [gene] locus=scaffold7238_2:27269:28441:+ [Complete] codon-table.11", "humangutMH0068_GL0025047 [gene] locus=scaffold2668_4:6952:8124:+ [Complete] codon-table.11", "humangutMH0096_GL0108095 [gene] locus=scaffold10502_7:3798:4970:+ [Complete] codon-table.11", "humangutMH0107_GL0014100 [gene] locus=scaffold94184_3:3232:4404:+ [Complete] codon-table.11", "humangutMH0108_GL0084746 [gene] locus=scaffold24961_2:3115:4287:- [Complete] codon-table.11", "humangutMH0110_GL0036574 [gene] locus=scaffold64034_1:21985:23157:- [Complete] codon-table.11", "humangutMH0118_GL0094753 [gene] locus=scaffold25193_11:6159:7331:- [Complete] codon-table.11", "humangutMH0204_GL0152049 [gene] locus=scaffold123145_1:6065:7237:- [Complete] codon-table.11", "humangutMH0319_GL0128255 [gene] locus=scaffold68360_3:154:1326:+ [Complete] codon-table.11", "humangutMH0413_GL0134704 [gene] locus=scaffold113148_1:5774:6946:- [Complete] codon-table.11", "humangutMH0439_GL0204787 [gene] locus=scaffold128360_1:19466:20638:+ [Complete] codon-table.11", "humangutO2_CD2_0_GL0092646 [gene] locus=scaffold23217_1:4473:5645:- [Complete] codon-table.11", "humangutO2_UC1-1_GL0135101 [gene] locus=scaffold82652_1:11269:12441:+ [Complete] codon-table.11", "humangutV1_CD49-0_GL0042171 [gene] locus=scaffold98_1:6271:7443:+ [Complete] codon-table.11", "humangutV1_FI09_GL0019029 [gene] locus=scaffold113036_3:3584:4756:+ [Complete] codon-table.11", "humangutV1_FI14_GL0197754 [gene] locus=scaffold4657_3:19502:20674:- [Complete] codon-table.11",</p>

"humangutV1.FI21\_GL0042399 [gene] locus=scaffold11131\_1:28543:29715:- [Complete] codon-table.11",

"humangutV1.UC12-4\_GL0087291 [gene] locus=scaffold46695\_1:6095:7267:+ [Complete] codon-table.11",

"humangutV1.UC17-2\_GL0138817 [gene] locus=scaffold101158\_2:8753:9925:+ [Complete] codon-table.11",

"humangutDLF013\_GL0071348 [gene] locus=scaffold15346\_3:2304:3476:+ [Complete] codon-table.11",

"humangutNOM012\_GL0077981 [gene] locus=scaffold47201\_8:3023:4195:- [Complete] codon-table.11",

"humangut764588959-stool1\_revised\_scaffold37899\_1\_gene92472 strand:- start:416 stop:1588 length:1173 start\_codon:yes stop\_codon:yes gene\_type:complete [Complete] codon-table.11",

"humangut340101.Vrad\_PD1405 [Complete]:- codon-table.11",

"mouseS-Fe1\_GL0032980 [gene] locus=scaffold1050\_1:65236:66408:+ [Complete] codon-table.11",

"mouseG1-1A\_GL0112135 [gene] locus=scaffold85946\_1:9974:11146:+ [Complete] codon-table.11",

"mouseG1-4A\_GL0002753 [gene] locus=scaffold255\_6:6975:8147:- [Complete] codon-table.11",

"pigPIG\_151\_GL0132399 [gene] locus=scaffold257136\_1:829:2001:+ [Complete] codon-table.11",

"pigPIG-042\_GL0083904 [gene] locus=scaffold91070\_1:3176:4348:+ [Complete] codon-table.11",

"pigPIG-042\_GL0107950 [gene] locus=scaffold40045\_4:18612:19784:+ [Complete] codon-table.11",

"pigBHZ-5B\_GL0196560 [gene] locus=scaffold1120\_5:1578:2750:+ [Complete] codon-table.11",

"rumen553\_GL0180945\_1 [gene] locus=scaffold6020\_1:9339:10511:-[Complete]",

"rumen553\_GL0344582\_1 [gene] locus=scaffold304915\_1:14287:15459:-[Complete]",

"rumen553\_GL0418645\_1 [gene] locus=scaffold113043\_2:120:1292:+[Complete]",

"rumen553\_GL0745339\_1 [gene] locus=scaffold77336\_4:40365:41537:-[Complete]",

"rumen552\_GL1330311\_1 [gene] locus=scaffold418063\_1:3715:4887:-[Complete]",

"rumen554\_GL0598331\_1 [gene] locus=scaffold200869\_1:918:2090:-[Complete]",

"rumen554\_GL1420526\_1 [gene] locus=scaffold18984\_1:2700:3872:+[Complete]",

"rumen554\_GL2381906\_1 [gene] locus=scaffold35339\_1:1115:2287:+[Complete]",

"rumen0081\_GL1835481\_1 [gene] locus=scaffold292226\_1:34868:36040:-[Complete]",

"rumen100058\_GL1296115\_1 [gene] locus=scaffold3360526\_1:2683:3855:-[Complete]",

"rumen100058\_GL1415020\_1 [gene] locus=scaffold1781521\_1:4254:5426:+[Complete]",

"rumen100058\_GL2060545\_1 [gene] locus=scaffold255740\_1:1392:2564:+[Complete]",

"rumen100058\_GL2074080\_1 [gene] locus=scaffold484796\_2:1768:2940:-[Complete]",

"rumen2009040\_GL1506655\_1 [gene] locus=scaffold424\_2:10634:11806:+[Complete]",

"rumen7049\_GL0177938\_1 [gene] locus=scaffold170653\_1:280:1452:-[Complete]",

"rumen7049\_GL1540641\_1 [gene] locus=scaffold591523\_1:826:1998:+[Complete]",

"cazygi|671712711|gb|AII64984.1| glycosidase [Bacteroides dorei]",

"cazygi|301161859|emb|CBW21403.1| conserved hypothetical protein [Bacteroides fragilis 638R]",

"cazygi|922660742|emb|CUA17426.1| 4-O-beta-D-mannosyl-D-glucose phosphorylase [Bacteroides fragilis]",

"cazygi|794204885|gb|AKA50876.1| glycosidase [Bacteroides fragilis]",

"cazygi|1042799867|gb|ANQ59514.1| glycosidase [Bacteroides fragilis]",

"cazygi|52215005|dbj|BAD47598.1| conserved hypothetical protein [Bacteroides fragilis YCH46]",

"cazygi|938483303|gb|ALJ47534.1| 4-O-beta-D-mannosyl-D-glucose phosphorylase [Bacteroides ovatus]",

"cazygi|149935157|gb|ABR41854.1| conserved hypothetical protein [Parabacteroides distasonis ATCC 8503]",

"cazygi|460564980|gb|AGH13967.1| glycosylase [Prevotella sp. Sc00026]"

["cazyCCgi|VCV21228.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Roseburia intestinalis L1-82]",

"cazy|AVM41762.1 glycosidase [Fastidiosipila sanguinis]",

"cazy|AYF38259.1 glycosidase [Ethanoligenens harbinense]",

"cazy|AYF41005.1 glycosidase [Ethanoligenens harbinense]",

"humangutMH0003\_GL0066421 [gene] locus=scaffold31568\_5:287:1465:- [Complete] codon-table.11",

"humangutMH0113\_GL0091133 [gene] locus=scaffold6516\_6:4173:5351:+ [Complete] codon-table.11",

"humangutMH0124\_GL0095539 [gene] locus=scaffold96089\_5:4645:5823:- [Complete] codon-table.11",

"humangutMH0143\_GL0013868 [gene] locus=scaffold18775\_4:2159:3337:+ [Complete] codon-table.11",

"humangutMH0200\_GL0131568 [gene] locus=scaffold17224\_1:6867:8045:- [Complete] codon-table.11",

"humangutMH0396\_GL0022730 [gene] locus=scaffold98811\_2:4136:5314:- [Lack 5'-end] codon-table.11",

"humangutMH0431\_GL0109398 [gene] locus=scaffold114921\_1:81485:82663:- [Complete] codon-table.11",

"humangutO2.UC37-1\_GL0054917 [gene] locus=scaffold50480\_4:50:1228:- [Lack 5'-end] codon-table.11",

"humangutSZEY-35A\_GL0075720 [gene] locus=scaffold8896\_1:5193:6371:+ [Complete] codon-table.11",

"humangutT2D-33A\_GL0089601 [gene] locus=scaffold18086\_5:30121:31299:- [Complete] codon-table.11",

"mouseS-Fe2\_GL0160680 [gene] locus=scaffold84515\_1:46293:47471:+ [Complete] codon-table.11",

"mouseG1-7A\_GL0023841 [gene] locus=scaffold10583\_7:9507:10685:+ [Complete] codon-table.11",

"mouse1-2\_GL0101012 [gene] locus=scaffold7366\_22:6163:7341:- [Complete] codon-table.11",

"mouse26\_GL0113777 [gene] locus=scaffold73750\_3:1126:2304:- [Complete] codon-table.11",

"mouse2-7\_GL0077041 [gene] locus=scaffold37832\_1:52:1230:- [Complete] codon-table.11",

"mouse7-7\_GL0001996 [gene] locus=scaffold62865\_1:9959:11137:- [Complete] codon-table.11",

"pigPIG-117\_GL0190472 [gene] locus=scaffold262986\_1:8033:9211:+ [Complete] codon-table.11",

"pigPIG-033\_GL0076532 [gene] locus=scaffold132591\_1:865:2043:- [Complete] codon-table.11",

"pigPIG-033\_GL0121405 [gene] locus=scaffold24127\_3:5365:6543:- [Complete] codon-table.11",

"pigPIG-043\_GL0020493 [gene] locus=C1594118\_1:200:1378:+ [Complete] codon-table.11",

"pigPIG-061\_GL0061187 [gene] locus=scaffold150548\_2:2264:3442:+ [Complete] codon-table.11",

"pigPIG-066\_GL0171037 [gene] locus=scaffold156896\_1:74:1252:- [Complete] codon-table.11",

"pigPIG-105\_GL0070140 [gene] locus=scaffold21854\_8:175:1353:- [Complete] codon-table.11",

"pigPIG-108\_GL0038609 [gene] locus=scaffold50953\_1:13642:14820:- [Complete] codon-table.11",

"pigPIG-109\_GL0153659 [gene] locus=scaffold15355\_2:101:1279:+ [Complete] codon-table.11",

"pigBHZ-4B\_GL0046982 [gene] locus=scaffold6788\_10:5028:6206:- [Complete] codon-table.11",

"pigBMZ-17B\_GL0130458 [gene] locus=scaffold31446\_2:852:2030:+ [Complete] codon-table.11",

"pigEYZ-120B\_GL0239890 [gene] locus=scaffold124621\_1:14640:15818:- [Complete] codon-table.11",

"rumen553\_GL0080408\_1 [gene] locus=scaffold389397\_1:289:1467:-[Complete]",

"rumen553\_GL0368033\_1 [gene] locus=scaffold42880\_1:939:2117:+[Complete]",

"rumen553\_GL0608442\_1 [gene] locus=scaffold99516\_2:18358:19536:+[Complete]",

"rumen553\_GL0672485\_1 [gene] locus=scaffold250358\_1:40472:41650:-[Complete]",

"rumen553\_GL0799271\_1 [gene] locus=scaffold285696\_1:2:1177:-[Lack 3'-end]",

"rumen552\_GL0196067\_1 [gene] locus=scaffold1044748\_1:19093:20271:-[Complete]",

"rumen552\_GL1374889\_1 [gene] locus=scaffold1084712\_1:1435:2613:-[Complete]",

"rumen583\_GL0314713\_1 [gene] locus=scaffold131305\_1:732:1910:+[Complete]",

"rumen583\_GL0754106\_1 [gene] locus=scaffold195983\_1:23761:24939:+[Complete]",

"rumen554\_GL0138869\_1 [gene] locus=scaffold288892\_1:859:2037:-[Complete]",

"rumen554\_GL0823804\_1 [gene] locus=scaffold1964144\_1:1691:2869:-[Complete]",

"rumen554\_GL2538377\_1 [gene] locus=scaffold618786\_1:150:1328:-[Complete]",

"rumen555\_GL2498922\_1 [gene] locus=scaffold1308004\_2:1032:2210:-[Complete]",

"rumen0081\_GL0200567\_1 [gene] locus=scaffold583614\_2:389:1567:+[Complete]",

"rumen0081\_GL0989309\_1 [gene] locus=scaffold391367\_2:395:1573:+[Complete]",

"rumen100058\_GL0662622\_1 [gene] locus=scaffold1264265\_3:2349:3527:-[Complete]",

"rumen2009040_GL0355188_1 [gene] locus=scaffold318654_1:1130:2308:-[Complete]",
"rumen2009040_GL1153821_1 [gene] locus=scaffold182269_4:4556:5734:+[Complete]",
"rumen2009040_GL1798234_1 [gene] locus=scaffold1815524_1:92:1270:-[Complete]",
"rumen2009040_GL2361669_1 [gene] locus=scaffold2277265_2:2813:3991:+[Complete]",
"rumen3042_GL2082550_1 [gene] locus=scaffold1268850_4:4066:5244:-[Complete]",
"rumen7049_GL1652958_1 [gene] locus=scaffold893802_4:6121:7299:+[Complete]",
"cazygi 295094605 emb CBK83696.1  Predicted glycosylase [Coprococcus sp. ART55/1]",
"cazygi 315469862 gb ADU26466.1  glycosidase related protein [Ethanoligenens harbinense YUAN-3]",
"cazygi 291537317 emb CBL10429.1  Predicted glycosylase [Roseburia intestinalis M50/1]",
"cazygi 291539263 emb CBL12374.1  Predicted glycosylase [Roseburia intestinalis XB6B4]",
["cazygi 1000297354 gb AML27056.1  putative glycosidase [Bacillus sp. N16-5]"]
["cazygi 1008894275 gb AMR25942.1  glycosidase [Hymenobacter sp. PAMC 26554]"]
["cazygi 1028462835 gb ANE45758.1  glycosidase [Paenibacillus swuensis]"]
["cazygi 1031984082 dbj BAV09483.1  predicted glycoside hydrolase [Filimonas lacunae]"]
["cazygi 1033477963 dbj BAV13071.1  glycosidase PH1107-related [Clostridium cellulovorans]",
"cazygi 302578871 gb ADL52883.1  glycosidase related protein [Clostridium cellulovorans 743B]"]
["cazygi 1042792181 gb ANQ52748.1  unk1-like protein [Flammeovirga sp. MY04]",
"cazygi 261868893 gb ACY02068.1  hypothetical protein [Flammeovirga yaeyamensis]"]
["cazygi 1049756037 gb ANY69291.1  glycosidase [Paenibacillus sp. BIHB4019]"]
["cazygi 169640140 gb ACA61147.1  conserved hypothetical protein [uncultured microorganism]",
"humangutMH0003_GL0049222 [gene] locus=scaffold17664_2:8391:9566:+ [Complete] codon-table.11",
"humangutMH0038_GL0001581 [gene] locus=scaffold2102_6:1247:2422:- [Complete] codon-table.11",
"humangutMH0143_GL0027387 [gene] locus=scaffold76777_2:3841:5016:+ [Complete] codon-table.11",
"humangutMH0198_GL0003384 [gene] locus=scaffold964_3:17833:19008:- [Complete] codon-table.11",
"humangutMH0220_GL0233763 [gene] locus=C1944239_1:11:1186:- [Complete] codon-table.11",
"humangutMH0250_GL0225137 [gene] locus=scaffold91081_4:1190:2365:- [Complete] codon-table.11",
"humangutMH0281_GL0021541 [gene] locus=scaffold20_3:5981:7156:- [Complete] codon-table.11",
"humangutMH0333_GL0065324 [gene] locus=scaffold55593_2:12263:13438:- [Complete] codon-table.11",
"humangutMH0404_GL0002420 [gene] locus=scaffold48203_4:24403:25578:- [Complete] codon-table.11",
"humangutO2_UC8-0_GL0042077 [gene] locus=scaffold31855_2:3308:4483:+ [Complete] codon-table.11",
"humangutV1_UC26-0_GL0097455 [gene] locus=scaffold2640_7:6674:7849:+ [Complete] codon-table.11",
"humangutDLM020_GL0058241 [gene] locus=scaffold14939_10:26:1201:- [Complete] codon-table.11",
"humangutDOM005_GL0054482 [gene] locus=scaffold5697_6:9236:10411:+ [Complete] codon-table.11",
"humangutNLM006_GL0090500 [gene] locus=scaffold24016_2:5835:7010:- [Complete] codon-table.11",
"humangutT2D-26A_GL0135482 [gene] locus=scaffold16630_2:801:1976:- [Complete] codon-table.11",
"mouseMC-6-1_GL0003210 [gene] locus=scaffold294_4:20864:22039:+ [Complete] codon-table.11",
"mouse3-1_GL0031926 [gene] locus=scaffold18314_1:24130:25305:+ [Complete] codon-table.11",
"mouse31_GL0057924 [gene] locus=scaffold36726_3:57584:58759:+ [Complete] codon-table.11",
"mouse40_GL0063271 [gene] locus=scaffold33833_11:3019:4194:- [Complete] codon-table.11",
"mouse7_GL0082073 [gene] locus=scaffold45200_2:6409:7584:+ [Complete] codon-table.11",
"pigPIG_127_GL0225872 [gene] locus=scaffold57456_1:2:1177:+ [Lack 5'-end] codon-table.11",
"pigPIG-002_GL0118353 [gene] locus=scaffold129520_1:1581:2756:- [Complete] codon-table.11",
"pigPIG-028_GL0219785 [gene] locus=scaffold57117_1:1:1176:+ [Lack 5'-end] codon-table.11",
"pigPIG-093_GL0085264 [gene] locus=scaffold80859_2:3:1178:+ [Lack 5'-end] codon-table.11",

"pigEYZ-378B_GL0010923 [gene] locus=C2385022_1:23046:24221:+ [Complete] codon-table.11",
"rumen554_GL2240865_1 [gene] locus=scaffold177812_3:28559:29734:-[Complete]",
"rumen2009040_GL1743916_1 [gene] locus=scaffold1072038_1:4245:5420:-[Complete]",
"rumen3042_GL1764059_1 [gene] locus=scaffold13938_4:5273:6448:-[Complete]"
["cazygi 177841338 gb ACB75590.1  glycosidase PH1107-related [Opitutus terrae PB90-1]"]
["cazygi 220000696 gb ACL77297.1  glycosidase PH1107-related [[Clostridium] cellulolyticum H10]"]
["cazygi 237684844 gb ACR12108.1  conserved hypothetical protein [Teredinibacter turnerae T7901]"]
["cazygi 247543793 gb ACT00812.1  glycosidase PH1107-related [Paenibacillus sp. JDR-2]"]
["cazygi 255346849 gb ACU06175.1  glycosidase PH1107-related [Pedobacter heparinus DSM 2366]"]
["cazygi 256039283 gb ACU62827.1  glycosidase PH1107-related [Chitinophaga pinensis DSM 2588]"]
["cazygi 262335521 gb ACY49318.1  glycosidase PH1107-related protein [Rhodothermus marinus DSM 4252],
"cazygi 345113502 gb AEN74334.1  glycosidase related protein [Rhodothermus marinus SG0.5JP17-172]"
["cazygi 284158781 gb ADB80102.1  glycosidase [uncultured microorganism]",
"cazygi 82524102 emb CAJ19137.1  conserved hypothetical protein [unidentified microorganism]",
"humangutMH00252_GL0130169 [gene] locus=scaffold46124_3:3552:4712:- [Complete] codon-table.11",
"mouse19_GL0059980 [gene] locus=scaffold6821_5:1223:2383:- [Complete] codon-table.11",
"pigPIG_119_GL0111674 [gene] locus=scaffold53781_2:761:1921:+ [Complete] codon-table.11",
"pigPIG-018_GL0182330 [gene] locus=scaffold12858_2:87701:88861:+ [Complete] codon-table.11",
"pigPIG-027_GL0246440 [gene] locus=scaffold83656_4:1373:2533:- [Complete] codon-table.11",
"pigBHZ-9B_GL0192845 [gene] locus=scaffold48502_3:19993:21153:+ [Complete] codon-table.11",
"rumen553_GL0780103_1 [gene] locus=scaffold410565_1:8371:9531:-[Complete]",
"rumen552_GL0626026_1 [gene] locus=scaffold1113599_1:132:1292:-[Complete]",
"rumen552_GL0940734_1 [gene] locus=scaffold696891_2:3677:4837:+[Complete]",
"rumen552_GL1700463_1 [gene] locus=scaffold1036305_1:3406:4566:-[Complete]",
"rumen554_GL1222817_1 [gene] locus=scaffold68735_4:6051:7211:+[Complete]",
"rumen554_GL1613293_1 [gene] locus=scaffold718363_1:1619:2779:+[Complete]",
"rumen555_GL0221201_1 [gene] locus=scaffold13840_1:649:1809:-[Complete]",
"rumen555_GL1629362_1 [gene] locus=scaffold120052_5:43473:44633:+[Complete]",
"rumen0081_GL0103663_1 [gene] locus=scaffold830863_2:1259:2419:-[Complete]",
"rumen0081_GL0134462_1 [gene] locus=scaffold98731_3:12335:13495:+[Complete]",
"rumen0081_GL0514060_1 [gene] locus=scaffold5614_1:8340:9500:+[Complete]",
"rumen0081_GL1036364_1 [gene] locus=scaffold454329_1:2137:3297:+[Complete]",
"rumen0081_GL1258454_1 [gene] locus=scaffold882583_1:798:1958:-[Complete]",
"rumen0081_GL1762675_1 [gene] locus=scaffold894285_1:840:2000:+[Complete]",
"rumen100058_GL0026523_1 [gene] locus=scaffold393135_3:1042:2202:+[Complete]",
"rumen2009040_GL3366046_1 [gene] locus=scaffold2399118_1:3222:4382:+[Complete]",
"rumen3042_GL0863569_1 [gene] locus=scaffold2513516_2:1667:2827:-[Complete]",
"rumen3042_GL2268751_1 [gene] locus=scaffold1869024_2:6750:7910:-[Complete]",
"rumen3042_GL2297951_1 [gene] locus=scaffold1001230_1:94:1254:+[Complete]",
"rumen7049_GL0275719_1 [gene] locus=scaffold2125146_1:3791:4951:+[Complete]"
["cazygi 294980251 gb ADF50716.1  glycosidase", " PH1107-related protein [Zunongwangia profunda SM-A87]"]
["cazygi 294983326 gb ADF53791.1  glycosidase", " PH1107-related protein [Zunongwangia profunda SM-A87]"]
["cazygi 306531536 gb ADN01070.1  putative glycosylase [Spirochaeta thermophila DSM 6192]",
"cazygi 339410803 gb AEJ60368.1  glycosidase related protein [Spirochaeta thermophila DSM 6578]"

["cazygi 311908637 gb ADQ19078.1  glycosidase related protein [Leadbetterella byssophila DSM 17132]"
["cazygi 315471962 gb ADU28565.1  glycosidase related protein [Bacillus cellulosiiticus DSM 2522]"
["cazygi 324974528 gb ADY53512.1  glycosidase related protein [Pseudopedobacter saltans DSM 12145]"
["cazygi 326549119 gb ADZ77504.1  glycosidase related protein [Sphingobacterium sp. 21]"
["cazygi 332174970 gb AEE24224.1  glycosidase related protein [Glaciecola sp. 4H-3-7+YE-5], "cazygi 409028202 gb AFV00487.1  hypothetical protein M5M_16780 [Simidiua agarivorans SA1 = DSM 21679]"
["cazygi 332330851 gb AEE47952.1  hypothetical protein Halhy_0038 [Haliscomenobacter hydrossis DSM 1100]"
["cazygi 332336263 gb AEE53364.1  glycosidase related protein [Haliscomenobacter hydrossis DSM 1100]"
["cazygi 357200024 gb AET57921.1  glycosidase like protein [Paenibacillus terrae HPL-003]"
["cazygi 361061660 gb AEW00652.1  glycosidase related protein [Niastella koreensis GR20-10]"
["cazygi 373946953 gb AEY67874.1  putative glycosylase [Clostridium sp. BNL1100]"
["cazygi 378568988 gb AFC29298.1  hypothetical protein PM3016_2410 [Paenibacillus mucilaginosus 3016], "cazygi 384090041 gb AFH61477.1  glycosidase [Paenibacillus mucilaginosus K02]", "cazygi 336297581 gb AEI40684.1  conserved hypothetical protein [Paenibacillus mucilaginosus KNP414]"
["cazygi 395811001 gb AFN73750.1  glycosidase PH1107-related protein [Melioribacter roseus P3M-2]"
["cazygi 407728379 dbj BAM48377.1  hypothetical protein AXY_22450 [Amphibacillus xylanus NBRC 15112]"
["cazygi 537743161 emb CDF80804.1  PH1107-like glycosidase [Formosa agariphila KMM 3901]"
["cazygi 570745708 gb AHF16220.1  glycosidase [Niabella soli DSM 19437]"
["cazygi 595617251 gb AHM60894.1  glycosidase-like protein [Flammeovirgaceae bacterium 311]"
["cazygi 610421555 gb AHW58759.1  glycosidase [Draconibacterium orientale]"
["cazygi 672715735 emb CDT00074.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Sphingobacterium sp. PM2-P1-29]"
["cazygi 673067755 emb CDZ25110.1  hypothetical protein CCDG5_2018 [[Clostridium] cellulosi]"
["cazygi 686546537 gb AIQ57233.1  glycosidase [Paenibacillus borealis], "cazygi 686557130 gb AIQ67824.1  glycosidase [Paenibacillus graminis], "cazygi 806911806 emb CQR54414.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Paenibacillus riograndensis SBR5]"
["cazygi 686552468 gb AIQ63163.1  glycosidase [Paenibacillus stellifer]"
["cazygi 808183734 gb AKD03278.1  glycosidase [Pontibacter korlensis]"
["cazygi 874567365 emb CRY96301.1  hypothetical protein [uncultured prokaryote], "pigPIG-018_GL0158480 [gene] locus=scaffold171626_2:17405:18559:+ [Complete] codon-table.11", "pigBHZ-9B_GL0146223 [gene] locus=scaffold94856_1:175:1329:+ [Complete] codon-table.11", "rumen552_GL0148742_1 [gene] locus=scaffold431873_1:24917:26071:-[Complete]", "rumen552_GL1731584_1 [gene] locus=scaffold10134_1:79333:80487:-[Complete]", "rumen554_GL1022204_1 [gene] locus=scaffold359402_2:1862:3016:-[Complete]", "rumen554_GL2723235_1 [gene] locus=scaffold23964_1:370:1524:+[Complete]", "rumen554_GL2929602_1 [gene] locus=scaffold181747_1:1742:2896:-[Complete]", "rumen0081_GL0118178_1 [gene] locus=scaffold1011559_2:13805:14959:+[Complete]", "rumen0081_GL0924944_1 [gene] locus=C39741617_1:24:1178:-[Complete]", "rumen100058_GL1676940_1 [gene] locus=scaffold587872_2:4351:5505:+[Complete]", "rumen3042_GL1475731_1 [gene] locus=scaffold2132912_1:3648:4802:-[Complete]", "rumen7049_GL1822588_1 [gene] locus=scaffold867003_2:2185:3339:-[Complete]"
["cazygi 88709570 gb EAR01803.1  hypothetical protein FB2170_14783 [Maribacter sp. HTCC2170]"
["cazygi 937828634 gb ALI98491.1  glycosidase [Rufibacter tibetensis]"
["cazygi 996008937 gb AMJ66328.1  glycosidase [Hymenobacter sp. PAMC 26628]"



<p>["cazy 996029876 gb AMJ87259.1  glycosidase [Alteromonas sp. Mac1]",  "cazy 996033740 gb AMJ91122.1  glycosidase [Alteromonas sp. Mac2]",  "cazy 1023067534 gb ANB2411.1  glycosidase [Alteromonas stellipolaris]"]</p>
<p>["cazy 998619555 dbj BAU55488.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Mucilagibacter gotjawali]"]</p>
<p>["cazy AOE54287.1 glycosidase [Flavobacterium psychrophilum]",  "cazy AOW17807.1 glycosidase [Polaribacter vadi]",  "cazy AWH86882.1 glycosidase [Flavobacterium sp. HYN0059]",  "cazy AWM14794.1 glycosidase [Flavobacterium sp. MEBIC07310]",  "cazy 947264404 gb ALM47942.1  glycosidase [Flavobacterium psychrophilum]"]</p>
<p>["cazy AOK90372.1 glycosidase [Paenibacillus polymyxa]",  "cazy APB69112.1 glycosidase [Paenibacillus polymyxa]",  "cazy APB73770.1 glycosidase [Paenibacillus polymyxa]",  "cazy APO61726.1 glycosidase [Paenibacillus polymyxa]",  "cazy ASR45393.1 glycosidase [Paenibacillus kribbensis]",  "cazy AUO06676.1 glycosidase [Paenibacillus sp. lzh-N1]",  "cazy AUS29147.1 glycosidase [Paenibacillus polymyxa]",  "cazy 920791919 gb ALA44438.1  glycosidase [Paenibacillus peoriae]",  "cazy 723615833 gb AIY09206.1  glycosidase [Paenibacillus polymyxa]",  "cazy 565677757 gb AHC22327.1  glycosidase [Paenibacillus polymyxa CR1]",  "cazy 305860624 gb ADM72412.1  glycosidase [Paenibacillus polymyxa E681]",  "cazy 392305251 emb CCI71614.1  hypothetical protein PPM_4807 [Paenibacillus polymyxa M1]",  "cazy 748408389 gb AJE51905.1  glycosidase [Paenibacillus polymyxa]",  "cazy 309249536 gb ADO59103.1  glycosidase [Paenibacillus polymyxa SC2]",  "cazy 595636231 gb AHM68489.1  glycosidase like protein [Paenibacillus polymyxa SQR-21]"]</p>
<p>["cazy AOM76025.1 glycosidase [Pedobacter steynii]",  "cazy 941976244 gb ALL07673.1  glycosidase [Pedobacter sp. PACM 27299]"]</p>
<p>["cazy AOS44739.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Lacunisphaera limnophila]",  "cazy 573475039 gb AHF92050.1  glycosidase [Opitutaceae bacterium TAV5]"]</p>
<p>["cazy AOS98644.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Microbulifer aggregans]"]</p>
<p>["cazy AOW21555.1 glycosidase [Lutibacter sp. LPB0138]"]</p>
<p>["cazy AOZ93121.1 glycosidase [Paenibacillus crassostreae]",  "cazy AWV32547.1 glycosidase [Paenibacillus odorifer]",  "cazy 686562510 gb AIQ73203.1  glycosidase [Paenibacillus odorifer]",  "cazy 690615645 gb AIQ16858.1  glycosidase [Paenibacillus sp. FSL H7-0357]",  "cazy 690621761 gb AIQ22775.1  glycosidase [Paenibacillus sp. FSL H7-0737]",  "cazy 686517730 gb AIQ28431.1  glycosidase [Paenibacillus sp. FSL P4-0081]",  "cazy 686523878 gb AIQ34578.1  glycosidase [Paenibacillus sp. FSL R5-0345]",  "cazy 686529466 gb AIQ40165.1  glycosidase [Paenibacillus sp. FSL R5-0912]",  "cazy 686535316 gb AIQ46014.1  glycosidase [Paenibacillus sp. FSL R7-0273]",  "cazy 686536683 gb AIQ47381.1  glycosidase [Paenibacillus sp. FSL R7-0273]",  "cazy 686542214 gb AIQ52911.1  glycosidase [Paenibacillus sp. FSL R7-0331]",  "cazy 686540928 gb AIQ51625.1  glycosidase [Paenibacillus sp. FSL R7-0331]",  "cazy 991824680 gb AMF93029.1  glycosidase [Vibrio fluvialis]",  "cazy 315181851 gb ADT88764.1  glycosidase PH1107-like protein [Vibrio furnissii NCTC 11218]"]</p>

"cazy 1042390253 gb ANQ24660.1  glycosidase [Vibrio natriegens]"
["cazy AOZ96976.1 glycoside hydrolase GH130 family [Butyrivibrio hungatei]", "cazy ASU28436.1 glycosidase [Blautia coxoides]", "humangut MH0193_GL0151565 [gene] locus=scaffold48753_8:30007:31176:+ [Complete] codon-table.11", "humangut MH0286_GL0027030 [gene] locus=scaffold1827_12:788:1957:+ [Complete] codon-table.11", "humangut O2_UC8-1_GL0175915 [gene] locus=scaffold27462_4:5020:6189:+ [Complete] codon-table.11", "humangut V1_CD25-4_GL0125785 [gene] locus=scaffold1855_23:471:1640:- [Complete] codon-table.11", "humangut V1_CD55-0_GL0019722 [gene] locus=scaffold99650_1:145:1314:- [Complete] codon-table.11", "mouse MC-0-1_GL0116189 [gene] locus=scaffold99096_2:7600:8769:+ [Complete] codon-table.11", "mouse MC-6-5_GL0126806 [gene] locus=scaffold97032_1:2216:3385:- [Complete] codon-table.11", "mouse 26_GL0143937 [gene] locus=scaffold53671_2:1130:2299:- [Complete] codon-table.11", "mouse 29_GL0004044 [gene] locus=scaffold98111_2:2151:3320:- [Complete] codon-table.11", "mouse 6-3_GL0066401 [gene] locus=scaffold85639_4:2267:3436:+ [Complete] codon-table.11", "mouse 8-1_GL0089436 [gene] locus=scaffold42344_7:2435:3604:- [Complete] codon-table.11", "pig PIG_140_GL0075906 [gene] locus=scaffold120029_9:1040:2209:+ [Complete] codon-table.11", "pig PIG_167_GL0213461 [gene] locus=scaffold59379_3:3:1169:- [Lack 3'-end] codon-table.11", "pig PIG_192_GL0047528 [gene] locus=scaffold19611_5:411:1580:- [Complete] codon-table.11", "pig PIG-001_GL0169553 [gene] locus=scaffold31187_9:1236:2405:+ [Complete] codon-table.11", "rumen 553_GL0620793_1 [gene] locus=scaffold430590_1:66040:67209:+[Complete]", "rumen 553_GL0720166_1 [gene] locus=scaffold70501_1:1602:2771:+[Complete]", "rumen 583_GL0267624_1 [gene] locus=scaffold337529_1:5774:6943:-[Complete]", "rumen 583_GL0281287_1 [gene] locus=scaffold149356_5:1144:2313:+[Complete]", "rumen 583_GL0726185_1 [gene] locus=scaffold1286_4:100582:101751:-[Complete]", "rumen 554_GL1011952_1 [gene] locus=scaffold1761809_1:1001:2170:-[Complete]", "rumen 555_GL1294657_1 [gene] locus=scaffold755112_1:10663:11832:-[Complete]", "rumen 0081_GL0043449_1 [gene] locus=scaffold1608509_3:795:1964:+[Complete]", "rumen 0081_GL1055791_1 [gene] locus=scaffold452820_5:1601:2770:-[Complete]", "rumen 100058_GL1310035_1 [gene] locus=scaffold2492651_1:2805:3974:-[Complete]", "cazy 1045290883 gb ANU75633.1  glycosidase [Blautia sp. YL58]"
["cazy APC39749.1 glycosidase [Clostridium estertheticum subsp. estertheticum]", "cazy AST56548.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Thermoanaerobacterium thermosaccharolyticum]", "cazy 389570925 gb AFK87330.1  glycosidase related protein [Thermoanaerobacterium saccharolyticum JW/SL-YS485]", "cazy 302778862 gb ADL69421.1  glycosidase-related [Thermoanaerobacterium thermosaccharolyticum DSM 571]", "cazy 433293730 gb AGB19552.1  putative glycosylase [Thermoanaerobacterium thermosaccharolyticum M0795]"
["cazy APO42890.1 glycosidase [Paenibacillus xylanexedens]", "cazy 954043270 gb ALP37035.1  glycosidase [Paenibacillus sp. IHB B 3084]"
["cazy APS38170.1 glycosidase [Salegentibacter sp. T436]"
["cazy APU99346.1 glycosidase [Sphingobacterium sp. B29]"
["cazy AQW92133.1 glycosidase [Elizabethkingia anophelis]", "cazy AQW95450.1 glycosidase [Elizabethkingia anophelis]", "cazy AQW99478.1 glycosidase [Elizabethkingia anophelis]", "cazy AQX03213.1 glycosidase [Elizabethkingia anophelis]", "cazy AQX51803.1 glycosidase [Elizabethkingia anophelis]", "cazy AQX90026.1 glycosidase [Elizabethkingia anophelis]"

"cazy ASV79344.1 glycosidase [Elizabethkingia anophelis]", "cazy ATC35185.1 glycosidase [Elizabethkingia anophelis R26]", "cazy ATC38825.1 glycosidase [Elizabethkingia anophelis Ag1]", "cazy ATC42505.1 glycosidase [Elizabethkingia anophelis]", "cazy ATC46181.1 glycosidase [Elizabethkingia anophelis]", "cazy AVF48890.1 glycosidase [Elizabethkingia anophelis]", "cazy AVF52886.1 glycosidase [Elizabethkingia anophelis]", "cazy 1016605842 gb AMX50912.1  glycosidase [Elizabethkingia anophelis]", "cazy 1008914382 gb AMR40816.1  glycosidase [Elizabethkingia anophelis]", "cazy 1016609514 gb AMX54304.1  glycosidase [Elizabethkingia anophelis]", "cazy 1016602155 gb AMX47452.1  glycosidase [Elizabethkingia anophelis]", "cazy 822872393 gb AKH94617.1  glycosidase [Elizabethkingia anophelis FMS-007]", "cazy 675104779 gb AIL46072.1  putative glycoside hydrolase [Elizabethkingia anophelis NUHP1]"
["cazy AQX07236.1 glycosidase [Elizabethkingia ursingii]", "cazy AQX84721.1 glycosidase [Elizabethkingia bruuniana]", "cazy ATL42876.1 glycosidase [Elizabethkingia miricola]", "cazy 769869649 gb AJW61891.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Elizabethkingia miricola]"]
["cazy ARK12512.1 glycosidase [Fibrella sp. ES10-3-2-2]"]
["cazy ASA19953.1 glycosidase [Paenibacillus donghaensis]"]
["cazy ASB48953.1 glycosidase [Alkalitalea saponilacus]"]
["cazy ASM65030.1 glycosidase [Bacteroides caccae", "humangutMH0013_GL0010528 [gene] locus=scaffold807_4:10769:11968:+ [Complete] codon-table.11"]
["cazy ASU33410.1 glycosidase [Mucilagibacter sp. BJC16-A31]", "cazy 379654489 gb AFD07545.1  putative glycosylase [Solitalea canadensis DSM 3403]"]
["cazy ATL47767.1 glycosidase [Chitinophaga caeni]"]
["cazy AUS97049.1 glycosidase [Pseudoclostridium thermosuccinogenes]"]
["cazy AVM54084.1 glycosidase [Bacteroides zoogloformans]", "humangutT2D-135A_GL0111577 [gene] locus=scaffold23013_2:18227:19411:- [Complete] codon-table.11", "mouse1A-dyr2-07_GL0081301 [gene] locus=scaffold10432_2:43704:44888:+ [Complete] codon-table.11", "pigPIG_164_GL0141403 [gene] locus=scaffold38986_1:1:1185:+ [Lack 5'-end] codon-table.11", "pigPIG-032_GL0049834 [gene] locus=scaffold19392_27:2:1186:+ [Lack 5'-end] codon-table.11", "rumen552_GL1114630_1 [gene] locus=scaffold712100_1:12124:13308:-[Complete]", "rumen552_GL1143618_1 [gene] locus=scaffold29684_2:1363:2547:-[Complete]", "rumen554_GL0725053_1 [gene] locus=scaffold2187960_1:7:1191:-[Complete]", "rumen0081_GL0541184_1 [gene] locus=scaffold699814_1:12309:13493:+[Complete]", "rumen100058_GL1537500_1 [gene] locus=scaffold12501_3:2673:3857:+[Complete]", "rumen2009040_GL3289829_1 [gene] locus=scaffold780654_4:9276:10460:+[Complete]"]
["cazy AVM58814.1 glycosidase [Bacteroides heparinolyticus]", "humangutMH0003_GL0073593 [gene] locus=scaffold9631_2:15512:16690:- [Complete] codon-table.11", "humangutMH0011_GL0024617 [gene] locus=scaffold24322_8:1613:2791:- [Complete] codon-table.11", "humangutMH0026_GL0049629 [gene] locus=scaffold14722_2:1362:2540:- [Complete] codon-table.11", "humangutMH0028_GL0037958 [gene] locus=scaffold35126_2:889:2067:+ [Complete] codon-table.11", "humangutMH0047_GL0029507 [gene] locus=scaffold8414_1:15652:16830:- [Complete] codon-table.11", "humangutMH0113_GL0004360 [gene] locus=scaffold75803_5:9495:10673:- [Complete] codon-table.11",

"humangutMH0114_GL0053775 [gene] locus=scaffold56431_1:4880:6058:- [Complete] codon-table.11",
"humangutMH0302_GL0099631 [gene] locus=scaffold9392_6:4002:5180:+ [Complete] codon-table.11",
"humangutMH0309_GL0054284 [gene] locus=scaffold4630_4:9523:10701:+ [Complete] codon-table.11",
"humangutMH0407_GL0070133 [gene] locus=scaffold73610_5:6747:7925:- [Complete] codon-table.11",
"humangutO2.UC24-2_GL0054273 [gene] locus=scaffold9775_18:4301:5479:- [Complete] codon-table.11",
"humangutO2.UC58-2_GL0152937 [gene] locus=scaffold3330_6:542:1720:- [Complete] codon-table.11",
"humangutV1.F135_GL0086344 [gene] locus=scaffold16157_6:165:1343:- [Complete] codon-table.11",
"humangutNOF013_GL0042737 [gene] locus=scaffold16252_2:138513:139691:+ [Complete] codon-table.11",
"humangutN085A_GL0065524 [gene] locus=scaffold44823_1:37093:38271:+ [Complete] codon-table.11",
"humangutT2D-48A_GL0083972 [gene] locus=scaffold18493_2:18681:19859:- [Complete] codon-table.11",
"mouseG1-1A_GL0110639 [gene] locus=scaffold85753_1:20501:21679:+ [Complete] codon-table.11",
"mouseGroup2-3A_GL0160146 [gene] locus=scaffold102179_3:1524:2702:- [Complete] codon-table.11",
"mouse10_GL0081707 [gene] locus=scaffold41461_1:46211:47389:+ [Complete] codon-table.11",
"mouse10_GL0091204 [gene] locus=C801888_1:7411:8589:+ [Complete] codon-table.11",
"mouse1A-dyr2-07_GL0066252 [gene] locus=scaffold13599_3:9593:10771:- [Complete] codon-table.11",
"pigPIG-031_GL0115019 [gene] locus=scaffold144823_1:761:1939:+ [Complete] codon-table.11",
"pigPIG-036_GL0021257 [gene] locus=scaffold156299_5:1816:2994:- [Complete] codon-table.11",
"rumen554_GL2845194_1 [gene] locus=scaffold34491_2:1193:2371:+[Complete]",
"rumen555_GL0766667_1 [gene] locus=scaffold209228_1:23209:24387:+[Complete]",
"cazygi 939201095 gb ALJ59268.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Bacteroides cellulosilyticus]",
"cazygi 319415146 gb ADV42257.1  glycosidase related protein [Bacteroides helcogenes P 36-108]",
"cazygi 149931592 gb ABR38290.1  conserved hypothetical protein [Bacteroides vulgatus ATCC 8482]",
"cazygi 941509130 gb ALK82665.1  Glycosidase-like Protein [Bacteroides vulgatus]",
"cazygi 294472386 gb ADE81775.1  conserved hypothetical protein [Prevotella ruminicola 23"]
["cazy AVR44603.1 glycosidase [Gramella sp. SH35]"]
["cazy AWB46384.1 glycosidase [Paenibacillus sp. CAA11]"]
"humangutMH0277_GL0018625 [gene] locus=scaffold4297_3:1193:2371:+ [Complete] codon-table.11",
"humangutMH0277_GL0036178 [gene] locus=scaffold6836_3:42511:43689:+ [Complete] codon-table.11",
"humangutDOF004_GL0062857 [gene] locus=scaffold19413_12:6329:7507:- [Complete] codon-table.11",
"cazygi 1031373314 gb ANF96696.1  glycosidase [Paenibacillus bovis]"
["cazy AWB65989.1 glycosidase [Catenovulum sp. CCB-QB4]"]
["cazy AWG26847.1 glycosidase [Flavobacterium kingsejongi]"
["cazy AWM35262.1 glycosidase [Hymenobacter nivis]"
["cazy AXB29279.1 glycosidase [Faecalibacterium prausnitzii]",
"humangutMH0004_GL0022947 [gene] locus=scaffold4876_6:5755:6945:+ [Complete] codon-table.11",
"humangutMH0143_GL0066610 [gene] locus=scaffold10045_5:67698:68888:- [Complete] codon-table.11",
"humangutMH0233_GL0007868 [gene] locus=scaffold65_1:7044:8234:- [Complete] codon-table.11",
"humangut706846339-stool1_revised_scaffold23726_3_gene129107 strand:- start:1014 stop:2204 length:1191 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",
"mouseMC-6-1_GL0107987 [gene] locus=scaffold75276_1:4575:5765:- [Complete] codon-table.11",
"mouse10_GL0064298 [gene] locus=scaffold8820_2:15495:16685:- [Complete] codon-table.11",
"pigPIG-173_GL0143313 [gene] locus=scaffold157290_1:3:1193:+ [Lack 5'-end] codon-table.11",
"pigPIG-019_GL0065321 [gene] locus=scaffold11801_1:514:1704:+ [Complete] codon-table.11",
"pigPIG-080_GL0106426 [gene] locus=scaffold141193_3:546:1736:+ [Complete] codon-table.11",

<p>"pigPIG-101_GL0023438 [gene] locus=scaffold56096_1:34:1224:- [Complete] codon-table.11",</p> <p>"rumen552_GL0517600_1 [gene] locus=scaffold11542_8:5683:6873:+[Complete]",</p> <p>"rumen554_GL1856714_1 [gene] locus=scaffold2142401_1:2198:3388:+[Complete]",</p> <p>"cazygi 295104426 emb CBL01970.1  Predicted glycosylase [Faecalibacterium prausnitzii SL3/3]"</p>
<p>["cazy AXE17606.1 glycosidase [Runella sp. HYN0085]"]</p>
<p>["cazy AXG75195.1 glycosidase [Flavobacterium arcticum]",</p> <p>"cazy AYO56875.1 glycosidase [Chryseobacterium sp. 6424]"</p>
<p>["cazy AXP79811.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Mariniflexile sp. TRM1-10]"</p>
<p>["cazy AXT62365.1 glycosidase [Aquimarina sp. AD10]"</p>
<p>["cazy AXV50322.1 glycosidase [Prevotella denticola]",</p> <p>"humangutV1_UC43-0_GL0082855 [gene] locus=scaffold13620_3:17502:18665:+ [Complete] codon-table.11",</p> <p>"mouseMC-0-1_GL0111200 [gene] locus=scaffold96950_3:7683:8846:- [Complete] codon-table.11",</p> <p>"pigPIG-137_GL0180063 [gene] locus=scaffold98100_2:487:1650:+ [Complete] codon-table.11",</p> <p>"pigPIG-022_GL0171437 [gene] locus=scaffold94455_3:857:2020:+ [Complete] codon-table.11",</p> <p>"pigPIG-030_GL0025138 [gene] locus=scaffold46777_11:3786:4949:- [Complete] codon-table.11",</p> <p>"pigPIG-041_GL0094226 [gene] locus=scaffold16_4:3117:4280:+ [Complete] codon-table.11",</p> <p>"pigPIG-041_GL0118777 [gene] locus=scaffold5184_7:1860:3023:- [Complete] codon-table.11",</p> <p>"pigPIG-071_GL0029070 [gene] locus=scaffold42364_1:7020:8183:- [Complete] codon-table.11",</p> <p>"pigBHZ-5B_GL0002271 [gene] locus=scaffold188566_1:138:1301:+ [Complete] codon-table.11",</p> <p>"pigBHZ-8B_GL0185313 [gene] locus=scaffold85542_5:1826:2991:- [Complete] codon-table.11",</p> <p>"pigDB-11B_GL0197709 [gene] locus=scaffold158518_2_1:21:1184:- [Complete] codon-table.11",</p> <p>"pigDB-512B_GL0024780 [gene] locus=scaffold100436_3:8755:9918:- [Complete] codon-table.11",</p> <p>"pigEYZ-378B_GL0053124 [gene] locus=scaffold100833_1:345:1508:+ [Complete] codon-table.11",</p> <p>"rumen553_GL0133960_1 [gene] locus=scaffold919_2:5650:6813:-[Complete]",</p> <p>"rumen553_GL0582149_1 [gene] locus=scaffold185_1.8064:9227:-[Complete]",</p> <p>"rumen553_GL0881969_1 [gene] locus=scaffold352799_3:13055:14218:-[Complete]",</p> <p>"rumen552_GL1114230_1 [gene] locus=scaffold306738_4:5283:6446:+[Complete]",</p> <p>"rumen552_GL1191325_1 [gene] locus=scaffold562209_3:1804:2967:+[Complete]",</p> <p>"rumen552_GL1475824_1 [gene] locus=scaffold419564_1:6005:7168:-[Complete]",</p> <p>"rumen552_GL1488809_1 [gene] locus=scaffold1115241_1:15561:16724:+[Complete]",</p> <p>"rumen552_GL1624036_1 [gene] locus=scaffold1093134_1:2605:3768:+[Complete]",</p> <p>"rumen554_GL0507290_1 [gene] locus=scaffold500042_1:3713:4876:-[Complete]",</p> <p>"rumen554_GL0829376_1 [gene] locus=scaffold2126898_1:3195:4358:-[Complete]",</p> <p>"rumen554_GL0886475_1 [gene] locus=scaffold49808_1:1162:2325:+[Complete]",</p> <p>"rumen554_GL1771620_1 [gene] locus=scaffold1542404_8:2001:3164:+[Complete]",</p> <p>"rumen554_GL1982279_1 [gene] locus=scaffold373070_2:8720:9883:+[Complete]",</p> <p>"rumen554_GL2030663_1 [gene] locus=scaffold896637_3:13:1176:-[Complete]",</p> <p>"rumen554_GL2072226_1 [gene] locus=scaffold14762_1:838:2001:-[Complete]",</p> <p>"rumen554_GL2151294_1 [gene] locus=scaffold518530_1:5283:6446:+[Complete]",</p> <p>"rumen554_GL2564007_1 [gene] locus=scaffold198438_1:3857:5020:-[Complete]",</p> <p>"rumen554_GL2594225_1 [gene] locus=scaffold1010330_2:4365:5528:+[Complete]",</p> <p>"rumen554_GL3098497_1 [gene] locus=scaffold531699_3:57:1220:+[Complete]",</p> <p>"rumen555_GL0508198_1 [gene] locus=scaffold1040298_1:374:1537:-[Complete]",</p> <p>"rumen555_GL0767275_1 [gene] locus=scaffold869588_1:14421:15584:-[Complete]",</p>

"rumen555_GL1143495_1 [gene] locus=scaffold1157453_1:3814:4977:-[Complete]",
"rumen555_GL2114163_1 [gene] locus=scaffold320623_3:3616:4779:-[Complete]",
"rumen555_GL2188078_1 [gene] locus=scaffold991361_1:1446:2609:+[Complete]",
"rumen0081_GL0218905_1 [gene] locus=scaffold1066063_2:196:1359:-[Complete]",
"rumen0081_GL0377878_1 [gene] locus=scaffold650509_1:1629:2792:-[Complete]",
"rumen0081_GL1244966_1 [gene] locus=scaffold579866_1:762:1925:+[Complete]",
"rumen0081_GL1262434_1 [gene] locus=scaffold631150_1:3088:4251:-[Complete]",
"rumen0081_GL1404169_1 [gene] locus=C39889247_1:575:1738:+[Complete]",
"rumen0081_GL1498948_1 [gene] locus=scaffold832430_1:688:1851:-[Lack 5'-end]",
"rumen0081_GL1680436_1 [gene] locus=scaffold825235_1:479:1642:-[Complete]",
"rumen100058_GL0753127_1 [gene] locus=scaffold94941_2:493:1656:-[Complete]",
"rumen100058_GL1356880_1 [gene] locus=scaffold1598668_2:2287:3450:+[Complete]",
"rumen100058_GL1414813_1 [gene] locus=scaffold1508233_4:2402:3565:-[Complete]",
"rumen100058_GL2113642_1 [gene] locus=scaffold1278622_3:2077:3240:+[Complete]",
"rumen100058_GL2560527_1 [gene] locus=scaffold832542_1:58:1221:-[Lack 5'-end]",
"rumen100058_GL2603941_1 [gene] locus=scaffold361223_9:4745:5908:-[Complete]",
"rumen100058_GL3499349_1 [gene] locus=C60815319_1:6495:7658:-[Complete]",
"rumen2009040_GL0248720_1 [gene] locus=scaffold1342030_1:1638:2801:+[Complete]",
"rumen2009040_GL1699258_1 [gene] locus=scaffold78944_1:5788:6951:+[Complete]",
"rumen2009040_GL1981669_1 [gene] locus=scaffold711804_1:4897:6060:-[Complete]",
"rumen2009040_GL3563154_1 [gene] locus=scaffold1311966_1:2321:3484:-[Complete]",
"rumen3042_GL0439631_1 [gene] locus=scaffold1215104_4:1333:2496:+[Complete]",
"rumen3042_GL0447709_1 [gene] locus=scaffold734523_2:693:1856:+[Complete]",
"rumen3042_GL1687329_1 [gene] locus=scaffold707710_2:31:1194:+[Complete]",
"rumen3042_GL2089833_1 [gene] locus=scaffold580603_1:2351:3514:+[Complete]",
"rumen7049_GL2274324_1 [gene] locus=scaffold1348347_1:7324:8487:+[Complete]",
"cazygi 326944448 gb AEA20333.1  hypothetical protein HMPREF9137_1951 [Prevotella denticola F0289]"
["cazy AXY73908.1 glycosidase [Pseudoflavitalea sp. 5GH32-13]"]
["cazy AYD47090.1 glycosidase [Arachidicoccus sp. KIS59-12]"]
["cazy AYL94098.1 glycosidase [Mucilagibacter sp. HYN0043]"]
["cazy AYQ73088.1 glycosidase [Cohnella sp. 18JY8-7]"]
["cazy BAX79320.1 glycosidase [Marinifilaceae bacterium SPP2]"]
["cazy SCD21900.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Proteiniphilum saccharofermentans]",
"humangutMH0381_GL0150559 [gene] locus=scaffold92566_2:2289:3470:- [Complete] codon-table.11",
"humangutDOM005_GL0042972 [gene] locus=scaffold6931_3:20973:22154:+ [Complete] codon-table.11",
"humangutT2D-113A_GL0104331 [gene] locus=scaffold12978_1:30168:31349:- [Complete] codon-table.11",
"humangut457424.BFAG_00180 [Complete]:- codon-table.11",
"cazygi 697634431 emb CEA16908.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Fermentimonas caenicola]"
["cazy SCV07061.1 hypothetical protein BACOV975_00817 [Bacteroides ovatus V975]",
"humangutMH0006_GL0115594 [gene] locus=scaffold224052_1:1361:2530:+ [Complete] codon-table.11",
"humangutMH0020_GL0011935 [gene] locus=scaffold3989_1:7411:8580:- [Complete] codon-table.11",
"humangutMH0287_GL0079244 [gene] locus=scaffold3631_2:1928:3097:- [Complete] codon-table.11",
"humangutMH0363_GL0030758 [gene] locus=scaffold89062_1:4745:5914:+ [Complete] codon-table.11",
"humangutNOF013_GL0050747 [gene] locus=scaffold5482_39:1583:2752:- [Complete] codon-table.11",

<p>"rumen553_GL0235336_1 [gene] locus=scaffold183563_1:612:1781:+[Complete]",</p> <p>"cazygii 938483432 gb ALJ47663.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Bacteroides ovatus]",</p> <p>"cazygii 295085672 emb CBK67195.1  Predicted glycosylase [Bacteroides xylanisolvens XB1A]"</p>
<p>["cazy SDS23678.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Mucilaginibacter mallensis]",</p> <p>"cazygii 336306901 gb AEI50003.1  glycosidase related protein [Runella slithyiformis DSM 19594]"</p>
<p>["cazy SjX74203.1 COG2152 predicted glycoside hydrolase [feces metagenome]",</p> <p>"mouseS-Fe10_GL0077674 [gene] locus=scaffold2319_4:16598:17755:+ [Complete] codon-table.11",</p> <p>"pigPIG-012_GL0198868 [gene] locus=scaffold175149_1:15138:16295:- [Complete] codon-table.11",</p> <p>"rumen554_GL1874810_1 [gene] locus=scaffold55901_2:3151:4308:-[Complete]",</p> <p>"rumen100058_GL1181547_1 [gene] locus=scaffold2365842_1:241:1398:+[Complete]",</p> <p>"rumen2009040_GL2571842_1 [gene] locus=scaffold1302178_1:1404:2561:-[Complete]"</p>
<p>["cazy SNX52632.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Thermoanaerobacterium sp. RBlITD]",</p> <p>"humangutMH0055_GL0070815 [gene] locus=scaffold34778_2:597:1778:+ [Complete] codon-table.11",</p> <p>"humangutMH0135_GL0080937 [gene] locus=scaffold1874_12:3739:4920:- [Complete] codon-table.11",</p> <p>"humangutMH0355_GL0026985 [gene] locus=scaffold59455_8:2250:3431:- [Complete] codon-table.11",</p> <p>"humangutO2_UC0_2_GL0081821 [gene] locus=scaffold37505_8:4778:5959:- [Complete] codon-table.11",</p> <p>"mouseMC-0-1_GL0086094 [gene] locus=scaffold75211_2:844:2025:- [Complete] codon-table.11",</p> <p>"mouseG1-1A_GL0008996 [gene] locus=scaffold3859_1:47826:49007:+ [Complete] codon-table.11",</p> <p>"mouse2-1_GL0026532 [gene] locus=scaffold83145_2:20129:21310:- [Complete] codon-table.11",</p> <p>"mouse2-1_GL0100763 [gene] locus=scaffold27245_8:482:1663:- [Complete] codon-table.11",</p> <p>"mouse2-3_GL0035308 [gene] locus=scaffold59252_3:16735:17916:- [Complete] codon-table.11",</p> <p>"mouse6-2_GL0021670 [gene] locus=scaffold52589_2:19565:20746:+ [Complete] codon-table.11",</p> <p>"mouse6-2_GL0056584 [gene] locus=scaffold27523_9:6716:7897:- [Complete] codon-table.11",</p> <p>"pigPIG-017_GL0066822 [gene] locus=scaffold165618_4:1007:2188:- [Complete] codon-table.11",</p> <p>"pigBHZ-11B_GL0063886 [gene] locus=scaffold18158_9:10158:11339:+ [Complete] codon-table.11",</p> <p>"rumen583_GL0572359_1 [gene] locus=scaffold335058_1:125034:126215:-[Complete]"</p>
<p>["humangut158458797-stool1_revised_C1254954_1_gene7695 strand:- start:155 stop:670 length:516 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut158458797-stool1_revised_C1330728_1_gene57635 strand:+ start:1451 stop:1921 length:471 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut158479027-stool1_revised_scaffold21677_1_gene16249 strand:- start:2 stop:565 length:564 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut158499257-stool2_revised_scaffold66254_1_gene37390 strand:- start:10217 stop:11395 length:1179 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut158499257-stool2_revised_scaffold72472_1_gene148447 strand:- start:4189 stop:5364 length:1176 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"rumen552_GL0548529_1 [gene] locus=scaffold662837_1:4322:5497:-[Complete]",</p> <p>"rumen555_GL0790964_1 [gene] locus=scaffold697095_7:1021:2196:+[Complete]",</p> <p>"rumen3042_GL0057553_1 [gene] locus=scaffold191918_7:888:2063:+[Complete]",</p> <p>"rumen7049_GL1338943_1 [gene] locus=scaffold1107426_5:618:1793:-[Complete]"</p>
<p>["humangut158802708-stool2_revised_scaffold19713_1_gene128431 strand:- start:813 stop:1223 length:411 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut158924089-stool1_revised_C357054_1_gene12204 strand:+ start:2 stop:1237 length:1236 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>

<p>["humangut159146620-stool1_revised_scaffold6399_1_gene5753 strand:- start:14096 stop:15346 length:1251 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut159207311-stool1_revised_scaffold15028_2_gene60096 strand:+ start:98 stop:778 length:681 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut159268001-stool1_revised_scaffold48948_1_gene45850 strand:- start:2 stop:520 length:519 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut159551223-stool1_revised_scaffold14178_1_gene131122 strand:- start:1 stop:546 length:546 start_codon:no stop_codon:no gene_type:incomplete [Lack both ends] codon-table.11", "rumen2009040_GL2806757_1 [gene] locus=scaffold15187_1:3:548:-[Lack both ends]"]</p>
<p>["humangut159551223-stool1_revised_scaffold22239_2_gene117759 strand:- start:2259 stop:2957 length:699 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut159551223-stool1_revised_scaffold22239_3_gene31179 strand:- start:3 stop:440 length:438 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut159551223-stool2_revised_C929707_1_gene3027 strand:+ start:1 stop:1302 length:1302 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut159571453-stool1_revised_C710594_1_gene87154 strand:- start:502 stop:1464 length:963 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "rumen0081_GL1646563_1 [gene] locus=scaffold888945_3:1:963:+[Lack 5'-end]", "cazygij643431560[gb]AIA99572.1  hypothetical protein [uncultured bacterium contig00010(2014)]"]</p>
<p>["humangut159814214-stool1_revised_scaffold14993_1_gene26555 strand:- start:2 stop:607 length:606 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11", "pigPIG_200_GL0162359 [gene] locus=scaffold89599_5:700:1305:+ [Lack 3'-end] codon-table.11"]</p>
<p>["humangut160603188-stool1_revised_C988630_1_gene107263 strand:- start:371 stop:1675 length:1305 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut686765762-stool1_revised_C472423_1_gene33724 strand:- start:1125 stop:2351 length:1227 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "rumen100058_GL1835902_1 [gene] locus=scaffold1661826_3:460:1686:+[Complete]"]</p>
<p>["humangut763496533-stool1_revised_C1161525_1_gene112770 strand:- start:2 stop:571 length:570 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut764062976-stool1_revised_C1264223_1_gene131035 strand:- start:1289 stop:1936 length:648 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "rumen3042_GL2264029_1 [gene] locus=scaffold1371059_2:208:855:-[Lack 5'-end]"]</p>
<p>["humangut764062976-stool1_revised_scaffold40568_3_gene149282 strand:+ start:6388 stop:7590 length:1203 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangutBGI001A_GL0024419 [gene] locus=scaffold7193_1:19067:20320:+ [Complete] codon-table.11", "rumen100058_GL3674533_1 [gene] locus=scaffold175438_2:1583:2836:-[Complete]"]</p>
<p>["humangutBGI089A_GL0084439 [gene] locus=scaffold47176_1:1:1221:+ [Lack 5'-end] codon-table.11", "rumen2009040_GL3443456_1 [gene] locus=scaffold2815356_1:1132:2352:+[Complete]"]</p>
<p>["humangutDLM018_GL0065366 [gene] locus=scaffold46582_5:3818:5011:- [Complete] codon-table.11", "pigBHZ-1B_GL0056960 [gene] locus=scaffold26544_1:7502:8695:- [Complete] codon-table.11", "pigBHZ-3B_GL0044984 [gene] locus=scaffold143974_1:8394:9587:- [Complete] codon-table.11", "rumen552_GL0302831_1 [gene] locus=scaffold397072_1:3349:4542:-[Complete]", "rumen552_GL0528208_1 [gene] locus=scaffold25689_2:33268:34461:-[Complete]",</p>



"rumen552_GL0891159_1 [gene] locus=scaffold306185_1:4343:5536:-[Complete]",
"rumen0081_GL1703369_1 [gene] locus=scaffold685453_4:388:1581:-[Complete]",
"rumen7049_GL0291338_1 [gene] locus=scaffold498578_2:3211:4404:+[Complete]"
["humangutDLM020_GL0047564 [gene] locus=scaffold4283_1:3:578:+ [Lack both ends] codon-table.11"]
["humangutDLM028_GL0015950 [gene] locus=scaffold44194_1:1:960:- [Lack both ends] codon-table.11"]
["humangutDOF008_GL0012963 [gene] locus=scaffold5558_23:452:868:+ [Lack 3'-end] codon-table.11"]
["humangutMH0001_GL0008963 [gene] locus=scaffold4941_9:21884:23056:+ [Complete] codon-table.11",
"humangutMH0006_GL0069639 [gene] locus=scaffold5771_4:1736:2908:+ [Complete] codon-table.11",
"humangutMH00212_GL0057095 [gene] locus=scaffold1862_26:4509:5681:+ [Complete] codon-table.11",
"humangutMH00229_GL0190805 [gene] locus=scaffold90208_2:4449:5621:+ [Complete] codon-table.11",
"humangutMH00260_GL0043424 [gene] locus=scaffold844_1:1138:2310:- [Complete] codon-table.11",
"humangutMH00373_GL0061364 [gene] locus=scaffold40690_3:1866:3038:+ [Complete] codon-table.11",
"humangutMH00433_GL0095455 [gene] locus=scaffold100358_3:241:1413:- [Complete] codon-table.11",
"humangutDLM028_GL0033958 [gene] locus=scaffold17607_13:1499:2671:- [Complete] codon-table.11",
"humangutDOM010_GL0020281 [gene] locus=scaffold6476_2:26932:28104:+ [Complete] codon-table.11",
"humangutT2D-45A_GL0047609 [gene] locus=scaffold76749_1:69782:70954:- [Complete] codon-table.11",
"mouseMC-6-1_GL0102367 [gene] locus=scaffold72393_2:1662:2834:+ [Complete] codon-table.11",
"mouseMC-6-2_GL0183039 [gene] locus=scaffold132992_1:105615:106787:+ [Complete] codon-table.11",
"mouseGroup2-2A_GL0001768 [gene] locus=scaffold194_1:16577:17749:+ [Complete] codon-table.11",
"mouseGroup2-3A_GL0155035 [gene] locus=scaffold97533_5:214:1386:+ [Complete] codon-table.11",
"mouse11_GL0042095 [gene] locus=scaffold90279_1:1019:2191:- [Complete] codon-table.11",
"mouse1-2_GL0036788 [gene] locus=scaffold29291_6:321:1493:- [Complete] codon-table.11",
"mouse4-1_GL0031568 [gene] locus=scaffold29527_1:21738:22910:+ [Complete] codon-table.11",
"mouse5-4_GL0028708 [gene] locus=scaffold51359_4:669:1841:- [Complete] codon-table.11",
"mouse6-1_GL0086335 [gene] locus=scaffold3735_1:18410:19582:+ [Complete] codon-table.11",
"pigPIG_196_GL0046463 [gene] locus=scaffold230571_1:94:1266:- [Complete] codon-table.11",
"pigPIG-001_GL0131188 [gene] locus=scaffold52084_1:15174:16346:+ [Complete] codon-table.11",
"pigPIG-007_GL0092032 [gene] locus=scaffold32192_4:106:1278:- [Complete] codon-table.11",
"pigPIG-024_GL0032316 [gene] locus=scaffold117195_4:2442:3614:+ [Complete] codon-table.11",
"pigPIG-025_GL0049563 [gene] locus=scaffold116655_1:134:1306:- [Complete] codon-table.11",
"pigPIG-026_GL0131158 [gene] locus=scaffold100689_1:3431:4603:+ [Complete] codon-table.11",
"pigPIG-039_GL0006796 [gene] locus=scaffold172054_1:4599:5771:+ [Complete] codon-table.11",
"pigPIG-084_GL0130316 [gene] locus=scaffold34714_3:1151:2323:- [Complete] codon-table.11",
"rumen553_GL0374550_1 [gene] locus=scaffold192374_1:70313:71485:+[Complete]",
"rumen583_GL0562823_1 [gene] locus=C5693781_1:12094:13266:+[Complete]",
"rumen554_GL0164185_1 [gene] locus=scaffold1890409_3:83:1255:+[Complete]",
"rumen554_GL0687568_1 [gene] locus=scaffold1598446_2:998:2170:+[Complete]",
"rumen554_GL1338144_1 [gene] locus=scaffold1192500_2:2501:3673:+[Complete]",
"rumen554_GL2685461_1 [gene] locus=scaffold1675218_5:171:1343:-[Complete]",
"rumen554_GL2922997_1 [gene] locus=scaffold665943_2:26:1198:-[Complete]",
"rumen555_GL2345541_1 [gene] locus=scaffold21142_2:8470:9642:+[Complete]",
"rumen100058_GL1062365_1 [gene] locus=scaffold1497823_4:6689:7861:+[Complete]",
"rumen100058_GL2538220_1 [gene] locus=scaffold171829_1:1536:2708:+[Complete]",
"rumen100058_GL3324879_1 [gene] locus=scaffold1542797_3:2066:3238:+[Complete]",

"rumen2009040\_GL3211682\_1 [gene] locus=scaffold2032426\_3:119:1291:-[Complete]",

"rumen2009040\_GL3280346\_1 [gene] locus=scaffold2478833\_1:626:1798:-[Complete]",

"rumen3042\_GL0860282\_1 [gene] locus=scaffold804980\_2:390:1562:+[Complete]",

"rumen7049\_GL1043269\_1 [gene] locus=scaffold1199013\_1:1301:2473:+[Complete]"

---

["humangutMH0001\_GL0012727 [gene] locus=scaffold3748\_3:1867:3042:- [Complete] codon-table.11",

"humangutMH0002\_GL0036601 [gene] locus=scaffold13906\_2:27627:28802:+ [Complete] codon-table.11",

"humangutMH0040\_GL0059391 [gene] locus=scaffold2869\_1\_1:6999:8174:+ [Complete] codon-table.11",

"humangutMH0100\_GL0160313 [gene] locus=scaffold5389\_46:1109:2284:- [Complete] codon-table.11",

"humangutMH0143\_GL0122660 [gene] locus=scaffold48916\_1:1397:2572:+ [Complete] codon-table.11",

"humangutMH0144\_GL0121801 [gene] locus=scaffold30658\_10:1282:2457:- [Complete] codon-table.11",

"humangutMH0149\_GL0065608 [gene] locus=scaffold3870\_10:13891:15066:+ [Complete] codon-table.11",

"humangutMH0161\_GL0177592 [gene] locus=scaffold71483\_1:9329:10504:+ [Complete] codon-table.11",

"humangutO2.UC22-1\_GL0078164 [gene] locus=scaffold10239\_8:5660:6835:- [Complete] codon-table.11",

"humangutV1.F137\_GL0083288 [gene] locus=scaffold84494\_6:225:1400:- [Complete] codon-table.11",

"humangutT2D-11A\_GL0038541 [gene] locus=scaffold59242\_6:11013:12188:- [Complete] codon-table.11",

"mouseS-Fe20\_GL0180051 [gene] locus=scaffold102347\_1:23471:24646:- [Complete] codon-table.11",

"mouseS-Fe3\_GL0155724 [gene] locus=scaffold20\_2:32522:33697:+ [Complete] codon-table.11",

"mouseMC-0-1\_GL0064821 [gene] locus=scaffold53168\_13:5126:6301:- [Complete] codon-table.11",

"mouseG1-5A\_GL0044807 [gene] locus=scaffold25393\_2:378:1553:- [Complete] codon-table.11",

"mouseG1-5A\_GL0112860 [gene] locus=scaffold77446\_3:51404:52579:- [Complete] codon-table.11",

"mouseG1-6A\_GL0023709 [gene] locus=scaffold9642\_11:418:1593:+ [Complete] codon-table.11",

"mouseGroup2-3A\_GL0194457 [gene] locus=scaffold125876\_2:53386:54561:- [Complete] codon-table.11",

"mouse20\_GL0026048 [gene] locus=scaffold37937\_1:1428:2603:- [Complete] codon-table.11",

"mouse2-2\_GL0076415 [gene] locus=scaffold14974\_4:37481:38656:+ [Complete] codon-table.11",

"mouse23\_GL0060739 [gene] locus=scaffold35607\_2:2034:3209:+ [Complete] codon-table.11",

"mouse7-3\_GL0008012 [gene] locus=scaffold1210\_7:218:1393:+ [Complete] codon-table.11",

"mouse7-8\_GL0102343 [gene] locus=scaffold68021\_1:1414:2589:+ [Complete] codon-table.11",

"mouse8-7\_GL0056549 [gene] locus=scaffold18483\_2:6803:7978:+ [Complete] codon-table.11",

"pigPIG\_144\_GL0102692 [gene] locus=scaffold2700\_5:27313:28488:- [Complete] codon-table.11",

"pigPIG\_151\_GL0035862 [gene] locus=scaffold15482\_1:6405:7580:- [Complete] codon-table.11",

"pigPIG\_154\_GL0044207 [gene] locus=scaffold38224\_2:916:2091:+ [Complete] codon-table.11",

"pigPIG\_207\_GL0027936 [gene] locus=scaffold253081\_1:22:1197:- [Complete] codon-table.11",

"pigPIG-001\_GL0136662 [gene] locus=scaffold53466\_8:1479:2654:- [Complete] codon-table.11",

"pigPIG-006\_GL0203904 [gene] locus=scaffold60412\_6:186:1361:- [Complete] codon-table.11",

"pigPIG-009\_GL0057076 [gene] locus=scaffold18352\_6:2384:3559:+ [Complete] codon-table.11",

"pigPIG-017\_GL0131673 [gene] locus=scaffold766\_5:1342:2517:+ [Complete] codon-table.11",

"pigPIG-023\_GL0120564 [gene] locus=scaffold148282\_1:75220:76395:+ [Complete] codon-table.11",

"pigPIG-033\_GL0192316 [gene] locus=C1724773\_1:999:2174:- [Complete] codon-table.11",

"pigPIG-039\_GL0000920 [gene] locus=scaffold91017\_9:9441:10616:+ [Complete] codon-table.11",

"pigPIG-106\_GL0046632 [gene] locus=scaffold17851\_9:7690:8865:- [Complete] codon-table.11",

"pigBHZ-11B\_GL00090195 [gene] locus=scaffold167910\_1:494:1669:- [Complete] codon-table.11",

"pigBHZ-2B\_GL0040230 [gene] locus=scaffold82168\_1:1:1176:- [Complete] codon-table.11",

"pigDB-530B\_GL0118605 [gene] locus=scaffold107655\_1:1937:3112:- [Complete] codon-table.11",

"rumen553\_GL0392614\_1 [gene] locus=scaffold37534\_3:1887:3062:-[Complete]",

<p>"rumen552_GL0987053_1 [gene] locus=scaffold1115340_1:4619:5794:-[Complete]",</p> <p>"rumen552_GL1341760_1 [gene] locus=scaffold137436_3:1187:2362:-[Complete]",</p> <p>"rumen583_GL0063681_1 [gene] locus=scaffold268085_3:55354:56529:+[Complete]",</p> <p>"rumen583_GL0159581_1 [gene] locus=scaffold172591_7:11717:12892:-[Complete]",</p> <p>"rumen583_GL0385136_1 [gene] locus=scaffold19862_2:1102:2277:-[Complete]",</p> <p>"rumen554_GL0264589_1 [gene] locus=scaffold21340_1:484:1659:+[Complete]",</p> <p>"rumen554_GL1088525_1 [gene] locus=scaffold977727_2:313:1488:+[Complete]",</p> <p>"rumen554_GL1230399_1 [gene] locus=C41612791_1:698:1873:-[Complete]",</p> <p>"rumen555_GL0512706_1 [gene] locus=scaffold81084_1:5267:6442:+[Complete]",</p> <p>"rumen555_GL1874408_1 [gene] locus=scaffold1378456_3:5285:6460:+[Complete]",</p> <p>"rumen0081_GL0989629_1 [gene] locus=C39771777_1:732:1907:-[Complete]",</p> <p>"rumen0081_GL2065341_1 [gene] locus=scaffold903959_2:1799:2974:+[Complete]",</p> <p>"rumen100058_GL1056176_1 [gene] locus=scaffold2252074_1:200:1372:-[Lack 3'-end]",</p> <p>"rumen100058_GL2978106_1 [gene] locus=C60508655_1:182:1357:+[Complete]",</p> <p>"rumen100058_GL3245501_1 [gene] locus=scaffold608862_5:3509:4684:+[Complete]",</p> <p>"cazygi 291530538 emb CBK96123.1  Predicted glycosylase [[Eubacterium] siraeum 70/3]",</p> <p>"cazygi 291557872 emb CBL34989.1  Predicted glycosylase [[Eubacterium] siraeum V10Sc8a]",</p> <p>"cazygi 345502714 gb AEN97397.1  glycosidase related protein [Roseburia hominis A2-183]",</p> <p>"cazygi 571258177 emb CCO04533.1  Glycoside Hydrolase Family 130 protein [Ruminococcus bicirculans]"</p>
<p>["humangutMH0002_GL0067890 [gene] locus=scaffold1153_5:38816:39982:- [Complete] codon-table.11",</p> <p>"humangutMH0047_GL0038238 [gene] locus=scaffold32713_3:84:1250:- [Complete] codon-table.11",</p> <p>"humangutMH0054_GL0074871 [gene] locus=scaffold5732_2:908:2074:- [Complete] codon-table.11",</p> <p>"humangutMH0169_GL0036039 [gene] locus=scaffold22380_12:19531:20697:- [Complete] codon-table.11",</p> <p>"humangutMH0310_GL0051694 [gene] locus=scaffold51993_1:48097:49263:- [Complete] codon-table.11",</p> <p>"humangutMH0383_GL0114832 [gene] locus=scaffold80173_1:29524:30690:+ [Complete] codon-table.11",</p> <p>"humangutMH0415_GL0044234 [gene] locus=scaffold135679_1:13191:14357:- [Complete] codon-table.11",</p> <p>"humangutT2D-22A_GL0100754 [gene] locus=scaffold67755_2:58456:59622:+ [Complete] codon-table.11",</p> <p>"mouseS-Fe10_GL0057060 [gene] locus=scaffold40113_2:33961:35127:+ [Complete] codon-table.11",</p> <p>"mouseS-Fe10_GL0110865 [gene] locus=scaffold56450_1:34120:35286:- [Complete] codon-table.11",</p> <p>"mouseMC-0-1_GL0077339 [gene] locus=scaffold66101_1:40905:42071:- [Complete] codon-table.11",</p> <p>"pigPIG-002_GL0141929 [gene] locus=scaffold120314_2:2882:4048:- [Complete] codon-table.11",</p> <p>"pigPIG-048_GL0142122 [gene] locus=scaffold43767_1:27875:29041:+ [Complete] codon-table.11",</p> <p>"rumen554_GL0757272_1 [gene] locus=scaffold7618_1:2460:3626:-[Complete]",</p> <p>"rumen554_GL1755958_1 [gene] locus=scaffold446293_2:1797:2963:+[Complete]",</p> <p>"rumen554_GL2967180_1 [gene] locus=scaffold102921_8:23227:24393:+[Complete]",</p> <p>"rumen555_GL0083736_1 [gene] locus=scaffold994071_3:91595:92761:-[Complete]",</p> <p>"rumen555_GL1538021_1 [gene] locus=scaffold809012_3:558:1724:+[Complete]",</p> <p>"rumen100058_GL2073289_1 [gene] locus=scaffold1330887_6:177:1343:-[Complete]",</p> <p>"rumen2009040_GL2061377_1 [gene] locus=scaffold1112673_1:4064:5230:-[Complete]",</p> <p>"rumen7049_GL2253545_1 [gene] locus=scaffold386514_3:805:1971:+[Complete]",</p> <p>"rumen7049_GL2779726_1 [gene] locus=scaffold1300485_1:2980:4146:-[Complete]",</p> <p>"cazygi 324318387 gb ADY36278.1  glycosidase related protein [Bacteroides salanitronis DSM 18170]"</p>
<p>["humangutMH0003_GL0003142 [gene] locus=scaffold31787_1:6057:7253:- [Complete] codon-table.11",</p> <p>"humangutMH0267_GL0221938 [gene] locus=scaffold88613_1:5752:6948:- [Complete] codon-table.11",</p>

<p>"humangutT2D-2A_GL0041562 [gene] locus=scaffold11956_2:300:1496:- [Lack 5'-end] codon-table.11",</p> <p>"mouse10_GL0084381 [gene] locus=scaffold21177_35:3024:4220:- [Complete] codon-table.11",</p> <p>"pigPIG-093_GL0016195 [gene] locus=scaffold73456_3:3:1199:+ [Lack 5'-end] codon-table.11",</p> <p>"pigBHZ-12B_GL0015966 [gene] locus=scaffold143672_2:8550:9746:- [Complete] codon-table.11",</p> <p>"rumen554_GL2814085_1 [gene] locus=scaffold2177694_1:103:1299:-[Complete]",</p> <p>"rumen554_GL3044073_1 [gene] locus=scaffold255068_1:5358:6554:-[Complete]",</p> <p>"rumen2009040_GL1607558_1 [gene] locus=scaffold14374_1:4043:5239:+[Complete]",</p> <p>"rumen3042_GL1567335_1 [gene] locus=scaffold609419_1:43:1239:-[Complete]",</p> <p>"cazygi 312443599 gb ADQ79955.1  glycosidase related protein [Paludibacter propionigenes WB4]"</p>
<p>["humangutMH0003_GL0040210 [gene] locus=scaffold9278_1:4837:6006:- [Complete] codon-table.11",</p> <p>"humangut763982056-stool1_revised_scaffold33383_4_gene91709 strand:- start:1361 stop:2530 length:1170 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangutMH0004_GL0014392 [gene] locus=scaffold3576_11:10154:11344:+ [Complete] codon-table.11",</p> <p>"humangutMH0016_GL0077493 [gene] locus=scaffold781_6:19537:20727:+ [Complete] codon-table.11",</p> <p>"humangutMH0142_GL0050877 [gene] locus=scaffold12269_6:1097:2287:- [Complete] codon-table.11",</p> <p>"humangutMH0146_GL0040498 [gene] locus=scaffold48645_1:19556:20746:+ [Complete] codon-table.11",</p> <p>"humangutMH0227_GL0085100 [gene] locus=scaffold57871_1:13279:14469:+ [Complete] codon-table.11",</p> <p>"humangutV1_CD37-4_GL0129659 [gene] locus=scaffold1237_4:318:1508:- [Lack 5'-end] codon-table.11",</p> <p>"humangutV1_CD38-0_GL0149408 [gene] locus=scaffold47721_2:21092:22282:+ [Complete] codon-table.11",</p> <p>"humangutNOF013_GL0005847 [gene] locus=scaffold11455_12:3385:4575:- [Complete] codon-table.11",</p> <p>"humangutT2D-113A_GL0017412 [gene] locus=scaffold39693_1:5489:6679:- [Complete] codon-table.11",</p> <p>"humangutT2D-135A_GL0097479 [gene] locus=scaffold4791_2:28290:29480:- [Complete] codon-table.11",</p> <p>"mouse1A-dyr2-07_GL0081296 [gene] locus=scaffold10432_2:34127:35317:+ [Complete] codon-table.11",</p> <p>"pigPIG_191_GL0129383 [gene] locus=scaffold66717_4:2548:3738:- [Lack 5'-end] codon-table.11",</p> <p>"pigPIG-004_GL0201947 [gene] locus=scaffold95810_1:2:11192:+ [Lack 5'-end] codon-table.11",</p> <p>"pigPIG-035_GL0179949 [gene] locus=scaffold49369_6:95:1285:- [Complete] codon-table.11",</p> <p>"pigBHZ-1B_GL0166577 [gene] locus=scaffold2900_1:8760:9950:- [Complete] codon-table.11",</p> <p>"rumen552_GL0765203_1 [gene] locus=scaffold188212_2:1693:2883:-[Complete]",</p> <p>"rumen555_GL0186127_1 [gene] locus=scaffold222754_1:21411:22601:+[Complete]",</p> <p>"rumen2009040_GL2207291_1 [gene] locus=scaffold383982_2:4701:5891:+[Complete]",</p> <p>"rumen2009040_GL2351849_1 [gene] locus=scaffold996819_1:14891:16081:+[Complete]"</p>
<p>["humangutMH0005_GL0003560 [gene] locus=scaffold18617_2:1:447:- [Lack 3'-end] codon-table.11"]</p>
<p>["humangutMH0008_GL0035219 [gene] locus=scaffold75_32:22073:23266:- [Complete] codon-table.11"]</p>
<p>"humangutMH0010_GL0028301 [gene] locus=scaffold17706_5:1453:2646:+ [Complete] codon-table.11",</p> <p>"humangutMH0088_GL0008413 [gene] locus=scaffold60292_2:6203:7396:- [Complete] codon-table.11",</p> <p>"humangutSZEY-39A_GL0012771 [gene] locus=scaffold23635_5:7654:8847:- [Complete] codon-table.11"]</p>
<p>["humangutMH0046_GL0006703 [gene] locus=scaffold16924_6:476:1084:+ [Lack 3'-end] codon-table.11"]</p>
<p>["humangutMH0053_GL0020379 [gene] locus=scaffold22014_2:2:439:+ [Lack 5'-end] codon-table.11",</p> <p>"rumen2009040_GL1996083_1 [gene] locus=scaffold809218_1:1:438:+[Lack 5'-end]",</p> <p>"rumen3042_GL2590115_1 [gene] locus=scaffold526261_1:433:870:-[Lack 5'-end]"</p>
<p>["humangutMH0053_GL0075282 [gene] locus=scaffold7906_13:9376:10569:+ [Complete] codon-table.11",</p> <p>"humangutMH0092_GL0158226 [gene] locus=scaffold39295_1:5340:6533:+ [Complete] codon-table.11",</p> <p>"mouse4-8_GL0099499 [gene] locus=scaffold61328_1:15238:16431:+ [Complete] codon-table.11",</p> <p>"pigPIG_119_GL0332247 [gene] locus=scaffold43880_29:768:1961:+ [Complete] codon-table.11",</p>

<p>"rumen553_GL0201985_1 [gene] locus=scaffold154648_1:14165:15358:-[Complete]",</p> <p>"rumen583_GL0464837_1 [gene] locus=scaffold107109_1:10:1203:-[Complete]",</p> <p>"rumen100058_GL1464037_1 [gene] locus=scaffold1214349_3:4269:5462:-[Complete]"</p>
<p>["humangutMH0055_GL0014394 [gene] locus=scaffold12333_5:3:419:+ [Lack 5'-end] codon-table.11",</p> <p>"pigPIG-043_GL0101446 [gene] locus=scaffold118544_2:245:661:- [Lack 5'-end] codon-table.11",</p> <p>"rumen7049_GL2623473_1 [gene] locus=scaffold1856051_1:111:527:-[Lack 5'-end]"</p>
<p>["humangutMH0060_GL0011435 [gene] locus=scaffold3787_2:1830:2537:- [Lack 5'-end] codon-table.11"]</p>
<p>["humangutMH0061_GL0035824 [gene] locus=scaffold26187_2:1262:2449:- [Complete] codon-table.11",</p> <p>"humangutMH0271_GL0008146 [gene] locus=scaffold22858_4:3394:4581:- [Complete] codon-table.11",</p> <p>"humangutV1_UC59-0_GL0075312 [gene] locus=scaffold50001_1:8606:9793:+ [Complete] codon-table.11",</p> <p>"humangutDLM013_GL0042248 [gene] locus=scaffold16696_3:2044:3231:- [Complete] codon-table.11",</p> <p>"humangutNOM023_GL0025373 [gene] locus=scaffold8794_4:144:1331:+ [Complete] codon-table.11",</p> <p>"humangut158924089-stool1_revised_scaffold11990_1_gene53457 strand:+ start:9800 stop:10987 length:1188 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"humangut160704339-stool1_revised_scaffold20757_2_gene65170 strand:+ start:88554 stop:89741 length:1188 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"humangut160765029-stool1_revised_scaffold21595_1_gene42009 strand:- start:35141 stop:36328 length:1188 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"humangut457390.HMPREF9010_00339 [Complete]:- codon-table.11",</p> <p>"rumen552_GL1643634_1 [gene] locus=scaffold437481_1:1382:2569:-[Complete]"</p>
<p>["humangutMH0071_GL0050647 [gene] locus=scaffold13703_7:12209:13426:+ [Complete] codon-table.11",</p> <p>"humangutO2_UC50-0_GL0126452 [gene] locus=scaffold87365_4:6651:7868:- [Complete] codon-table.11",</p> <p>"humangut765094712-stool1_revised_scaffold5918_1_gene43451 strand:+ start:3918 stop:5135 length:1218 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"humangut411476.BACOVA_02090 [Complete]:- codon-table.11"]</p>
<p>["humangutMH0077_GL0038788 [gene] locus=scaffold26758_11:620:1669:- [Lack 5'-end] codon-table.11"]</p>
<p>["humangutMH0077_GL0069156 [gene] locus=C1110387_1:1:759:+ [Lack both ends] codon-table.11"]</p>
<p>["humangutMH0086_GL0043702 [gene] locus=scaffold3420_19:149:1336:- [Complete] codon-table.11",</p> <p>"humangutMH0169_GL0014591 [gene] locus=scaffold90896_3:5721:6908:+ [Complete] codon-table.11",</p> <p>"mouseG1-5A_GL0181295 [gene] locus=scaffold134836_1:10977:12164:- [Complete] codon-table.11",</p> <p>"mouse2-3_GL0031397 [gene] locus=scaffold235_3:7064:8251:- [Complete] codon-table.11",</p> <p>"pigPIG_115_GL0135634 [gene] locus=scaffold144786_1:209:1396:- [Complete] codon-table.11",</p> <p>"rumen2009040_GL2733267_1 [gene] locus=scaffold679350_1:2268:3455:+[Complete]"</p>
<p>["humangutMH0106_GL0063906 [gene] locus=scaffold758_13:312:698:+ [Lack 3'-end] codon-table.11"]</p>
<p>["humangutMH0141_GL0045172 [gene] locus=scaffold90823_2:59452:60723:- [Complete] codon-table.11",</p> <p>"pigEYZ-362B_GL0213996 [gene] locus=scaffold64315_1:2838:4109:+ [Complete] codon-table.11"]</p>
<p>["humangutMH0150_GL0029065 [gene] locus=scaffold26200_7:3:1046:+ [Lack both ends] codon-table.11"]</p>
<p>["humangutMH0154_GL0052097 [gene] locus=scaffold72395_2:2:619:- [Lack 3'-end] codon-table.11",</p> <p>"rumen554_GL2215439_1 [gene] locus=scaffold640454_4:141:758:+[Lack 3'-end]"</p>
<p>["humangutMH0158_GL0020995 [gene] locus=scaffold73_5:547:1941:- [Complete] codon-table.11"]</p>
<p>["humangutMH0175_GL0008390 [gene] locus=scaffold5723_3:8628:9797:+ [Complete] codon-table.11",</p> <p>"humangutV1_CD15-3_GL0043751 [gene] locus=scaffold36254_15:2353:3522:- [Complete] codon-table.11",</p> <p>"humangutV1_UC14-1_GL0016015 [gene] locus=scaffold7083_11:304:1473:- [Complete] codon-table.11",</p> <p>"humangutV1_UC40-1_GL0189893 [gene] locus=scaffold26751_3:50075:51244:- [Complete] codon-table.11",</p>

"humangutT2D-57A_GL0089819 [gene] locus=scaffold37237_2:48502:49671:- [Complete] codon-table.11",
"mouseS-Fe10_GL0020481 [gene] locus=scaffold62188_1:15006:16175:- [Complete] codon-table.11",
"mouseMC-0-1_GL0000741 [gene] locus=scaffold182_2:1677:2846:+ [Complete] codon-table.11",
"mouseMC-0-1_GL0097520 [gene] locus=scaffold86236_8:883:2052:+ [Complete] codon-table.11",
"mouseMC-6-2_GL0172729 [gene] locus=scaffold131564_1:27302:28471:+ [Complete] codon-table.11",
"mouseMC-6-3_GL0073206 [gene] locus=scaffold51250_1:1502:2671:- [Complete] codon-table.11",
"mouseG1-1A_GL0086557 [gene] locus=scaffold69184_2:28379:29548:- [Complete] codon-table.11",
"mouse1A-dyr2-07_GL0077917 [gene] locus=scaffold30795_6:18113:19282:- [Complete] codon-table.11",
"mouse4-1_GL0047775 [gene] locus=scaffold62147_1:73815:74984:+ [Complete] codon-table.11",
"pigPIG-031_GL0058312 [gene] locus=scaffold110073_3:2:1171:+ [Lack 5'-end] codon-table.11",
"rumen553_GL0098295_1 [gene] locus=scaffold295983_2:2588:3757:+[Complete]",
"rumen553_GL0293893_1 [gene] locus=scaffold354547_1:12051:13220:+[Complete]",
"rumen553_GL0533049_1 [gene] locus=scaffold81146_1:24886:26055:-[Complete]",
"rumen553_GL0770667_1 [gene] locus=scaffold119161_1:16572:17741:-[Complete]",
"rumen553_GL0805459_1 [gene] locus=scaffold183561_1:1086:2255:+[Complete]",
"rumen552_GL0986920_1 [gene] locus=scaffold127796_2:7380:8549:-[Complete]",
"rumen552_GL1043400_1 [gene] locus=scaffold209443_2:5010:6179:-[Complete]",
"rumen552_GL1104510_1 [gene] locus=scaffold1115005_1:25884:27053:+[Complete]",
"rumen583_GL0766550_1 [gene] locus=scaffold280980_1:26443:27612:-[Complete]",
"rumen554_GL0710234_1 [gene] locus=scaffold320099_2:4450:5619:-[Complete]",
"rumen554_GL0903399_1 [gene] locus=scaffold360775_1:16715:17884:-[Complete]",
"rumen554_GL1512054_1 [gene] locus=scaffold144087_3:211:1380:+[Complete]",
"rumen554_GL2005306_1 [gene] locus=scaffold18673_1:97:1266:-[Complete]",
"rumen554_GL2346766_1 [gene] locus=scaffold84744_2:1230:2399:-[Complete]",
"rumen555_GL0739033_1 [gene] locus=scaffold168963_2:11384:12553:+[Complete]",
"rumen555_GL2164851_1 [gene] locus=scaffold1262900_1:12081:13250:+[Complete]",
"rumen0081_GL0834214_1 [gene] locus=scaffold1778304_1:216:1385:+[Complete]",
"rumen0081_GL0861054_1 [gene] locus=scaffold102262_2:2898:4067:+[Complete]",
"rumen0081_GL2320442_1 [gene] locus=scaffold697257_1:53555:54724:-[Complete]",
"rumen100058_GL0730810_1 [gene] locus=scaffold3230704_2:1372:2541:-[Complete]",
"rumen100058_GL1140795_1 [gene] locus=scaffold3123978_2:2:1171:+[Lack 5'-end]",
"rumen100058_GL1382710_1 [gene] locus=scaffold1446962_3:12479:13648:-[Complete]",
"rumen100058_GL1713671_1 [gene] locus=scaffold3260277_1:1017:2186:-[Complete]",
"rumen100058_GL1870643_1 [gene] locus=scaffold831521_2:3236:4405:-[Complete]",
"rumen100058_GL2879678_1 [gene] locus=scaffold2011468_1:77:1246:-[Complete]",
"rumen100058_GL2882754_1 [gene] locus=scaffold2160084_1:97:1266:+[Complete]",
"rumen100058_GL3753782_1 [gene] locus=scaffold519037_1:1585:2754:+[Complete]",
"rumen2009040_GL0755339_1 [gene] locus=scaffold134393_1:1164:2333:-[Complete]",
"rumen2009040_GL2002423_1 [gene] locus=scaffold638974_6:23852:25021:-[Complete]",
"rumen3042_GL2710176_1 [gene] locus=scaffold456468_4:1590:2759:-[Complete]"
["humangutMH0181_GL104159 [gene] locus=scaffold148_2:1:447:- [Lack 3'-end] codon-table.11"]
["humangutMH0181_GL0119730 [gene] locus=scaffold148_1:5514:6188:- [Lack 5'-end] codon-table.11",
"rumen7049_GL2326404_1 [gene] locus=scaffold399270_1:3779:4453:-[Lack 5'-end]"
["humangutMH0183_GL0124654 [gene] locus=scaffold57416_2:665:1348:- [Lack 5'-end] codon-table.11"]

["humangutMH0189_GL0061360 [gene] locus=scaffold5399_7:13426:14622:+ [Complete] codon-table.11"]
["humangutMH0193_GL0079553 [gene] locus=scaffold80193_1:6442:7626:- [Complete] codon-table.11", "humangutMH0346_GL0012872 [gene] locus=scaffold91286_1:73757:74941:+ [Complete] codon-table.11", "humangutO2.UC7-1_GL0002488 [gene] locus=scaffold7596_2:22867:24051:+ [Complete] codon-table.11", "humangutV1.CD42-0_GL0134459 [gene] locus=scaffold3497_9:378:1562:+ [Complete] codon-table.11", "mouseS-Fe8_GL0202730 [gene] locus=scaffold84136_4:26492:27676:+ [Complete] codon-table.11", "mouseMC-0-1_GL0081615 [gene] locus=scaffold70529_1:4761:5945:- [Complete] codon-table.11", "mouseGroup2-1A_GL0071200 [gene] locus=scaffold49224_2:144:1328:+ [Complete] codon-table.11", "mouse3-6_GL0024704 [gene] locus=scaffold28367_2:7518:8702:+ [Complete] codon-table.11", "pigDB-510B_GL0206545 [gene] locus=scaffold49419_2:2273:3457:+ [Complete] codon-table.11", "rumen554_GL0769618_1 [gene] locus=scaffold370046_1:386:1570:+[Complete]"]
["humangutMH0197_GL0075607 [gene] locus=scaffold39932_1:1229:2377:+ [Complete] codon-table.11"]
["humangutMH0197_GL0097441 [gene] locus=C1904641_1:217:744:- [Lack 5'-end] codon-table.11"]
["humangutMH0197_GL0103303 [gene] locus=scaffold89255_1:3:653:- [Lack 3'-end] codon-table.11"]
["humangutMH0198_GL0043816 [gene] locus=scaffold44551_1:347:1261:+ [Lack 3'-end] codon-table.11"]
["humangutMH0200_GL0168561 [gene] locus=scaffold19653_1:10723:12000:- [Complete] codon-table.11"]
["humangutMH0203_GL0230351 [gene] locus=scaffold10958_6:967:2178:+ [Complete] codon-table.11", "mouseGroup2-3A_GL0127943 [gene] locus=scaffold74719_1:14518:15729:- [Complete] codon-table.11", "mouse2-2_GL0057371 [gene] locus=scaffold117963_5:22906:24117:+ [Complete] codon-table.11"]
["humangutMH0206_GL0205749 [gene] locus=scaffold152889_1:3:554:- [Lack 3'-end] codon-table.11"]
["humangutMH0229_GL0174354 [gene] locus=scaffold129056_1:1153:2364:+ [Complete] codon-table.11"]
["humangutMH0233_GL0001986 [gene] locus=scaffold24485_3:3:836:+ [Lack 5'-end] codon-table.11", "humangutV1.UC37-0_GL0072500 [gene] locus=scaffold19643_12:2:835:+ [Lack 5'-end] codon-table.11", "rumen100058_GL3508998_1 [gene] locus=scaffold491945_2:2:835:+[Lack 5'-end]"]
["humangutMH0234_GL0092685 [gene] locus=scaffold17765_28:1:1197:+ [Lack 5'-end] codon-table.11"]
["humangutMH0239_GL0155111 [gene] locus=scaffold10725_5:3212:4375:+ [Complete] codon-table.11", "rumen553_GL0025787_1 [gene] locus=scaffold425815_1:7629:8792:+[Complete]", "rumen0081_GL2522705_1 [gene] locus=scaffold1391530_3:119:1279:+[Lack 3'-end]"]
["humangutMH0243_GL0036444 [gene] locus=scaffold76437_2:1:645:+ [Lack 5'-end] codon-table.11", "rumen3042_GL1083413_1 [gene] locus=scaffold85108_2:2:646:+[Lack 5'-end]"]
["humangutMH0243_GL0087501 [gene] locus=scaffold76437_1:22166:22651:+ [Lack 3'-end] codon-table.11"]
["humangutMH0245_GL0164712 [gene] locus=scaffold19950_17:1:459:- [Lack 3'-end] codon-table.11", "rumen100058_GL1426300_1 [gene] locus=scaffold412313_8:3:461:-[Lack 3'-end]"]
["humangutMH0247_GL0065460 [gene] locus=scaffold3604_3:9122:10354:+ [Complete] codon-table.11"]
["humangutMH0250_GL0282662 [gene] locus=scaffold85700_1:3:533:- [Lack 3'-end] codon-table.11"]
["humangutMH0251_GL0042591 [gene] locus=scaffold19287_3:1:1500:- [Lack 3'-end] codon-table.11"]
["humangutMH0260_GL0038292 [gene] locus=scaffold87671_1:158:916:+ [Lack 3'-end] codon-table.11"]
["humangutMH0260_GL0046878 [gene] locus=scaffold103034_1:2:511:- [Lack both ends] codon-table.11"]
["humangutMH0260_GL0095703 [gene] locus=scaffold39193_15:2497:3636:+ [Complete] codon-table.11"]
["humangutMH0266_GL0001165 [gene] locus=scaffold15158_8:163:639:- [Lack 5'-end] codon-table.11"]
["humangutMH0266_GL0022658 [gene] locus=scaffold29203_10:3373:4527:+ [Complete] codon-table.11"]
["humangutMH0266_GL0082076 [gene] locus=scaffold3083_15:2:625:- [Lack 3'-end] codon-table.11"]
["humangutMH0266_GL0106114 [gene] locus=scaffold29683_1:2:475:- [Lack 3'-end] codon-table.11",

"humangutMH0403_GL0154505 [gene] locus=scaffold81282_1:2:475:- [Lack 3'-end] codon-table.11"
"humangutMH0267_GL0078594 [gene] locus=scaffold25085_7:2:796:+ [Lack 5'-end] codon-table.11", "rumen3042_GL1054393_1 [gene] locus=scaffold17865_2:2:796:+[Lack 5'-end]"
"humangutMH0271_GL0060042 [gene] locus=scaffold25955_5:85:771:+ [Lack 3'-end] codon-table.11"
"humangutMH0276_GL0215010 [gene] locus=C1978076_1:1:561:- [Lack 3'-end] codon-table.11", "mouse20_GL0049333 [gene] locus=scaffold88136_5:2:562:- [Lack 3'-end] codon-table.11"
"humangutMH0287_GL0048636 [gene] locus=scaffold63999_1:44240:45394:+ [Complete] codon-table.11", "rumen7049_GL0174478_1 [gene] locus=scaffold26723_4:867:2021:-[Lack 5'-end]"
"humangutMH0302_GL0088302 [gene] locus=scaffold62124_1:9329:10327:+ [Complete] codon-table.11"
"humangutMH0309_GL0064688 [gene] locus=scaffold37913_3:2:628:+ [Lack 5'-end] codon-table.11"
"humangutMH0309_GL0096983 [gene] locus=scaffold37913_2:167:655:+ [Lack 3'-end] codon-table.11"
"humangutMH0315_GL0027374 [gene] locus=scaffold15353_1:1:567:- [Lack 3'-end] codon-table.11"
"humangutMH0318_GL0144813 [gene] locus=scaffold97586_2:3:809:- [Lack 3'-end] codon-table.11"
"humangutMH0319_GL0012399 [gene] locus=scaffold73619_4:648:1886:+ [Complete] codon-table.11", "pigPIG_202_GL0230914 [gene] locus=scaffold237116_1:17896:19134:+ [Complete] codon-table.11"
"humangutMH0355_GL0031281 [gene] locus=C2003740_1:3:599:- [Lack both ends] codon-table.11", "rumen554_GL0269222_1 [gene] locus=scaffold1445625_4:3:602:+[Lack 5'-end]", "rumen0081_GL2326714_1 [gene] locus=scaffold838015_1:1:600:+[Lack 5'-end]"
"humangutMH0355_GL0112804 [gene] locus=scaffold93624_5:1898:3064:+ [Complete] codon-table.11", "mouse7-1_GL0034863 [gene] locus=scaffold72_16:4814:5980:+ [Complete] codon-table.11"
"humangutMH0357_GL0093535 [gene] locus=scaffold6302_5:262:873:+ [Lack 3'-end] codon-table.11"
"humangutMH0358_GL0063993 [gene] locus=scaffold7965_1:2:478:- [Lack 3'-end] codon-table.11"
"humangutMH0362_GL0062124 [gene] locus=scaffold106578_1:5100:6281:- [Complete] codon-table.11"
"humangutMH0363_GL0120444 [gene] locus=scaffold17645_9:1:930:+ [Lack both ends] codon-table.11"
"humangutMH0364_GL0127490 [gene] locus=scaffold13251_4:1:813:- [Lack 3'-end] codon-table.11"
"humangutMH0374_GL0078912 [gene] locus=scaffold82649_3:5617:6297:+ [Lack 3'-end] codon-table.11"
"humangutMH0377_GL0151261 [gene] locus=scaffold73020_3:653:1129:+ [Lack 3'-end] codon-table.11", "pigZXZ-2B_GL0174477 [gene] locus=scaffold69697_1:367:843:+ [Lack 3'-end] codon-table.11"
"humangutMH0382_GL0012715 [gene] locus=scaffold7953_12:2:913:+ [Lack 5'-end] codon-table.11"
"humangutMH0394_GL0045810 [gene] locus=scaffold10293_15:2:499:+ [Lack 5'-end] codon-table.11", "rumen552_GL1380709_1 [gene] locus=scaffold503799_1:1:498:+[Lack 5'-end]"
"humangutMH0402_GL0056181 [gene] locus=scaffold70513_3:223:1209:- [Complete] codon-table.11"
"humangutMH0402_GL0221154 [gene] locus=scaffold10526_6:4980:6188:- [Complete] codon-table.11", "pigPIG-054_GL0165253 [gene] locus=scaffold157312_1:12154:13362:+ [Complete] codon-table.11", "pigPIG-055_GL0196683 [gene] locus=scaffold8432_2:22:1230:+ [Complete] codon-table.11"
"humangutMH0404_GL0163934 [gene] locus=scaffold3587_11:156:944:+ [Lack 3'-end] codon-table.11"
"humangutMH0411_GL0010782 [gene] locus=scaffold693_1:1884:2549:+ [Complete] codon-table.11"
"humangutMH0414_GL0042138 [gene] locus=scaffold13440_8:187:1533:+ [Complete] codon-table.11"
"humangutMH0416_GL0214784 [gene] locus=scaffold50630_5:4:954:- [Complete] codon-table.11"
"humangutMH0419_GL0051194 [gene] locus=scaffold93199_1:1:498:- [Lack 3'-end] codon-table.11", "pigPIG_138_GL0080226 [gene] locus=scaffold147754_1:191:688:+ [Lack 3'-end] codon-table.11"
"humangutMH0420_GL0064849 [gene] locus=scaffold5278_1:1369:4221:- [Complete] codon-table.11", "humangutO2.CD3-0-PT_GL0002951 [gene] locus=scaffold88260_1:12389:15241:+ [Complete] codon-table.11"



["humangutMH0425_GL0001000 [gene] locus=scaffold110_8:1223:2149:- [Complete] codon-table.11"]
["humangutMH0426_GL0161889 [gene] locus=scaffold10744_4:1047:2252:- [Complete] codon-table.11", "humangutO2_UC6-0_GL0015540 [gene] locus=scaffold10453_2:37136:38338:+ [Lack 3'-end] codon-table.11"]
["humangutMH0428_GL0023013 [gene] locus=scaffold35487_1:3:767:- [Lack 3'-end] codon-table.11"]
["humangutMH0431_GL0054417 [gene] locus=scaffold115150_1:51638:52126:+ [Lack 3'-end] codon-table.11", "humangutNOF010_GL0094281 [gene] locus=scaffold48727_12:11853:12341:+ [Lack 3'-end] codon-table.11"]
["humangutMH0437_GL0054519 [gene] locus=scaffold9441_16:2026:3099:+ [Lack 3'-end] codon-table.11"]
["humangutMH0439_GL0071704 [gene] locus=scaffold116113_1:806:1951:- [Complete] codon-table.11", "rumen583_GL0325328_1 [gene] locus=scaffold76910_2:8503:9648:-[Lack 5'-end]", "rumen2009040_GL0533400_1 [gene] locus=scaffold336820_1:238:1383:+[Complete]", "rumen2009040_GL2980251_1 [gene] locus=scaffold132598_2:1235:2380:-[Lack 5'-end]", "rumen7049_GL1338378_1 [gene] locus=scaffold1587737_2:15:1160:-[Complete]"]
["humangutMH0439_GL0188834 [gene] locus=scaffold4226_2:140:1216:- [Lack 5'-end] codon-table.11"]
["humangutMH0443_GL0182786 [gene] locus=scaffold52476_4:1:1809:- [Lack 3'-end] codon-table.11"]
["humangutMH0447_GL0161554 [gene] locus=scaffold2816_1:2439:3596:- [Complete] codon-table.11"]
["humangutMH0454_GL0202719 [gene] locus=scaffold33667_1:1:633:+ [Lack 5'-end] codon-table.11", "humangut764588959-stool1_revised_scaffold37375_1_gene66956 strand:+ start:2 stop:634 length:633 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangutMH0457_GL0023585 [gene] locus=scaffold51546_2:2:613:- [Lack both ends] codon-table.11"]
["humangutMH0457_GL0138585 [gene] locus=scaffold43943_7:316:798:+ [Lack 3'-end] codon-table.11", "mouse7_GL0070851 [gene] locus=scaffold4107_3:145:627:+ [Lack 3'-end] codon-table.11", "rumen7049_GL2519476_1 [gene] locus=scaffold2250314_2:1:483:-[Lack 3'-end]"]
["humangutN006A_GL0039158 [gene] locus=scaffold26845_5:1:702:+ [Lack 5'-end] codon-table.11"]
["humangutN006A_GL0056549 [gene] locus=scaffold61875_3:2:853:+ [Lack 5'-end] codon-table.11"]
["humangutN038A_GL0028817 [gene] locus=scaffold1158_2:682:1872:- [Complete] codon-table.11"]
["humangutN075A_GL0061161 [gene] locus=scaffold48837_1:25141:26328:- [Complete] codon-table.11", "humangut158337416-stool2_revised_C1037800_1_gene78616 strand:+ start:1721 stop:2908 length:1188 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "rumen100058_GL3253793_1 [gene] locus=scaffold841137_1:2702:3889:+[Complete]", "rumen2009040_GL2731047_1 [gene] locus=scaffold432748_1:205:1392:-[Complete]"]
["humangutN085A_GL0029153 [gene] locus=scaffold8604_2:2:586:+ [Lack both ends] codon-table.11", "rumen3042_GL1835188_1 [gene] locus=scaffold590073_1:2:586:+[Lack both ends]"]
["humangutNLM015_GL0015696 [gene] locus=scaffold22524_2:4109:4981:+ [Complete] codon-table.11", "mouse1A-dyr4-07_GL0070332 [gene] locus=scaffold24038_1:371:1243:- [Complete] codon-table.11"]
["humangutNLM022_GL0049460 [gene] locus=scaffold43914_1:1:711:- [Lack 3'-end] codon-table.11"]
["humangutNLM023_GL0044946 [gene] locus=scaffold21510_4:3:989:- [Lack 3'-end] codon-table.11"]
["humangutNLM031_GL0013903 [gene] locus=scaffold21775_7:2976:5030:+ [Lack 3'-end] codon-table.11"]
["humangutNOF006_GL0036819 [gene] locus=scaffold9781_6:479:892:- [Lack 5'-end] codon-table.11"]
["humangutNOM020_GL0049765 [gene] locus=scaffold31130_2:2:928:- [Lack 3'-end] codon-table.11"]
["humangutNOM023_GL0036783 [gene] locus=scaffold8794_7:1:801:+ [Lack both ends] codon-table.11"]
["humangutO2_UC12-2_GL0120407 [gene] locus=scaffold2961_5:2:580:+ [Lack 5'-end] codon-table.11", "pigSYZ-481B_GL0086675 [gene] locus=scaffold28811_2:3:581:+ [Lack 5'-end] codon-table.11"]
["humangutO2_UC22-1_GL0118828 [gene] locus=scaffold9468_1:2:787:- [Lack both ends] codon-table.11"]

["humangutO2.UC28-1_GL0023149 [gene] locus=scaffold112925_2:3:644:- [Lack 3'-end] codon-table.11"]
["humangutO2.UC28-1_GL0171115 [gene] locus=scaffold112925_1:209:709:- [Lack 5'-end] codon-table.11", "humangutT2D-51A_GL0130607 [gene] locus=scaffold36233_1:2:502:+ [Lack 5'-end] codon-table.11", "rumen583_GL0522900_1 [gene] locus=C5102750_1:48:548:-[Lack 5'-end]"]
["humangutO2.UC3-0_GL0141339 [gene] locus=scaffold74815_2:4974:5621:+ [Complete] codon-table.11"]
["humangutO2.UC40-1_GL0087978 [gene] locus=scaffold6773_3:1:1533:+ [Lack both ends] codon-table.11"]
["humangutO2.UC40-2_GL0126302 [gene] locus=scaffold82685_2:4602:6173:- [Complete] codon-table.11"]
["humangutO2.UC41-0_GL0074405 [gene] locus=scaffold59061_9:3:662:- [Lack 3'-end] codon-table.11"]
["humangutO2.UC43-0_GL0024596 [gene] locus=scaffold4362_14:3340:4506:+ [Complete] codon-table.11"]
["humangutO2.UC47-1_GL0106516 [gene] locus=scaffold31155_4:560:1333:+ [Lack 3'-end] codon-table.11"]
["humangutO2.UC48-1_GL0200602 [gene] locus=scaffold21500_3:1:657:- [Lack both ends] codon-table.11"]
["humangutO2.UC52-0_GL0007460 [gene] locus=scaffold34267_4:3:749:+ [Lack both ends] codon-table.11"]
["humangutO2.UC58-0_GL0099707 [gene] locus=scaffold28582_3:1:507:+ [Lack both ends] codon-table.11"]
["humangutO2.UC58-0_GL0144409 [gene] locus=scaffold28582_4:1:540:+ [Lack both ends] codon-table.11"]
["humangutO2.UC9-1_GL0104818 [gene] locus=scaffold69048_7:3:1283:+ [Lack 5'-end] codon-table.11"]
["humangutSZEY-40A_GL0052629 [gene] locus=scaffold986_10:2:799:+ [Lack 5'-end] codon-table.11", "pigPIG_189_GL0107784 [gene] locus=scaffold39191_1:3:800:+ [Lack 5'-end] codon-table.11"]
["humangutSZEY-66A_GL0034879 [gene] locus=scaffold34398_2:1:651:- [Lack both ends] codon-table.11"]
["humangutSZEY-69A_GL0075907 [gene] locus=scaffold5091_8:404:1294:- [Lack 5'-end] codon-table.11"]
["humangutSZEY-79A_GL0078725 [gene] locus=scaffold32900_2:2:742:- [Lack 3'-end] codon-table.11"]
["humangutT2D-49A_GL0008767 [gene] locus=scaffold50534_1:5529:6788:+ [Complete] codon-table.11"]
["humangutT2D-62A_GL0033315 [gene] locus=scaffold1006_10:662:1849:+ [Complete] codon-table.11", "mouseG1-1A_GL0067551 [gene] locus=scaffold50327_3:1192:2379:- [Complete] codon-table.11", "mouse20_GL0137765 [gene] locus=scaffold37707_1:9311:10498:- [Complete] codon-table.11", "mouse2-2_GL0113805 [gene] locus=scaffold7847_23:1534:2721:+ [Complete] codon-table.11", "mouse35_GL0008207 [gene] locus=scaffold1654_3:2226:3413:+ [Complete] codon-table.11", "mouse6-2_GL0012583 [gene] locus=scaffold27665_1:85621:86808:- [Complete] codon-table.11", "pigPIG_155_GL0209039 [gene] locus=scaffold258678_1:893:2080:- [Lack 5'-end] codon-table.11", "pigPIG_203_GL0040935 [gene] locus=scaffold36594_20:6579:7766:+ [Complete] codon-table.11", "rumen583_GL0089164_1 [gene] locus=scaffold62306_4:3479:4666:+[Complete]", "rumen554_GL1823487_1 [gene] locus=scaffold1579573_1:2949:4136:-[Complete]", "rumen2009040_GL1448770_1 [gene] locus=scaffold1685413_3:281:1468:-[Complete]"]
["humangutT2D-63A_GL0039325 [gene] locus=scaffold25495_1:3:527:+ [Lack both ends] codon-table.11"]
["humangutV1.CD15-3_GL0028475 [gene] locus=scaffold15479_33:3328:4536:+ [Complete] codon-table.11"]
["humangutV1.CD2-0-PT_GL0057437 [gene] locus=scaffold8057_11:3687:4205:- [Lack 5'-end] codon-table.11"]
["humangutV1.CD38-0_GL0186310 [gene] locus=scaffold47721_3:5732:6916:+ [Complete] codon-table.11"]
["humangutV1.CD40-0_GL0148977 [gene] locus=scaffold16169_1:575:1327:- [Lack 5'-end] codon-table.11", "rumen7049_GL1876747_1 [gene] locus=scaffold688033_1:280:1032:-[Lack 5'-end]"]
["humangutV1.CD40-0_GL0163227 [gene] locus=scaffold16169_2:2:385:- [Lack 3'-end] codon-table.11", "rumen7049_GL1900126_1 [gene] locus=scaffold286734_1:2:385:-[Lack 3'-end]"]
["humangutV1.CD48-0_GL0049853 [gene] locus=scaffold21729_1:2:757:- [Lack both ends] codon-table.11"]
["humangutV1.CD53-0_GL0063667 [gene] locus=scaffold17550_7:7770:8960:+ [Complete] codon-table.11", "mouse1A-dyr3-06_GL0048311 [gene] locus=scaffold4151_1:56118:57308:- [Complete] codon-table.11",

"cazygi 938475461 gb ALJ39693.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Bacteroides thetaiotaomicron]", "cazygi 29340341 gb AAO78134.1  putative glycosylase [Bacteroides thetaiotaomicron VPI-5482]"
["humangutV1.CD6-0-PT_GL0073017 [gene] locus=scaffold127996_2:9399:10625:+ [Complete] codon-table.11", "rumen552_GL0764241_1 [gene] locus=scaffold492656_2:1179:2405:+[Complete]"]
["humangutV1.FI03_GL0003294 [gene] locus=C977374_1:2:394:- [Lack 3'-end] codon-table.11"]
["humangutV1.FI14_GL0257660 [gene] locus=scaffold84882_5:1:1053:- [Lack 3'-end] codon-table.11"]
["humangutV1.FI16_GL0184215 [gene] locus=scaffold3794_11:2:616:+ [Lack 5'-end] codon-table.11", "pigPIG_204_GL0014757 [gene] locus=scaffold104647_12:1:615:+ [Lack 5'-end] codon-table.11"]
["humangutV1.FI27_GL0059160 [gene] locus=scaffold234_7:9683:10894:- [Lack 5'-end] codon-table.11"]
["humangutV1.FI27_GL0066186 [gene] locus=scaffold83213_2:2:1183:+ [Lack 5'-end] codon-table.11", "humangut763536994-stool2_revised_scaffold69911_4_gene146893 strand:+ start:3 stop:1184 length:1182 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "mouseS-Fe10_GL0165818 [gene] locus=scaffold65784_1:21413:22594:+ [Complete] codon-table.11"]
["humangutV1.FI28_GL0079660 [gene] locus=scaffold56031_13:1:615:+ [Lack 5'-end] codon-table.11"]
["humangutV1.FI28_GL0152998 [gene] locus=scaffold41976_2:6995:7672:- [Complete] codon-table.11"]
["humangutV1.UC10-2_GL0174527 [gene] locus=scaffold31422_1:4720:5499:+ [Complete] codon-table.11"]
["humangutV1.UC10-2_GL0175130 [gene] locus=scaffold12243_18:2991:4220:+ [Lack 3'-end] codon-table.11", "rumen554_GL1492779_1 [gene] locus=scaffold1360138_2:8350:9582:+[Complete]"]
["humangutV1.UC11-5_GL0014113 [gene] locus=scaffold14897_18:2462:3118:+ [Lack 3'-end] codon-table.11", "rumen2009040_GL0388548_1 [gene] locus=scaffold1851692_1:371:1027:+[Lack 3'-end]"]
["humangutV1.UC11-5_GL0059799 [gene] locus=scaffold5864_5:1:645:+ [Lack both ends] codon-table.11"]
["humangutV1.UC17-2_GL0111873 [gene] locus=scaffold51891_2:1:702:- [Lack both ends] codon-table.11", "rumen552_GL0685303_1 [gene] locus=scaffold854013_3:68:772:-[Lack 5'-end]"]
["humangutV1.UC26-4_GL0151511 [gene] locus=scaffold63765_2:1965:3146:- [Complete] codon-table.11"]
["humangutV1.UC34-0_GL0105732 [gene] locus=scaffold11144_1:7:1209:- [Lack 5'-end] codon-table.11", "mouse1-6_GL0039815 [gene] locus=scaffold13603_1:237:1439:+ [Complete] codon-table.11", "mouse3-8_GL0031525 [gene] locus=scaffold2846_10:4675:5877:+ [Complete] codon-table.11", "rumen555_GL0654298_1 [gene] locus=scaffold1034900_1:10147:11349:-[Complete]", "rumen555_GL2385602_1 [gene] locus=scaffold283062_4:5069:6271:-[Complete]"]
["humangutV1.UC40-1_GL0150341 [gene] locus=scaffold11381_7:2:514:- [Lack 3'-end] codon-table.11"]
["humangutV1.UC47-4_GL0163825 [gene] locus=scaffold11314_18:79:1275:- [Complete] codon-table.11", "mouse5-1_GL0006217 [gene] locus=scaffold12825_5:985:2181:- [Complete] codon-table.11", "mouse5-1_GL0032035 [gene] locus=scaffold24858_2:4732:5928:- [Complete] codon-table.11", "rumen553_GL0846782_1 [gene] locus=scaffold2814_1:18038:19234:-[Complete]", "rumen0081_GL0064711_1 [gene] locus=scaffold335362_3:1279:2475:+[Complete]"]
["mouse1-1_GL0104836 [gene] locus=scaffold12767_20:1545:2723:- [Complete] codon-table.11"]
["mouse1A-dyr4-07_GL0092877 [gene] locus=scaffold24445_1:1671:2780:+ [Lack 3'-end] codon-table.11"]
["mouse2-5_GL0068669 [gene] locus=scaffold23663_4:6848:8095:- [Complete] codon-table.11"]
["mouse20_GL0104041 [gene] locus=scaffold1396_4:57:581:+ [Lack 3'-end] codon-table.11"]
["mouse20_GL0150465 [gene] locus=scaffold13756_3:4154:5320:+ [Complete] codon-table.11", "rumen553_GL0707227_1 [gene] locus=scaffold102953_3:5352:6518:+[Complete]", "rumen552_GL0099297_1 [gene] locus=scaffold386055_1:171:1337:+[Complete]", "rumen552_GL0252065_1 [gene] locus=scaffold506907_1:373:1539:-[Complete]",

"rumen552_GL0841846_1 [gene] locus=scaffold210469_1:6959:8125:-[Complete]",
"rumen554_GL1845448_1 [gene] locus=scaffold681740_1:3931:5097:+[Complete]",
"rumen554_GL2479742_1 [gene] locus=scaffold26282_1:909:2075:-[Complete]",
"rumen0081_GL1224068_1 [gene] locus=C39762997_1:65:1231:+[Complete]",
"rumen100058_GL0167877_1 [gene] locus=scaffold3028_5:1451:2617:+[Complete]",
"rumen100058_GL1244672_1 [gene] locus=scaffold3366082_1:1672:2838:-[Complete]",
"rumen100058_GL3140985_1 [gene] locus=scaffold798435_2:57:1223:-[Complete]",
"rumen100058_GL3835232_1 [gene] locus=scaffold1577825_2:672:1838:+[Complete]",
"rumen2009040_GL1917829_1 [gene] locus=scaffold1594294_1:1937:3103:-[Complete]",
"rumen2009040_GL2269736_1 [gene] locus=scaffold2329482_1:5312:6478:-[Complete]",
"rumen2009040_GL2642793_1 [gene] locus=scaffold1358709_10:662:1828:+[Complete]",
"rumen3042_GL0131095_1 [gene] locus=scaffold2454318_1:356:1522:+[Complete]",
"rumen3042_GL1485888_1 [gene] locus=scaffold2612311_1:1189:2355:+[Complete]",
"rumen3042_GL2268688_1 [gene] locus=scaffold1295952_5:2154:3320:-[Complete]"
["mouse29_GL0095889 [gene] locus=scaffold46844_2:157:540:- [Lack 5'-end] codon-table.11"]
["mouse3-6_GL0009578 [gene] locus=scaffold63212_1:6391:7623:- [Complete] codon-table.11"]
["mouse37_GL0036091 [gene] locus=scaffold36633_1:3:590:+ [Lack both ends] codon-table.11"]
["mouse4-3_GL0027379 [gene] locus=scaffold23007_5:1:666:- [Lack 3'-end] codon-table.11", "rumen2009040_GL0697873_1 [gene] locus=scaffold2007056_1:2:667:+[Lack both ends]"
["mouse4-7_GL0053583 [gene] locus=scaffold24657_2:1473:2186:+ [Complete] codon-table.11"]
["mouse40_GL0003047 [gene] locus=scaffold3733_5:2:871:+ [Lack 5'-end] codon-table.11"]
["mouse52_GL0066171 [gene] locus=C1229355_1:1236:2558:- [Complete] codon-table.11"]
["mouse7-5_GL0099089 [gene] locus=scaffold62478_1:1999:3198:- [Complete] codon-table.11"]
["mouse8-1_GL0096154 [gene] locus=scaffold21121_4:3:887:- [Lack both ends] codon-table.11"]
["mouse8-2_GL0031752 [gene] locus=scaffold30695_2:1:642:+ [Lack 5'-end] codon-table.11"]
["mouse8-2_GL0086414 [gene] locus=scaffold30695_1:1313:1804:+ [Lack 3'-end] codon-table.11"]
["mouse8-3_GL0003506 [gene] locus=scaffold64522_1:9192:10358:+ [Complete] codon-table.11", "pigPIG_161_GL0158104 [gene] locus=scaffold37546_2:2713:3879:+ [Complete] codon-table.11", "pigDB-11B_GL0076554 [gene] locus=scaffold24_2:33303:34469:+ [Complete] codon-table.11", "pigDB-511B_GL0014654 [gene] locus=scaffold67850_2:1964:3130:- [Complete] codon-table.11", "pigEYZ-120B_GL0301365 [gene] locus=scaffold51536_3:3060:4226:- [Complete] codon-table.11", "rumen583_GL0021794_1 [gene] locus=C5676937_1:4700:5866:+[Complete]", "rumen3042_GL2088050_1 [gene] locus=scaffold525157_3:49:1212:+[Lack 3'-end]", "cazygii326543192(gb)ADZ85051.1] glycosidase related protein [Clostridium lentocellum DSM 5427]"
["mouseG1-1A_GL0035773 [gene] locus=scaffold23651_3:32:697:- [Lack 5'-end] codon-table.11", "rumen2009040_GL1823158_1 [gene] locus=scaffold2243758_1:2418:3083:-[Lack 5'-end]"
["mouseG1-2A_GL0065747 [gene] locus=scaffold47004_3:1:561:- [Lack 3'-end] codon-table.11"]
["mouseG1-3A_GL0079207 [gene] locus=scaffold49653_6:1:858:+ [Lack 5'-end] codon-table.11"]
["mouseG1-6A_GL0052078 [gene] locus=scaffold27249_7:1024:1536:- [Lack 5'-end] codon-table.11", "rumen100058_GL0670777_1 [gene] locus=scaffold2791858_1:1:513:+[Lack 5'-end]"
["mouseG1-6A_GL0052079 [gene] locus=scaffold27249_8:1:549:- [Lack 3'-end] codon-table.11"]
["mouseG1-6A_GL0074666 [gene] locus=scaffold41234_6:2:790:- [Lack 3'-end] codon-table.11"]
["mouseGroup2-2A_GL0060717 [gene] locus=scaffold39236_3:2263:3501:- [Complete] codon-table.11"]

["mouseGroup2-3A_GL0015006 [gene] locus=scaffold3514_12:60:842:- [Lack 5'-end] codon-table.11"]
["mouseGroup2-3A_GL0026300 [gene] locus=scaffold9194_7:1:609:- [Lack 3'-end] codon-table.11"]
["mouseGroup2-4A_GL0130929 [gene] locus=scaffold114663_1:1:513:+ [Lack 5'-end] codon-table.11"]
["mouseGroup2-5A_GL0103129 [gene] locus=scaffold70021_2:2:925:- [Lack 3'-end] codon-table.11", "rumen2009040_GL1397020_1 [gene] locus=scaffold626237_1:3:926:-[Lack 3'-end]"]
["mouseGroup2-8A_GL0147181 [gene] locus=scaffold121907_8:1339:1806:- [Lack 5'-end] codon-table.11", "rumen553_GL0852252_1 [gene] locus=scaffold112080_3:2:469:+[Lack 5'-end]", "rumen554_GL2300168_1 [gene] locus=scaffold792886_4:3:470:+[Lack 5'-end]"]
["mouseGroup2-8A_GL0147182 [gene] locus=scaffold121907_9:2:688:- [Lack 3'-end] codon-table.11", "mouse8-6_GL0028013 [gene] locus=scaffold62741_1:47:733:+ [Lack 3'-end] codon-table.11"]
["mouseMC-0-1_GL0110427 [gene] locus=scaffold96537_1:2:598:- [Lack both ends] codon-table.11", "rumen552_GL1573339_1 [gene] locus=scaffold785128_1:2:598:+[Lack both ends]"]
["mouseMC-6-1_GL0074889 [gene] locus=scaffold49658_1:281:1348:+ [Lack 3'-end] codon-table.11", "rumen553_GL0598341_1 [gene] locus=scaffold368919_2:1130:2200:-[Lack 5'-end]"]
["mouseMC-6-2_GL0115419 [gene] locus=scaffold91199_2:2:652:- [Lack both ends] codon-table.11"]
["mouseMC-6-2_GL0152441 [gene] locus=scaffold122298_1:1:663:+ [Lack 5'-end] codon-table.11", "rumen554_GL0411802_1 [gene] locus=scaffold1143481_1:1:663:+[Lack 5'-end]", "rumen0081_GL0859080_1 [gene] locus=scaffold697899_2:2:664:+[Lack 5'-end]"]
["mouseMC-6-3_GL0095494 [gene] locus=scaffold70992_2:8783:9967:+ [Complete] codon-table.11"]
["mouseMC-6-4_GL0117573 [gene] locus=scaffold83323_2:2:550:+ [Lack 5'-end] codon-table.11", "rumen100058_GL3004017_1 [gene] locus=scaffold1710841_1:2:550:+[Lack 5'-end]"]
["mouseMH-6-2_GL0099477 [gene] locus=scaffold78797_3:6912:8150:+ [Complete] codon-table.11"]
["mouseS-Fe11_GL0022259 [gene] locus=scaffold14952_1:3063:4277:- [Complete] codon-table.11", "rumen0081_GL1908540_1 [gene] locus=scaffold4735_6:1749:2963:+[Complete]"]
["mouseS-Fe12_GL0125823 [gene] locus=scaffold37891_1:1:507:- [Lack 3'-end] codon-table.11"]
["mouseS-Fe20_GL0157906 [gene] locus=scaffold87368_1:2:643:+ [Lack both ends] codon-table.11", "pigPIG_144_GL0269360 [gene] locus=scaffold71900_2:3:644:+ [Lack both ends] codon-table.11", "rumen7049_GL0142595_1 [gene] locus=scaffold374494_2:2:646:+[Lack 5'-end]"]
["mouseS-Fe20_GL0184469 [gene] locus=scaffold103466_2:3:581:- [Lack both ends] codon-table.11"]
["mouseS-Fe2_GL0149456 [gene] locus=scaffold6259_8:1:981:- [Lack 3'-end] codon-table.11", "mouseG1-5A_GL0120339 [gene] locus=scaffold84034_12:1:984:+ [Lack 5'-end] codon-table.11"]
["mouseS-Fe3_GL0012630 [gene] locus=scaffold109608_3:2:457:- [Lack 3'-end] codon-table.11"]
["mouseS-Fe3_GL0182180 [gene] locus=scaffold5576_11:291:743:- [Lack 5'-end] codon-table.11"]
["mouseS-Fe8_GL0062201 [gene] locus=C1788575_1:2:754:+ [Lack both ends] codon-table.11"]
["mouseS-Fe8_GL0076295 [gene] locus=scaffold44585_1:12619:14178:+ [Complete] codon-table.11"]
["mouseS-Fe9_GL0254040 [gene] locus=scaffold105458_7:1:627:- [Lack both ends] codon-table.11"]
["pigBHZ-10B_GL0256708 [gene] locus=scaffold5679_1:1304:2524:+ [Complete] codon-table.11"]
["pigBHZ-11B_GL0034540 [gene] locus=scaffold196728_2:128305:129498:+ [Complete] codon-table.11"]
["pigBHZ-2B_GL0075359 [gene] locus=scaffold166132_1:1:945:- [Lack 3'-end] codon-table.11", "rumen2009040_GL1807090_1 [gene] locus=scaffold2927015_1:1:945:+[Lack both ends]"]
["pigBHZ-4B_GL0153379 [gene] locus=scaffold164132_1:214:951:- [Lack 5'-end] codon-table.11"]
["pigBHZ-4B_GL0202887 [gene] locus=scaffold22706_2:2:562:+ [Lack 5'-end] codon-table.11", "rumen554_GL2975678_1 [gene] locus=scaffold2182415_1:1:561:+[Lack 5'-end]"]

["pigBHZ-6B_GL0161101 [gene] locus=scaffold99203_1:2:1084:- [Lack both ends] codon-table.11"]
["pigBHZ-9B_GL0092637 [gene] locus=scaffold5837_1:1:1107:- [Lack 3'-end] codon-table.11"]
["pigBMZ-17B_GL0022145 [gene] locus=scaffold116002_7:430:1446:+ [Lack 3'-end] codon-table.11"]
["pigBMZ-17B_GL0100030 [gene] locus=scaffold91060_1:2:724:- [Lack both ends] codon-table.11"]
["pigBMZ-2B_GL0014517 [gene] locus=scaffold50928_4:3:719:- [Lack 3'-end] codon-table.11"]
["pigDB-510B_GL0212637 [gene] locus=scaffold32625_4:1595:2266:- [Lack 5'-end] codon-table.11"]
["pigDB-517B_GL0101001 [gene] locus=scaffold127221_1:75:512:+ [Lack 3'-end] codon-table.11"]
["pigEYZ-183B_GL0159281 [gene] locus=scaffold18455_2:1:555:+ [Lack both ends] codon-table.11", "rumen100058_GL1180685_1 [gene] locus=scaffold1351010_1:3:557:-[Lack both ends]", "rumen100058_GL3225001_1 [gene] locus=scaffold1584546_2:2:556:+[Lack both ends]", "rumen2009040_GL0483093_1 [gene] locus=C53189378_1:1:555:-[Lack both ends]"]
["pigEYZ-192B_GL0068258 [gene] locus=scaffold123997_1:819:2030:- [Complete] codon-table.11"]
["pigEYZ-378B_GL0169238 [gene] locus=scaffold93268_4:1:903:- [Lack both ends] codon-table.11"]
["pigEYZ-381B_GL0163816 [gene] locus=scaffold205315_1:426:896:- [Lack 5'-end] codon-table.11"]
["pigEYZ-468B_GL0016892 [gene] locus=scaffold59667_1:1:576:- [Lack both ends] codon-table.11", "rumen555_GL0499687_1 [gene] locus=scaffold1402685_1:3:581:+[Lack 5'-end]", "rumen2009040_GL3653300_1 [gene] locus=scaffold2933610_1:1:579:+[Lack 5'-end]"]
["pigEYZ-566B_GL0134779 [gene] locus=C1416983_1:3:815:- [Lack 3'-end] codon-table.11"]
["pigEYZ-592B_GL0151096 [gene] locus=scaffold37532_1:1:549:+ [Lack both ends] codon-table.11", "rumen2009040_GL1991920_1 [gene] locus=scaffold764530_6:3:551:-[Lack both ends]"]
["pigEYZ-611B_GL0059729 [gene] locus=scaffold133290_2:3:647:- [Lack 3'-end] codon-table.11"]
["pigEYZ-615B_GL0085856 [gene] locus=scaffold39063_1:33:638:+ [Lack 3'-end] codon-table.11"]
["pigEYZ-652B_GL0050351 [gene] locus=scaffold127622_2:780:1364:- [Lack 5'-end] codon-table.11"]
["pigPIG-001_GL0084092 [gene] locus=scaffold112621_2:23174:24376:+ [Complete] codon-table.11", "pigPIG-027_GL0132459 [gene] locus=scaffold13426_11:2576:3778:- [Lack 5'-end] codon-table.11", "rumen552_GL1686014_1 [gene] locus=scaffold446346_1:657:1859:+[Complete]", "rumen554_GL2104050_1 [gene] locus=scaffold102241_1:336:1538:-[Complete]", "rumen0081_GL1300854_1 [gene] locus=scaffold1788767_2:1976:3178:+[Complete]", "rumen7049_GL2676190_1 [gene] locus=scaffold766563_7:6575:7777:+[Complete]"]
["pigPIG-006_GL0003381 [gene] locus=scaffold79667_1:3:761:- [Lack 3'-end] codon-table.11"]
["pigPIG-006_GL0107362 [gene] locus=scaffold102332_1:1:774:- [Lack both ends] codon-table.11", "rumen553_GL0437579_1 [gene] locus=scaffold66463_1:5117:5893:-[Lack 5'-end]"]
["pigPIG-007_GL0170892 [gene] locus=scaffold36575_5:2:367:+ [Lack 5'-end] codon-table.11"]
["pigPIG-007_GL0195730 [gene] locus=scaffold36575_3:369:887:+ [Lack 3'-end] codon-table.11"]
["pigPIG-011_GL0208843 [gene] locus=scaffold104732_1:3:527:+ [Lack both ends] codon-table.11"]
["pigPIG-011_GL0212040 [gene] locus=scaffold8823_3:5184:6383:- [Complete] codon-table.11", "rumen554_GL0552620_1 [gene] locus=scaffold2138255_1:199:1398:-[Complete]", "rumen554_GL0776369_1 [gene] locus=scaffold28152_2:6087:7286:+[Complete]", "rumen100058_GL3148890_1 [gene] locus=scaffold478250_2:747:1946:+[Complete]", "rumen2009040_GL3531659_1 [gene] locus=scaffold283956_1:47:1246:-[Complete]", "rumen3042_GL2020338_1 [gene] locus=scaffold2076113_1:2611:3810:-[Complete]"]
["pigPIG-012_GL0150881 [gene] locus=scaffold35901_1:1:729:+ [Lack both ends] codon-table.11", "rumen100058_GL1430674_1 [gene] locus=scaffold1928015_2:409:1137:+[Lack 3'-end]"]

<p>["pigPIG-017_GL0017516 [gene] locus=scaffold1616_2:2136:3302:- [Complete] codon-table.11",</p> <p>"rumen553_GL0501507_1 [gene] locus=scaffold34527_2:1421:2587:-[Complete]",</p> <p>"rumen552_GL1485570_1 [gene] locus=scaffold626980_2:57117:58283:+[Complete]",</p> <p>"rumen554_GL2211671_1 [gene] locus=scaffold33847_1:259:1425:-[Complete]",</p> <p>"rumen554_GL2600831_1 [gene] locus=scaffold204795_1:106:1272:-[Complete]",</p> <p>"rumen554_GL2810335_1 [gene] locus=scaffold231054_2:583:1749:+[Complete]",</p> <p>"rumen554_GL2910917_1 [gene] locus=scaffold542701_1:195:1361:-[Complete]",</p> <p>"rumen554_GL3157872_1 [gene] locus=scaffold2075507_2:3659:4825:+[Complete]",</p> <p>"rumen555_GL1580309_1 [gene] locus=scaffold1536785_1:11780:12946:-[Complete]",</p> <p>"rumen0081_GL0263207_1 [gene] locus=scaffold99592_1:7085:8251:-[Complete]",</p> <p>"rumen0081_GL0480546_1 [gene] locus=scaffold156774_3:149:1315:+[Complete]",</p> <p>"rumen0081_GL2110370_1 [gene] locus=scaffold786666_4:1519:2685:-[Complete]",</p> <p>"rumen0081_GL2298606_1 [gene] locus=scaffold34203_1:538:1704:+[Complete]",</p> <p>"rumen100058_GL1773084_1 [gene] locus=scaffold740572_1:843:2009:-[Complete]",</p> <p>"rumen100058_GL2010090_1 [gene] locus=scaffold1257179_4:532:1698:-[Complete]",</p> <p>"rumen100058_GL2011063_1 [gene] locus=C60783253_1:304:1470:+[Complete]",</p> <p>"rumen100058_GL2237142_1 [gene] locus=scaffold1037187_1:3721:4887:-[Complete]",</p> <p>"rumen2009040_GL0521284_1 [gene] locus=scaffold147283_2:24:1190:+[Complete]",</p> <p>"rumen2009040_GL1349272_1 [gene] locus=scaffold530263_1:1070:2236:-[Complete]",</p> <p>"rumen2009040_GL3530282_1 [gene] locus=scaffold23780_1:1175:2341:+[Complete]",</p> <p>"rumen3042_GL1010274_1 [gene] locus=scaffold2404816_1:6147:7313:+[Complete]"</p>
<p>["pigPIG-017_GL0172359 [gene] locus=scaffold29954_2:919:2100:- [Lack 5'-end] codon-table.11",</p> <p>"rumen552_GL1525844_1 [gene] locus=scaffold131085_2:215:1396:-[Complete]",</p> <p>"rumen554_GL1096797_1 [gene] locus=scaffold1746292_1:892:2073:+[Complete]",</p> <p>"rumen555_GL0162025_1 [gene] locus=scaffold479522_1:1260:2441:+[Complete]",</p> <p>"rumen0081_GL0761903_1 [gene] locus=scaffold55494_2:553:1734:+[Complete]",</p> <p>"rumen100058_GL1839944_1 [gene] locus=scaffold12460_1:2683:3864:-[Lack 5'-end]",</p> <p>"rumen2009040_GL0867123_1 [gene] locus=scaffold2352423_1:6:1187:-[Complete]",</p> <p>"rumen3042_GL0391091_1 [gene] locus=scaffold10271_2:481:1662:+[Complete]",</p> <p>"rumen3042_GL1303090_1 [gene] locus=scaffold370611_1:53:1234:-[Lack 5'-end]",</p> <p>"rumen3042_GL1591543_1 [gene] locus=scaffold1583907_4:399:1580:-[Complete]"</p>
<p>["pigPIG-018_GL0014696 [gene] locus=scaffold119816_1:3:533:- [Lack 3'-end] codon-table.11"]</p>
<p>["pigPIG-020_GL0005672 [gene] locus=scaffold105618_4:3794:4963:+ [Complete] codon-table.11",</p> <p>"rumen3042_GL2582720_1 [gene] locus=scaffold484113_2:12530:13699:-[Complete]",</p> <p>"rumen7049_GL1546302_1 [gene] locus=scaffold92776_6:167:1336:+[Complete]"</p>
<p>["pigPIG-020_GL0035751 [gene] locus=scaffold174384_1:3:584:+ [Lack both ends] codon-table.11"]</p>
<p>["pigPIG-023_GL0023071 [gene] locus=scaffold65895_1:1:573:- [Lack both ends] codon-table.11",</p> <p>"rumen100058_GL0477677_1 [gene] locus=C58269829_1:3:575:-[Lack 3'-end]"</p>
<p>["pigPIG-026_GL0007526 [gene] locus=scaffold105900_1:1:651:+ [Lack 5'-end] codon-table.11",</p> <p>"rumen553_GL0303320_1 [gene] locus=scaffold398815_2:2:652:+[Lack 5'-end]",</p> <p>"rumen2009040_GL3153638_1 [gene] locus=scaffold764681_1:1:651:+[Lack 5'-end]",</p> <p>"rumen3042_GL2518797_1 [gene] locus=scaffold1571394_1:1:651:+[Lack 5'-end]"</p>
<p>["pigPIG-026_GL0013259 [gene] locus=scaffold81048_2:2:1159:+ [Lack 5'-end] codon-table.11",</p> <p>"rumen552_GL1221272_1 [gene] locus=scaffold619406_1:5513:6670:-[Complete]",</p>

"rumen2009040_GL2065926_1 [gene] locus=scaffold1065072_1:518:1675:-[Lack 5'-end]"
["pigPIG-026_GL0130063 [gene] locus=scaffold112759_1:1:564:+ [Lack 5'-end] codon-table.11"]
["pigPIG-026_GL0193814 [gene] locus=scaffold114_12:4262:5008:+ [Lack 3'-end] codon-table.11"]
["pigPIG-026_GL0248028 [gene] locus=scaffold60158_1:2357:3580:+ [Complete] codon-table.11"]
["pigPIG-027_GL0041928 [gene] locus=scaffold80042_1:3:476:+ [Lack 5'-end] codon-table.11", "rumen3042_GL2172007_1 [gene] locus=scaffold1967034_1:77:550:-[Lack 5'-end]"
["pigPIG-029_GL0031350 [gene] locus=scaffold22653_6:3:530:+ [Lack both ends] codon-table.11"]
["pigPIG-031_GL0065486 [gene] locus=scaffold100115_3:690:1664:+ [Lack 3'-end] codon-table.11"]
["pigPIG-031_GL0184492 [gene] locus=scaffold4264_2:3:578:+ [Lack 5'-end] codon-table.11", "pigPIG-034_GL0183281 [gene] locus=scaffold104881_1:3:575:+ [Lack both ends] codon-table.11"]
["pigPIG-033_GL0201605 [gene] locus=scaffold39444_1:3:818:+ [Lack both ends] codon-table.11"]
["pigPIG-034_GL0075039 [gene] locus=scaffold145714_2:8552:9391:+ [Complete] codon-table.11"]
["pigPIG-035_GL0076964 [gene] locus=scaffold4108_2:5911:6447:- [Lack 5'-end] codon-table.11"]
["pigPIG-035_GL0142973 [gene] locus=scaffold113295_1:2:940:- [Lack 3'-end] codon-table.11", "rumen555_GL2185050_1 [gene] locus=scaffold1241617_1:1:939:+[Lack both ends]"
["pigPIG-035_GL0143396 [gene] locus=C1702293_1:1:747:+ [Lack 5'-end] codon-table.11", "rumen3042_GL1313175_1 [gene] locus=scaffold12436_3:1181:1927:-[Lack 5'-end]", "rumen3042_GL2802106_1 [gene] locus=scaffold1587930_1:7803:8549:-[Lack 5'-end]"
["pigPIG-036_GL0166384 [gene] locus=scaffold107511_2:196:633:- [Lack 5'-end] codon-table.11", "rumen100058_GL0050368_1 [gene] locus=scaffold675000_3:2:439:+[Lack 5'-end]"
["pigPIG-037_GL0127005 [gene] locus=scaffold82022_5:177:971:+ [Lack 3'-end] codon-table.11"]
["pigPIG-038_GL0128508 [gene] locus=scaffold208995_2:1244:2473:+ [Complete] codon-table.11", "pigPIG-082_GL0061069 [gene] locus=scaffold48565_2:2246:3475:- [Complete] codon-table.11"]
["pigPIG-038_GL0157334 [gene] locus=scaffold205231_3:3:800:+ [Lack 5'-end] codon-table.11"]
["pigPIG-038_GL0173146 [gene] locus=scaffold108992_2:23406:24671:+ [Complete] codon-table.11"]
["pigPIG-044_GL0139262 [gene] locus=scaffold51992_17:2573:3235:- [Lack 5'-end] codon-table.11"]
["pigPIG-044_GL0160786 [gene] locus=scaffold51992_18:2:469:- [Lack 3'-end] codon-table.11"]
["pigPIG-045_GL0086006 [gene] locus=scaffold120143_1:1379:2458:+ [Lack 3'-end] codon-table.11"]
["pigPIG-045_GL0165944 [gene] locus=scaffold45985_4:713:1708:- [Complete] codon-table.11"]
["pigPIG-046_GL0076681 [gene] locus=scaffold103983_1:1:456:+ [Lack 5'-end] codon-table.11"]
["pigPIG-046_GL0190036 [gene] locus=scaffold132072_3:117:602:+ [Lack 3'-end] codon-table.11"]
["pigPIG-058_GL0014194 [gene] locus=scaffold204438_2:2:589:+ [Lack both ends] codon-table.11", "rumen554_GL1020366_1 [gene] locus=scaffold1719517_1:3:590:+[Lack both ends]"
["pigPIG-058_GL0242172 [gene] locus=scaffold213269_2:2:505:- [Lack both ends] codon-table.11"]
["pigPIG-079_GL0015783 [gene] locus=scaffold78110_4:3:632:+ [Lack both ends] codon-table.11"]
["pigPIG-081_GL0069460 [gene] locus=scaffold54785_1:15372:16550:- [Complete] codon-table.11"]
["pigPIG-081_GL0070629 [gene] locus=scaffold49609_1:5474:6700:- [Complete] codon-table.11"]
["pigPIG-082_GL0156754 [gene] locus=scaffold68717_3:3:707:+ [Lack both ends] codon-table.11", "rumen555_GL0384859_1 [gene] locus=scaffold884172_1:2:706:-[Lack both ends]"
["pigPIG-083_GL0170487 [gene] locus=scaffold63230_21:2:1129:+ [Lack 5'-end] codon-table.11", "rumen100058_GL0775549_1 [gene] locus=scaffold2096722_1:120:1244:+[Lack 3'-end]"
["pigPIG-084_GL0114584 [gene] locus=scaffold13539_18:1:933:- [Lack 3'-end] codon-table.11", "rumen553_GL0859605_1 [gene] locus=scaffold100021_1:9385:10317:+[Lack 3'-end]"



["pigPIG-085_GL0107466 [gene] locus=scaffold130200_1:3:563:+ [Lack both ends] codon-table.11"]
["pigPIG-091_GL0053548 [gene] locus=scaffold161822_1:14463:15920:- [Complete] codon-table.11"]
["pigPIG-093_GL0033145 [gene] locus=scaffold65710_1:10422:11711:- [Complete] codon-table.11"]
["pigPIG-094_GL0136337 [gene] locus=scaffold151664_2:1456:2307:- [Lack 5'-end] codon-table.11"]
["pigPIG-094_GL0195080 [gene] locus=scaffold4599_7:2:955:+ [Lack 5'-end] codon-table.11"]
["pigPIG-095_GL0141942 [gene] locus=scaffold42740_4:3668:4963:+ [Complete] codon-table.11"]
["pigPIG-097_GL0062624 [gene] locus=scaffold87566_1:3:794:+ [Lack both ends] codon-table.11", "rumen100058_GL0632391_1 [gene] locus=scaffold1560285_3:3:797:+[Lack 5'-end]"]
["pigPIG-097_GL0075270 [gene] locus=scaffold85507_1:657:1229:+ [Lack 3'-end] codon-table.11"]
["pigPIG-103_GL0008850 [gene] locus=scaffold175724_1:3:656:- [Lack 3'-end] codon-table.11", "pigPIG-103_GL0269847 [gene] locus=scaffold175723_1:3:656:- [Lack 3'-end] codon-table.11", "pigBMZ-1B_GL0037337 [gene] locus=scaffold76326_1:1:654:- [Lack both ends] codon-table.11", "rumen0081_GL1284696_1 [gene] locus=scaffold1769067_1:1:654:-[Lack 3'-end]", "rumen3042_GL2115542_1 [gene] locus=C52164284_1:3:656:-[Lack 3'-end]"]
["pigPIG-106_GL0188443 [gene] locus=scaffold67583_1:1570:3729:+ [Lack 3'-end] codon-table.11"]
["pigPIG-108_GL0134942 [gene] locus=scaffold41440_2:2:1132:- [Lack 3'-end] codon-table.11"]
["pigPIG-109_GL0075251 [gene] locus=scaffold15250_2:21:500:- [Lack 5'-end] codon-table.11"]
["pigPIG-110_GL0001971 [gene] locus=scaffold57452_8:23299:24480:- [Complete] codon-table.11"]
["pigPIG-110_GL0147213 [gene] locus=scaffold22146_4:1:675:+ [Lack 5'-end] codon-table.11", "rumen2009040_GL1194740_1 [gene] locus=scaffold2792895_5:199:873:-[Lack 5'-end]"]
["pigPIG_111_GL0048555 [gene] locus=scaffold145756_2:1:531:+ [Lack both ends] codon-table.11"]
["pigPIG_114_GL0016970 [gene] locus=scaffold9464_4:2:553:- [Lack both ends] codon-table.11"]
["pigPIG_120_GL0208425 [gene] locus=C2070008_1:12:884:- [Lack 5'-end] codon-table.11"]
["pigPIG_123_GL0290744 [gene] locus=scaffold33_1:3:515:- [Complete] codon-table.11"]
["pigPIG_124_GL0253480 [gene] locus=scaffold127978_1:2055:2555:+ [Complete] codon-table.11"]
["pigPIG_125_GL0120815 [gene] locus=scaffold71681_1:842:2026:- [Complete] codon-table.11", "rumen0081_GL0510562_1 [gene] locus=scaffold200904_3:2016:3200:+[Complete]", "rumen7049_GL1461122_1 [gene] locus=scaffold903821_14:408:1592:-[Complete]"]
["pigPIG_126_GL0031494 [gene] locus=scaffold78398_1:3291:3761:+ [Complete] codon-table.11"]
["pigPIG_127_GL0155405 [gene] locus=C2337582_1:249:707:+ [Complete] codon-table.11"]
["pigPIG_128_GL0080714 [gene] locus=scaffold15833_2:355:1005:+ [Lack 3'-end] codon-table.11"]
["pigPIG_133_GL0082333 [gene] locus=scaffold114942_2:1:615:- [Lack 3'-end] codon-table.11"]
["pigPIG_135_GL0053887 [gene] locus=scaffold48752_2:2:811:+ [Lack 5'-end] codon-table.11", "rumen2009040_GL0202502_1 [gene] locus=scaffold1050783_1:1:810:+[Lack 5'-end]"]
["pigPIG_138_GL0203883 [gene] locus=scaffold59906_3:124:669:+ [Lack 3'-end] codon-table.11"]
["pigPIG_151_GL0084007 [gene] locus=scaffold188087_9:2:796:- [Lack both ends] codon-table.11"]
["pigPIG_151_GL0327709 [gene] locus=scaffold254836_6:2:1033:- [Lack 3'-end] codon-table.11"]
["pigPIG_155_GL0140171 [gene] locus=scaffold71559_1:1:582:+ [Lack both ends] codon-table.11"]
["pigPIG_156_GL0222712 [gene] locus=scaffold125662_2:2487:3239:- [Complete] codon-table.11"]
["pigPIG_157_GL0113023 [gene] locus=scaffold92247_5:2:916:- [Lack 3'-end] codon-table.11"]
["pigPIG_162_GL0239358 [gene] locus=C3366578_1:568:1551:- [Lack 5'-end] codon-table.11", "rumen3042_GL2148850_1 [gene] locus=scaffold1281627_1:1628:2611:-[Complete]"]
["pigPIG_173_GL0175765 [gene] locus=scaffold230225_4:1537:2787:- [Complete] codon-table.11",

"pigPIG-019_GL0155432 [gene] locus=scaffold48980_3:1255:2505:- [Complete] codon-table.11"
"pigPIG_173_GL0198560 [gene] locus=scaffold181858_4:3:932:+ [Lack 5'-end] codon-table.11", "rumen7049_GL2020500_1 [gene] locus=scaffold2252006_1:3:932:+[Lack 5'-end]"
"pigPIG_175_GL0060567 [gene] locus=scaffold108852_1_1:1563:2015:- [Lack 5'-end] codon-table.11"
"pigPIG_176_GL0069010 [gene] locus=scaffold204640_1:2:655:+ [Lack both ends] codon-table.11"
"pigPIG_186_GL0168224 [gene] locus=scaffold18482_2:2:565:+ [Lack both ends] codon-table.11"
"pigPIG_187_GL0057039 [gene] locus=C2545629_1:3:410:- [Lack 3'-end] codon-table.11"
"pigPIG_190_GL0017562 [gene] locus=scaffold141127_3:2:505:+ [Lack 5'-end] codon-table.11", "rumen100058_GL0269459_1 [gene] locus=scaffold56688_1:3:506:+[Lack 5'-end]"
"pigPIG_196_GL0038436 [gene] locus=scaffold233365_1:3:515:- [Lack both ends] codon-table.11"
"pigPIG_197_GL0000064 [gene] locus=C3418714_1:3310:4551:- [Complete] codon-table.11", "rumen100058_GL2992077_1 [gene] locus=scaffold434594_7:2498:3739:+[Complete]"
"pigPIG_198_GL0088713 [gene] locus=scaffold254369_1:3:563:+ [Lack both ends] codon-table.11"
"pigPIG_198_GL0261592 [gene] locus=scaffold559_5:2415:3431:+ [Complete] codon-table.11"
"pigPIG_201_GL0250193 [gene] locus=scaffold68270_4:2:739:+ [Lack both ends] codon-table.11"
"pigPIG_204_GL0024241 [gene] locus=scaffold104647_11:961:1479:+ [Lack 3'-end] codon-table.11"
"pigPIG_205_GL0135979 [gene] locus=scaffold176768_5:3:467:+ [Lack 5'-end] codon-table.11", "pigPIG-001_GL0200696 [gene] locus=scaffold24103_2:102:566:- [Lack 5'-end] codon-table.11"
"pigPIG_207_GL0143531 [gene] locus=scaffold8278_9:22:798:+ [Lack 3'-end] codon-table.11"
"pigPIG_208_GL0114492 [gene] locus=scaffold224521_2:2:784:+ [Lack both ends] codon-table.11"
"pigSYZ-428B_GL0135299 [gene] locus=scaffold104686_1:2:640:- [Lack both ends] codon-table.11"
"pigSYZ-428B_GL0190954 [gene] locus=scaffold77153_1:1:774:- [Lack both ends] codon-table.11"
"pigZXZ-7B_GL0151617 [gene] locus=scaffold119190_2:23:511:- [Lack 5'-end] codon-table.11"
"rumen0081_GL0065389_1 [gene] locus=scaffold555547_1:1:516:+[Lack both ends]", "rumen2009040_GL0561469_1 [gene] locus=scaffold1535209_1:2:517:-[Lack both ends]"
"rumen0081_GL0127716_1 [gene] locus=scaffold1034514_2:2:844:+[Lack 5'-end]"
"rumen0081_GL0338636_1 [gene] locus=scaffold412998_5:1269:1973:+[Lack 3'-end]"
"rumen0081_GL0411089_1 [gene] locus=scaffold1487438_1:3:599:-[Lack both ends]"
"rumen0081_GL0460747_1 [gene] locus=scaffold112280_2:2:1036:+[Lack 5'-end]"
"rumen0081_GL0488420_1 [gene] locus=C38714956_1:3:599:-[Lack 3'-end]", "rumen100058_GL1539564_1 [gene] locus=scaffold493414_3:3:599:-[Lack 3'-end]"
"rumen0081_GL0553385_1 [gene] locus=scaffold804545_7:390:1268:+[Lack 3'-end]"
"rumen0081_GL0612888_1 [gene] locus=scaffold1949880_1:52:705:+[Lack 3'-end]"
"rumen0081_GL0618138_1 [gene] locus=scaffold485236_1:2:640:+[Lack both ends]"
"rumen0081_GL0642831_1 [gene] locus=scaffold1832181_1:25:840:-[Lack 5'-end]", "rumen100058_GL3367416_1 [gene] locus=scaffold1731703_2:2:817:+[Lack 5'-end]"
"rumen0081_GL0654196_1 [gene] locus=scaffold23987_2:1014:1817:-[Lack 5'-end]"
"rumen0081_GL0717890_1 [gene] locus=scaffold1925290_2:2:910:+[Lack both ends]"
"rumen0081_GL0766424_1 [gene] locus=scaffold659499_2:303:854:+[Lack 3'-end]", "rumen100058_GL1730935_1 [gene] locus=scaffold2642523_2:129:680:+[Lack 3'-end]"
"rumen0081_GL0822409_1 [gene] locus=scaffold860226_2:182:1081:+[Lack 3'-end]", "rumen7049_GL2418659_1 [gene] locus=scaffold1619286_1:3:902:-[Lack 3'-end]"
"rumen0081_GL0914263_1 [gene] locus=scaffold1651922_1:656:1327:-[Lack 5'-end]"

"rumen100058_GL3795401_1 [gene] locus=scaffold80547_5:1:669:-[Lack both ends]"
"rumen0081_GL0932054_1 [gene] locus=scaffold1308780_1:1:567:+[Lack 5'-end]", "rumen7049_GL2755930_1 [gene] locus=scaffold113374_1:1:567:+[Lack 5'-end]"
"rumen0081_GL0935094_1 [gene] locus=scaffold1960186_3:3:683:+[Lack 5'-end]", "rumen100058_GL3376008_1 [gene] locus=scaffold3274052_1:2:682:+[Lack 5'-end]"
"rumen0081_GL0959534_1 [gene] locus=scaffold675900_2:224:1381:+[Complete]"
"rumen0081_GL1081048_1 [gene] locus=scaffold1792095_1:3:692:+[Lack 5'-end]"
"rumen0081_GL1287041_1 [gene] locus=scaffold821699_4:571:1071:-[Lack 5'-end]", "rumen2009040_GL1630589_1 [gene] locus=scaffold2545047_1:1:501:+[Lack 5'-end]"
"rumen0081_GL1294364_1 [gene] locus=scaffold1486322_1:290:886:+[Lack 3'-end]"
"rumen0081_GL1333276_1 [gene] locus=scaffold543317_1:928:1971:+[Lack 3'-end]"
"rumen0081_GL1465181_1 [gene] locus=scaffold1486322_2:2:454:+[Lack 5'-end]"
"rumen0081_GL1475424_1 [gene] locus=scaffold1740690_1:659:1420:+[Lack 3'-end]"
"rumen0081_GL1600238_1 [gene] locus=scaffold491436_1:332:1285:-[Lack 5'-end]"
"rumen0081_GL1693393_1 [gene] locus=scaffold1779572_1:445:906:+[Lack 3'-end]"
"rumen0081_GL1742662_1 [gene] locus=scaffold72493_8:1:438:-[Lack 3'-end]"
"rumen0081_GL1809516_1 [gene] locus=scaffold1960186_2:141:590:+[Lack 3'-end]"
"rumen0081_GL1935353_1 [gene] locus=scaffold1125193_1:2:697:-[Lack both ends]"
"rumen0081_GL1978628_1 [gene] locus=scaffold1601377_1:3:566:-[Lack both ends]"
"rumen0081_GL2055008_1 [gene] locus=C39340957_1:3:731:-[Lack 3'-end]"
"rumen0081_GL2122343_1 [gene] locus=scaffold1075911_5:3:800:-[Lack 3'-end]"
"rumen0081_GL2136272_1 [gene] locus=scaffold739655_1:3:635:-[Lack both ends]"
"rumen0081_GL2300849_1 [gene] locus=scaffold1124614_2:120:620:+[Lack 3'-end]"
"rumen0081_GL2407674_1 [gene] locus=scaffold980628_1:3356:4189:-[Lack 5'-end]"
"rumen0081_GL2446631_1 [gene] locus=scaffold929589_1:3:560:+[Lack both ends]"
"rumen0081_GL2453009_1 [gene] locus=scaffold717067_1:3:569:-[Lack 3'-end]"
"rumen0081_GL2484873_1 [gene] locus=C39086163_1:307:846:+[Lack 3'-end]", "rumen100058_GL2238021_1 [gene] locus=scaffold2718570_2:3:542:-[Lack both ends]", "rumen100058_GL2526240_1 [gene] locus=scaffold1296534_9:1:540:-[Lack 3'-end]"
"rumen100058_GL0004149_1 [gene] locus=scaffold1160113_1:3:728:+[Lack both ends]"
"rumen100058_GL0027684_1 [gene] locus=scaffold2981749_3:1:705:-[Lack 3'-end]"
"rumen100058_GL0079033_1 [gene] locus=scaffold1645549_2:1:618:-[Lack both ends]"
"rumen100058_GL0198858_1 [gene] locus=scaffold1730225_3:2:931:+[Lack both ends]"
"rumen100058_GL0266682_1 [gene] locus=scaffold1013398_2:2984:3499:-[Lack 5'-end]"
"rumen100058_GL0277713_1 [gene] locus=scaffold348243_2:34:1170:-[Lack 5'-end]"
"rumen100058_GL0284935_1 [gene] locus=scaffold620998_1:1:774:+[Lack 5'-end]"
"rumen100058_GL0316493_1 [gene] locus=scaffold3132681_1:44:586:+[Lack 3'-end]"
"rumen100058_GL0321424_1 [gene] locus=scaffold2801014_1:1:495:+[Lack 5'-end]"
"rumen100058_GL0393593_1 [gene] locus=scaffold1896703_3:1:435:-[Lack 3'-end]"
"rumen100058_GL0395059_1 [gene] locus=scaffold71213_2:758:1360:+[Lack 3'-end]"
"rumen100058_GL0421491_1 [gene] locus=scaffold3263654_1:2:535:+[Lack both ends]"
"rumen100058_GL0434644_1 [gene] locus=scaffold2706756_1:3:590:-[Lack 3'-end]"
"rumen100058_GL0462394_1 [gene] locus=scaffold150431_3:431:1024:-[Lack 5'-end]"

"rumen100058_GL0575058_1 [gene] locus=scaffold3082305_1:222:1433:+[Lack 3'-end]", "rumen2009040_GL1003917_1 [gene] locus=scaffold31292_2:1817:3031:+[Complete]"
"rumen100058_GL0578732_1 [gene] locus=C59582458_1:3:833:-[Lack both ends]"
"rumen100058_GL0671260_1 [gene] locus=scaffold2654340_1:99:602:+[Lack 3'-end]"
"rumen100058_GL0684755_1 [gene] locus=scaffold2188772_3:1:546:-[Lack 3'-end]", "rumen2009040_GL3028990_1 [gene] locus=scaffold473151_1:3:548:-[Lack 3'-end]"
"rumen100058_GL0697017_1 [gene] locus=scaffold1340323_1:147:1112:-[Lack 5'-end]"
"rumen100058_GL0791227_1 [gene] locus=scaffold447185_1:1:528:+[Lack both ends]"
"rumen100058_GL0900473_1 [gene] locus=scaffold2613189_2:1145:2335:+[Complete]"
"rumen100058_GL0934105_1 [gene] locus=C59009796_1:3:686:-[Lack both ends]", "rumen3042_GL0279852_1 [gene] locus=scaffold377932_1:3:686:-[Lack 3'-end]"
"rumen100058_GL0944679_1 [gene] locus=scaffold1815004_1:1:585:+[Lack 5'-end]"
"rumen100058_GL0986726_1 [gene] locus=scaffold1543466_1:3:770:-[Lack both ends]"
"rumen100058_GL1004470_1 [gene] locus=scaffold471899_1:3:554:+[Lack both ends]"
"rumen100058_GL1027453_1 [gene] locus=scaffold2325489_1:1:621:+[Lack 5'-end]"
"rumen100058_GL1057231_1 [gene] locus=scaffold1947780_3:1:594:-[Lack both ends]"
"rumen100058_GL1077138_1 [gene] locus=scaffold11652_2:1:738:-[Lack both ends]"
"rumen100058_GL1131842_1 [gene] locus=scaffold1602790_2:1:669:+[Lack both ends]", "rumen100058_GL3833831_1 [gene] locus=scaffold2507506_1:816:1484:+[Lack 3'-end]"
"rumen100058_GL1163277_1 [gene] locus=scaffold2470163_1:1:501:+[Lack both ends]"
"rumen100058_GL1306731_1 [gene] locus=scaffold1053781_1:1:1086:+[Lack 5'-end]"
"rumen100058_GL1334981_1 [gene] locus=C59411520_1:373:780:+[Lack 3'-end]"
"rumen100058_GL1341542_1 [gene] locus=scaffold965193_2:1:972:-[Lack 3'-end]"
"rumen100058_GL1371219_1 [gene] locus=scaffold2723488_1:1:504:+[Lack both ends]"
"rumen100058_GL1477150_1 [gene] locus=scaffold2280115_4:3:1055:-[Lack 3'-end]", "rumen100058_GL2631011_1 [gene] locus=scaffold2686552_1:225:1277:+[Lack 3'-end]"
"rumen100058_GL1525332_1 [gene] locus=scaffold191575_5:848:2032:-[Complete]"
"rumen100058_GL1527366_1 [gene] locus=scaffold3269640_1:202:729:+[Lack 3'-end]"
"rumen100058_GL1610277_1 [gene] locus=C58477178_1:1:600:+[Lack both ends]"
"rumen100058_GL1672120_1 [gene] locus=scaffold51761_1:1999:2880:+[Lack 3'-end]", "rumen3042_GL1999019_1 [gene] locus=scaffold1526490_3:1:882:-[Lack both ends]"
"rumen100058_GL1733252_1 [gene] locus=scaffold1969723_1:1:432:+[Lack 5'-end]", "rumen2009040_GL0377437_1 [gene] locus=scaffold643565_2:123:554:-[Lack 5'-end]"
"rumen100058_GL1742050_1 [gene] locus=scaffold2118762_1:3:614:-[Lack both ends]"
"rumen100058_GL1832360_1 [gene] locus=scaffold4654_1:1:960:-[Lack both ends]"
"rumen100058_GL1863710_1 [gene] locus=scaffold735331_2:2:847:+[Lack 5'-end]"
"rumen100058_GL1942038_1 [gene] locus=scaffold1704790_1:1:807:+[Lack 5'-end]"
"rumen100058_GL1966424_1 [gene] locus=scaffold1699302_1:231:1298:-[Lack 5'-end]"
"rumen100058_GL2002393_1 [gene] locus=scaffold2632189_2:2:640:-[Lack both ends]"
"rumen100058_GL2044991_1 [gene] locus=C59153038_1:1:717:-[Lack both ends]"
"rumen100058_GL2093037_1 [gene] locus=scaffold1802786_4:1:750:-[Lack both ends]"
"rumen100058_GL2119256_1 [gene] locus=scaffold491945_1:57:554:+[Lack 3'-end]"
"rumen100058_GL2124701_1 [gene] locus=scaffold903292_1:1:1467:+[Lack both ends]"

["rumen100058_GL2154870_1 [gene] locus=scaffold2411437_1:2:577:-[Lack both ends]", "rumen3042_GL2123395_1 [gene] locus=scaffold2337499_2:740:1315:+[Lack 3'-end]"]
["rumen100058_GL2161628_1 [gene] locus=scaffold1091202_10:2443:3210:-[Lack 5'-end]", "rumen7049_GL1201810_1 [gene] locus=scaffold1800922_1:1:765:+[Lack both ends]"]
["rumen100058_GL2223364_1 [gene] locus=scaffold797009_2:82:1173:-[Lack 5'-end]"]
["rumen100058_GL2284088_1 [gene] locus=scaffold1927667_1:280:1044:-[Lack 5'-end]"]
["rumen100058_GL2284288_1 [gene] locus=C59357534_1:1:765:+[Lack both ends]", "rumen7049_GL1233574_1 [gene] locus=scaffold702118_1:3:767:-[Lack both ends]"]
["rumen100058_GL2306076_1 [gene] locus=scaffold3338912_1:2:985:-[Lack both ends]"]
["rumen100058_GL2313150_1 [gene] locus=scaffold428931_3:1:498:-[Lack both ends]"]
["rumen100058_GL2365617_1 [gene] locus=scaffold462401_1:3:731:-[Lack both ends]"]
["rumen100058_GL2418955_1 [gene] locus=scaffold639873_4:1:507:+[Lack both ends]"]
["rumen100058_GL2423702_1 [gene] locus=scaffold2748936_1:1:1071:+[Lack 5'-end]"]
["rumen100058_GL2519575_1 [gene] locus=scaffold2762265_3:2:634:+[Lack 5'-end]"]
["rumen100058_GL2676087_1 [gene] locus=scaffold661069_1:3:761:+[Lack both ends]"]
["rumen100058_GL2686420_1 [gene] locus=scaffold837914_2:1593:2132:-[Lack 5'-end]", "rumen100058_GL2781152_1 [gene] locus=scaffold1985187_1:2:541:+[Lack 5'-end]", "rumen100058_GL3309756_1 [gene] locus=scaffold363913_2_1:2:541:+[Lack 5'-end]", "rumen2009040_GL3107657_1 [gene] locus=scaffold1949313_1:1:540:+[Lack 5'-end]"]
["rumen100058_GL2822485_1 [gene] locus=scaffold1219105_2:3055:3753:+[Lack 3'-end]"]
["rumen100058_GL2901305_1 [gene] locus=scaffold57323_3:3:527:+[Lack both ends]"]
["rumen100058_GL2999709_1 [gene] locus=scaffold2889118_1:2:544:+[Lack both ends]"]
["rumen100058_GL3013027_1 [gene] locus=scaffold2805555_1:1:573:-[Lack both ends]", "rumen3042_GL2705622_1 [gene] locus=scaffold1332620_1:2:574:-[Lack both ends]"]
["rumen100058_GL3051751_1 [gene] locus=scaffold1406293_7:566:1837:-[Complete]"]
["rumen100058_GL3144445_1 [gene] locus=scaffold1670612_1:2:535:-[Lack both ends]"]
["rumen100058_GL3221420_1 [gene] locus=scaffold2843119_1:2:409:-[Lack 3'-end]"]
["rumen100058_GL3356970_1 [gene] locus=scaffold189592_1:2:862:-[Lack both ends]"]
["rumen100058_GL3520852_1 [gene] locus=scaffold3335149_1:3:734:+[Lack 5'-end]"]
["rumen100058_GL3529071_1 [gene] locus=scaffold504382_1:1:1005:+[Lack 5'-end]"]
["rumen100058_GL3536391_1 [gene] locus=scaffold1916298_8:396:827:+[Lack 3'-end]"]
["rumen100058_GL3596268_1 [gene] locus=scaffold998408_2:1500:1928:+[Lack 3'-end]"]
["rumen100058_GL3684077_1 [gene] locus=scaffold1020301_2:2:463:+[Lack 5'-end]"]
["rumen100058_GL3761704_1 [gene] locus=scaffold3344023_1:1:618:+[Lack 5'-end]"]
["rumen100058_GL3859024_1 [gene] locus=scaffold485768_2:1:555:+[Lack both ends]"]
["rumen2009040_GL0019714_1 [gene] locus=scaffold2196920_1:1:651:+[Lack 5'-end]"]
["rumen2009040_GL0033547_1 [gene] locus=scaffold2996455_1:3:704:-[Lack 3'-end]"]
["rumen2009040_GL0148138_1 [gene] locus=scaffold728582_1:56:766:-[Lack 5'-end]"]
["rumen2009040_GL0160630_1 [gene] locus=scaffold1253254_3:3:494:+[Lack 5'-end]"]
["rumen2009040_GL0218699_1 [gene] locus=scaffold1339460_1:3:440:-[Lack 3'-end]"]
["rumen2009040_GL0224302_1 [gene] locus=scaffold2988751_1:2:811:-[Lack 3'-end]", "rumen7049_GL1713502_1 [gene] locus=scaffold1801653_3:2:811:+[Lack both ends]"]
["rumen2009040_GL0270988_1 [gene] locus=scaffold1454338_3:2:559:+[Lack both ends]"]

["rumen2009040_GL0357720_1 [gene] locus=scaffold1779755_3:1:588:+[Lack both ends]"]
["rumen2009040_GL0474796_1 [gene] locus=scaffold2421990_1:2:1006:+[Lack both ends]"]
["rumen2009040_GL0480478_1 [gene] locus=scaffold897786_1:2:763:-[Lack 3'-end]"]
["rumen2009040_GL0488748_1 [gene] locus=scaffold409690_2:303:998:+[Lack 3'-end]", "rumen3042_GL1408264_1 [gene] locus=scaffold1569385_3:30:725:+[Lack 3'-end]"]
["rumen2009040_GL0498920_1 [gene] locus=scaffold416704_2:2:661:+[Lack 5'-end]"]
["rumen2009040_GL0551496_1 [gene] locus=scaffold1667458_2:147:572:-[Lack 5'-end]", "rumen2009040_GL1985329_1 [gene] locus=scaffold624415_1:341:766:-[Lack 5'-end]"]
["rumen2009040_GL0607240_1 [gene] locus=scaffold2281443_8:2:799:+[Lack 5'-end]"]
["rumen2009040_GL0633993_1 [gene] locus=scaffold75155_3:1447:2619:+[Complete]", "cazygl 332181646 gb AEE17334.1  glycosidase related protein [Treponema brennaborensis DSM 12168]"]
["rumen2009040_GL0673296_1 [gene] locus=scaffold2641184_4:2:901:+[Lack 5'-end]"]
["rumen2009040_GL0678530_1 [gene] locus=scaffold2678330_1:3:1004:+[Lack 5'-end]"]
["rumen2009040_GL0693900_1 [gene] locus=scaffold95706_2:2:502:+[Lack both ends]", "rumen2009040_GL1576731_1 [gene] locus=scaffold2943023_1:2:502:-[Lack both ends]"]
["rumen2009040_GL0697332_1 [gene] locus=C55196181_1:740:1150:-[Lack 5'-end]"]
["rumen2009040_GL0791868_1 [gene] locus=scaffold1078780_2:1:1059:+[Lack 5'-end]"]
["rumen2009040_GL0818151_1 [gene] locus=scaffold2914414_1:2:544:+[Lack 5'-end]"]
["rumen2009040_GL0859896_1 [gene] locus=scaffold1256819_3:1157:2290:-[Lack 5'-end]"]
["rumen2009040_GL0895446_1 [gene] locus=scaffold582346_1:3:734:+[Lack 5'-end]"]
["rumen2009040_GL0895532_1 [gene] locus=scaffold693684_1:3:1010:+[Lack 5'-end]"]
["rumen2009040_GL0897993_1 [gene] locus=scaffold1783831_1:1:939:+[Lack both ends]"]
["rumen2009040_GL0974319_1 [gene] locus=scaffold2038548_1:1:990:+[Lack 5'-end]"]
["rumen2009040_GL0996574_1 [gene] locus=scaffold12975_1:839:1795:+[Lack 3'-end]"]
["rumen2009040_GL1049229_1 [gene] locus=scaffold2453597_1:1:825:+[Lack 5'-end]"]
["rumen2009040_GL1088314_1 [gene] locus=scaffold3070946_1:1:573:+[Lack 5'-end]", "rumen3042_GL1979964_1 [gene] locus=scaffold1170010_2:74:646:-[Lack 5'-end]"]
["rumen2009040_GL1094453_1 [gene] locus=scaffold2150285_1:1:678:+[Lack 5'-end]"]
["rumen2009040_GL1163272_1 [gene] locus=scaffold705478_1:1:831:+[Lack 5'-end]"]
["rumen2009040_GL1215461_1 [gene] locus=scaffold1334207_1:845:1318:+[Lack 3'-end]"]
["rumen2009040_GL1227174_1 [gene] locus=scaffold2582807_1:1:501:-[Lack both ends]"]
["rumen2009040_GL1297949_1 [gene] locus=scaffold2677149_1:457:882:+[Lack 3'-end]"]
["rumen2009040_GL1305280_1 [gene] locus=scaffold3002734_1:54934:56220:+[Complete]"]
["rumen2009040_GL1309675_1 [gene] locus=C54365707_1:192:755:+[Lack 3'-end]", "rumen2009040_GL2211219_1 [gene] locus=scaffold437521_1:1:564:-[Lack 3'-end]"]
["rumen2009040_GL1331816_1 [gene] locus=scaffold2978926_1:3:632:-[Lack 3'-end]"]
["rumen2009040_GL1417614_1 [gene] locus=scaffold992072_4:1:507:+[Lack both ends]"]
["rumen2009040_GL1438960_1 [gene] locus=scaffold1407695_3:3:530:+[Lack both ends]"]
["rumen2009040_GL1641622_1 [gene] locus=scaffold3013358_1:3:434:-[Lack 3'-end]"]
["rumen2009040_GL1656174_1 [gene] locus=scaffold1358075_2:1:792:-[Lack 3'-end]", "rumen3042_GL0867391_1 [gene] locus=scaffold1508821_2:1:792:-[Lack 3'-end]"]
["rumen2009040_GL1663378_1 [gene] locus=scaffold389369_2:10005:10607:-[Lack 5'-end]", "rumen7049_GL0447593_1 [gene] locus=scaffold1934473_3:1:603:+[Lack 5'-end]"]

["rumen2009040_GL1688301_1 [gene] locus=scaffold5458_4:2:991:+[Lack 5'-end]"]
["rumen2009040_GL1717716_1 [gene] locus=scaffold3054854_1:3:842:-[Lack both ends]"]
["rumen2009040_GL1749906_1 [gene] locus=scaffold2046819_1:2:643:+[Lack both ends]"]
["rumen2009040_GL1761748_1 [gene] locus=scaffold2804267_1:88:549:-[Lack 5'-end]"]
["rumen2009040_GL1807313_1 [gene] locus=C53084701_1:1:468:-[Lack 3'-end]"]
["rumen2009040_GL1842570_1 [gene] locus=scaffold783087_2:83:526:+[Lack 3'-end]"]
["rumen2009040_GL1938062_1 [gene] locus=scaffold2528382_1:262:1254:+[Lack 3'-end]", "rumen2009040_GL2485922_1 [gene] locus=scaffold48956_3:539:1531:+[Lack 3'-end]", "rumen2009040_GL2916504_1 [gene] locus=scaffold417233_1:3:995:-[Lack 3'-end]"]
["rumen2009040_GL2025858_1 [gene] locus=scaffold2345354_1:1:567:+[Lack both ends]"]
["rumen2009040_GL2050729_1 [gene] locus=scaffold396189_10:6479:8968:+[Complete]"]
["rumen2009040_GL2064896_1 [gene] locus=scaffold1767939_1:1:585:+[Lack both ends]"]
["rumen2009040_GL2070374_1 [gene] locus=scaffold921679_10:2:1225:+[Lack both ends]"]
["rumen2009040_GL2172593_1 [gene] locus=scaffold820164_8:431:952:+[Lack 3'-end]", "rumen3042_GL0215080_1 [gene] locus=C50220895_1:3:524:+[Lack both ends]"]
["rumen2009040_GL2243740_1 [gene] locus=scaffold3000142_1:447:1289:-[Lack 5'-end]", "rumen7049_GL1920804_1 [gene] locus=scaffold15914_1:1:843:+[Lack 5'-end]"]
["rumen2009040_GL2249617_1 [gene] locus=scaffold1670928_1:2:1240:+[Lack 5'-end]"]
["rumen2009040_GL2271978_1 [gene] locus=scaffold773586_1:3:587:-[Lack both ends]"]
["rumen2009040_GL2331927_1 [gene] locus=scaffold2424432_5:3:1103:+[Lack 5'-end]"]
["rumen2009040_GL2393911_1 [gene] locus=scaffold2981852_1:1:663:+[Lack both ends]"]
["rumen2009040_GL2418094_1 [gene] locus=scaffold1388705_2:1018:1464:+[Lack 3'-end]"]
["rumen2009040_GL2438299_1 [gene] locus=C54306259_1:215:742:+[Lack 3'-end]"]
["rumen2009040_GL2485217_1 [gene] locus=scaffold2673757_1:559:1587:-[Lack 5'-end]", "rumen7049_GL1880013_1 [gene] locus=C53224398_1:413:1441:-[Lack 5'-end]"]
["rumen2009040_GL2529504_1 [gene] locus=scaffold1866361_5:2:643:+[Lack 5'-end]"]
["rumen2009040_GL2570907_1 [gene] locus=scaffold2401081_2:2:919:+[Lack both ends]"]
["rumen2009040_GL2610461_1 [gene] locus=C54775105_1:380:859:-[Complete]"]
["rumen2009040_GL2643327_1 [gene] locus=scaffold862223_1:3:1091:+[Lack both ends]"]
["rumen2009040_GL2709124_1 [gene] locus=C54511778_1:3:797:+[Lack both ends]"]
["rumen2009040_GL2721007_1 [gene] locus=scaffold1171574_2:8401:9675:-[Complete]"]
["rumen2009040_GL2733548_1 [gene] locus=scaffold851585_2:682:1527:-[Lack 5'-end]"]
["rumen2009040_GL2738335_1 [gene] locus=scaffold965356_3:3:581:-[Lack both ends]"]
["rumen2009040_GL2949201_1 [gene] locus=scaffold1286518_1:5832:7055:+[Complete]"]
["rumen2009040_GL2985393_1 [gene] locus=scaffold33866_2:177:599:-[Lack 5'-end]"]
["rumen2009040_GL3014932_1 [gene] locus=scaffold1934946_2:3:941:+[Lack both ends]"]
["rumen2009040_GL3032962_1 [gene] locus=scaffold2608996_1:713:1159:+[Lack 3'-end]"]
["rumen2009040_GL3047245_1 [gene] locus=scaffold389369_3:2:532:-[Lack 3'-end]"]
["rumen2009040_GL3078576_1 [gene] locus=scaffold2277849_4:1051:2241:+[Complete]"]
["rumen2009040_GL3142931_1 [gene] locus=scaffold1863408_1:1:513:+[Lack both ends]"]
["rumen2009040_GL3145717_1 [gene] locus=scaffold3049593_1:1:549:+[Lack 5'-end]"]
["rumen2009040_GL3238168_1 [gene] locus=scaffold1928698_1:1:579:+[Lack both ends]"]
["rumen2009040_GL3249940_1 [gene] locus=scaffold143873_2:1:651:-[Lack both ends]"]

["rumen2009040_GL3261152_1 [gene] locus=scaffold238312_2:2:520:-[Lack both ends]"]
["rumen2009040_GL3301528_1 [gene] locus=C54978614_1:3:686:-[Lack 3'-end]"]
["rumen2009040_GL3327642_1 [gene] locus=scaffold2312858_1:2:538:-[Lack both ends]"]
["rumen2009040_GL3389735_1 [gene] locus=scaffold2257468_5:497:943:-[Lack 5'-end]"]
["rumen2009040_GL3484547_1 [gene] locus=scaffold2191915_1:2:673:+[Lack both ends]"]
["rumen2009040_GL3501091_1 [gene] locus=scaffold2196175_1:2:715:-[Lack 3'-end]"]
["rumen2009040_GL3586942_1 [gene] locus=scaffold363271_2:3:506:+[Lack 5'-end]"]
["rumen2009040_GL3650488_1 [gene] locus=scaffold1244479_2:141:725:+[Lack 3'-end]"]
["rumen2009040_GL3659099_1 [gene] locus=scaffold1585469_2:3:713:+[Lack 5'-end]"]
["rumen2009040_GL3660357_1 [gene] locus=scaffold3065062_2:1825:2694:-[Lack 5'-end]"]
["rumen3042_GL0000077_1 [gene] locus=scaffold1572661_1:1:558:+[Lack both ends]"]
["rumen3042_GL0032891_1 [gene] locus=scaffold2042204_4:2:514:-[Lack 3'-end]"]
["rumen3042_GL0081640_1 [gene] locus=scaffold1163097_1:817:1590:+[Lack 3'-end]"]
["rumen3042_GL0082423_1 [gene] locus=C50851480_1:3:626:+[Lack both ends]"]
["rumen3042_GL0360627_1 [gene] locus=scaffold338216_3:1956:3143:+[Complete]"]
["rumen3042_GL0486652_1 [gene] locus=C50290333_1:2:535:-[Lack both ends]"]
["rumen3042_GL0507881_1 [gene] locus=C50438823_1:3:554:-[Lack both ends]"]
["rumen3042_GL0529802_1 [gene] locus=scaffold166668_2:1:546:-[Lack 3'-end]"]
["rumen3042_GL0590771_1 [gene] locus=C50713299_1:3:599:-[Lack both ends]"]
["rumen3042_GL0640649_1 [gene] locus=scaffold613841_7:2022:2600:+[Lack 3'-end]"]
["rumen3042_GL0649954_1 [gene] locus=C50870129_1:3:629:-[Lack both ends]"]
["rumen3042_GL0670870_1 [gene] locus=scaffold856979_2:2:841:+[Lack 5'-end]"]
["rumen3042_GL0712183_1 [gene] locus=scaffold652095_2:3:506:+[Lack both ends]"]
["rumen3042_GL0822304_1 [gene] locus=scaffold1113388_2:2:751:-[Lack 3'-end]"]
["rumen3042_GL1082206_1 [gene] locus=scaffold1465853_1:1:435:+[Lack 5'-end]"]
["rumen3042_GL1098498_1 [gene] locus=scaffold2069073_1:3714:5009:+[Complete]"]
["rumen3042_GL1107395_1 [gene] locus=scaffold1093396_4:5500:5928:+[Lack 3'-end]"]
["rumen3042_GL1207560_1 [gene] locus=scaffold680221_1:3:605:-[Lack both ends]"]
["rumen3042_GL1383982_1 [gene] locus=scaffold832128_3:2:517:+[Lack 5'-end]"]
["rumen3042_GL1395732_1 [gene] locus=scaffold9535_3:41:526:-[Lack 5'-end]"]
["rumen3042_GL1401776_1 [gene] locus=scaffold1017850_7:1243:1728:+[Lack 3'-end]"]
["rumen3042_GL1442982_1 [gene] locus=scaffold1276484_2:2:868:-[Lack 3'-end]"]
["rumen3042_GL1513349_1 [gene] locus=scaffold522873_2:1:1053:+[Lack both ends]"]
["rumen3042_GL1529368_1 [gene] locus=scaffold1435774_1:884:1336:+[Lack 3'-end]"]
["rumen3042_GL1545277_1 [gene] locus=scaffold895734_1:1:600:+[Lack both ends]"]
["rumen3042_GL1599579_1 [gene] locus=scaffold960666_2:482:895:+[Lack 3'-end]"]
["rumen3042_GL1611192_1 [gene] locus=scaffold1102841_4:1:393:+[Lack 5'-end]"]
["rumen3042_GL1626821_1 [gene] locus=scaffold826559_15:2:874:+[Lack 5'-end]"]
["rumen3042_GL1789684_1 [gene] locus=scaffold1371059_3:1:483:-[Lack 3'-end]"]
["rumen3042_GL1953498_1 [gene] locus=scaffold1144998_5:2:718:-[Lack 3'-end]"]
["rumen3042_GL1980838_1 [gene] locus=scaffold5434_2:598:1038:-[Lack 5'-end]"]
["rumen3042_GL2039966_1 [gene] locus=scaffold1913087_5:1:1059:+[Lack 5'-end]"]
["rumen3042_GL2046699_1 [gene] locus=scaffold1462991_2:1:519:-[Lack both ends]"]



["rumen3042_GL2187846_1 [gene] locus=scaffold832128_2:1:609:+[Lack both ends]"]
["rumen3042_GL2213686_1 [gene] locus=scaffold320746_6:1:573:-[Lack both ends]"]
["rumen3042_GL2285557_1 [gene] locus=scaffold308203_2:121:573:-[Lack 5'-end]"]
["rumen3042_GL2300975_1 [gene] locus=scaffold2062302_3:1:603:+[Lack 5'-end]"]
["rumen3042_GL2356167_1 [gene] locus=C52066558_1:469:1275:+[Lack 3'-end]"]
["rumen3042_GL2378167_1 [gene] locus=scaffold2466948_1:1:582:-[Lack both ends]"]
["rumen3042_GL2417136_1 [gene] locus=scaffold700330_1:2:406:-[Lack 3'-end]"]
["rumen3042_GL2527931_1 [gene] locus=scaffold2529999_1:1:516:+[Lack 5'-end]"]
["rumen552_GL0039216_1 [gene] locus=scaffold1080482_1:836:2038:-[Complete]"]
["rumen552_GL0085050_1 [gene] locus=scaffold540319_1:677:1840:-[Complete]", "rumen552_GL0154928_1 [gene] locus=scaffold1115299_1:12069:13232:-[Complete]", "rumen0081_GL1513998_1 [gene] locus=scaffold722337_2:362:1525:+[Complete]", "rumen2009040_GL0484223_1 [gene] locus=scaffold842821_3:813:1976:-[Complete]", "rumen3042_GL0831827_1 [gene] locus=scaffold1802866_1:1918:3081:-[Complete]", "rumen3042_GL2393851_1 [gene] locus=scaffold2033295_1:570:1733:+[Complete]"]
["rumen552_GL0242863_1 [gene] locus=scaffold459412_2:3:590:-[Lack both ends]"]
["rumen552_GL0286565_1 [gene] locus=scaffold110901_2:3:890:-[Lack 3'-end]"]
["rumen552_GL0369668_1 [gene] locus=scaffold46347_2:2:643:+[Lack both ends]"]
["rumen552_GL0500598_1 [gene] locus=scaffold214801_2:7619:8800:-[Complete]"]
["rumen552_GL0548147_1 [gene] locus=scaffold281878_2:57425:58606:-[Complete]", "rumen555_GL2221632_1 [gene] locus=scaffold391993_1:93:1274:-[Complete]", "rumen100058_GL3492508_1 [gene] locus=scaffold373571_1:732:1913:+[Complete]", "rumen2009040_GL3559534_1 [gene] locus=scaffold1810933_1:279:1460:+[Complete]", "rumen3042_GL1654790_1 [gene] locus=scaffold246360_2:789:1970:+[Complete]"]
["rumen552_GL0582563_1 [gene] locus=scaffold470902_1:1:993:+[Lack both ends]", "rumen555_GL1019427_1 [gene] locus=scaffold132038_1:81:1073:+[Lack 3'-end]"]
["rumen552_GL0699265_1 [gene] locus=scaffold586952_1:16201:17385:-[Complete]"]
["rumen552_GL0721882_1 [gene] locus=scaffold524092_2:48285:49523:+[Complete]", "rumen0081_GL1802801_1 [gene] locus=scaffold174182_1:5853:7091:-[Complete]", "rumen2009040_GL1532117_1 [gene] locus=scaffold587927_2:1686:2924:-[Complete]", "rumen2009040_GL1575957_1 [gene] locus=scaffold489926_1:1242:2480:+[Complete]"]
["rumen552_GL0771921_1 [gene] locus=scaffold1027624_4:1:705:+[Lack both ends]", "rumen100058_GL1497917_1 [gene] locus=scaffold331685_6:1088:1795:-[Lack 5'-end]"]
["rumen552_GL0777748_1 [gene] locus=scaffold422006_1:1:1014:+[Lack 5'-end]"]
["rumen552_GL0840318_1 [gene] locus=scaffold255115_3:3:491:-[Lack 3'-end]"]
["rumen552_GL0844521_1 [gene] locus=scaffold713861_5:3010:3741:-[Lack 5'-end]"]
["rumen552_GL1249044_1 [gene] locus=scaffold369563_1:1:537:+[Lack 5'-end]"]
["rumen552_GL1264658_1 [gene] locus=scaffold290549_2:1467:2054:-[Lack 5'-end]"]
["rumen552_GL1417868_1 [gene] locus=scaffold954837_1:2:469:-[Lack 3'-end]"]
["rumen552_GL1478576_1 [gene] locus=scaffold576867_1:3:818:-[Lack 3'-end]"]
["rumen552_GL1487998_1 [gene] locus=scaffold1064081_2:102:1091:+[Lack 3'-end]"]
["rumen552_GL1503956_1 [gene] locus=scaffold149647_1:938:1633:-[Lack 5'-end]", "rumen100058_GL1685929_1 [gene] locus=scaffold556929_2:2:697:+[Lack 5'-end]"]

"rumen100058_GL2854153_1 [gene] locus=scaffold1175549_1:1:696:+[Lack 5'-end]"
"rumen552_GL1568100_1 [gene] locus=C21196678_1:1:471:-[Lack 3'-end]", "rumen100058_GL3505946_1 [gene] locus=scaffold3284786_1:128:598:+[Lack 3'-end]"
"rumen552_GL1593398_1 [gene] locus=C21827437_1:1:834:+[Lack both ends]"
"rumen552_GL1689901_1 [gene] locus=scaffold921789_1:2:652:-[Lack 3'-end]"
"rumen553_GL0032227_1 [gene] locus=scaffold284480_1:221:850:-[Lack 5'-end]"
"rumen553_GL0049253_1 [gene] locus=scaffold182048_1:151:612:-[Lack 5'-end]"
"rumen553_GL0094054_1 [gene] locus=scaffold44886_6:2:589:+[Lack both ends]"
"rumen553_GL0104245_1 [gene] locus=scaffold48459_1:2:826:-[Lack 3'-end]", "rumen553_GL0163953_1 [gene] locus=scaffold433511_1:2:826:-[Lack 3'-end]"
"rumen553_GL0105999_1 [gene] locus=scaffold57686_1:8066:9217:-[Complete]", "rumen552_GL0631529_1 [gene] locus=scaffold1026447_1:1848:2999:-[Complete]", "rumen552_GL1141348_1 [gene] locus=scaffold649643_3:278:1429:-[Complete]", "rumen554_GL2237796_1 [gene] locus=scaffold1021761_3:371:1522:+[Complete]", "rumen555_GL0791420_1 [gene] locus=scaffold55176_1:556:1707:+[Complete]", "rumen555_GL1977253_1 [gene] locus=scaffold429328_2:2885:4036:-[Complete]", "rumen0081_GL0347789_1 [gene] locus=scaffold9084_2:355:1506:-[Complete]", "rumen3042_GL1357986_1 [gene] locus=scaffold830021_2:1113:2264:-[Complete]"
"rumen553_GL0120895_1 [gene] locus=scaffold9924_1:135:1016:+[Lack 3'-end]"
"rumen553_GL0127650_1 [gene] locus=C7765883_1:13079:14320:-[Complete]"
"rumen553_GL0136564_1 [gene] locus=scaffold102846_5:7726:8931:-[Lack 5'-end]", "rumen554_GL1996354_1 [gene] locus=scaffold248758_5:29404:30609:-[Complete]"
"rumen553_GL0136884_1 [gene] locus=scaffold122658_7:2:1009:+[Lack 5'-end]"
"rumen553_GL0187129_1 [gene] locus=scaffold8660_4:476:1657:-[Complete]", "rumen583_GL0789265_1 [gene] locus=scaffold123359_1:399:1580:-[Complete]", "rumen554_GL0152551_1 [gene] locus=scaffold949638_2:1511:2692:+[Complete]", "rumen555_GL1400296_1 [gene] locus=scaffold364272_1:352:1533:+[Complete]", "rumen100058_GL0097486_1 [gene] locus=scaffold749237_1:3946:5127:-[Complete]", "rumen100058_GL2831528_1 [gene] locus=scaffold2732103_1:1612:2793:+[Complete]", "rumen7049_GL1440001_1 [gene] locus=scaffold1049146_2:1557:2738:-[Complete]"
"rumen553_GL0188465_1 [gene] locus=scaffold25813_1:490:1578:-[Lack 5'-end]"
"rumen553_GL0334707_1 [gene] locus=scaffold201627_1:2:376:-[Lack 3'-end]"
"rumen553_GL0387359_1 [gene] locus=scaffold335962_2:45:1277:-[Lack 5'-end]"
"rumen553_GL0579940_1 [gene] locus=scaffold192080_2:2:559:+[Lack both ends]"
"rumen553_GL0598510_1 [gene] locus=scaffold112080_2:1983:2696:+[Lack 3'-end]", "rumen553_GL0892836_1 [gene] locus=scaffold24477_5:1:714:+[Lack both ends]", "rumen0081_GL1007375_1 [gene] locus=scaffold731738_1:120:833:+[Lack 3'-end]"
"rumen553_GL0617458_1 [gene] locus=C7520020_1:1:828:-[Lack 3'-end]", "rumen100058_GL1891813_1 [gene] locus=scaffold2096473_3:183:1010:+[Lack 3'-end]"
"rumen553_GL0781215_1 [gene] locus=scaffold432384_1:202:1281:-[Lack 5'-end]", "rumen555_GL0742391_1 [gene] locus=C28670528_1:2:1078:-[Lack 3'-end]"
"rumen553_GL0807801_1 [gene] locus=scaffold92562_2:5954:7120:-[Complete]", "rumen2009040_GL0346636_1 [gene] locus=scaffold808408_2:7184:8350:-[Complete]"

<p>"rumen553_GL0862617_1 [gene] locus=scaffold105027_1:238:792:-[Lack 5'-end]",</p> <p>"rumen7049_GL2283102_1 [gene] locus=C51488427_1:1:552:+[Lack both ends]"</p>
<p>"rumen553_GL0904326_1 [gene] locus=scaffold329167_4:2:697:-[Lack both ends]"</p>
<p>"rumen553_GL0907209_1 [gene] locus=scaffold177577_1:3:716:+[Lack 5'-end]",</p> <p>"rumen100058_GL3039379_1 [gene] locus=scaffold832335_7:1260:1973:-[Lack 5'-end]",</p> <p>"rumen100058_GL3231998_1 [gene] locus=scaffold2351752_5:1:714:+[Lack 5'-end]",</p> <p>"rumen3042_GL1141595_1 [gene] locus=scaffold419096_2:1:714:+[Lack 5'-end]"</p>
<p>"rumen553_GL0917056_1 [gene] locus=scaffold217147_1:2:664:-[Lack 3'-end]"</p>
<p>"rumen554_GL0012127_1 [gene] locus=scaffold42727_2:140:1063:+[Lack 3'-end]"</p>
<p>"rumen554_GL0054969_1 [gene] locus=scaffold813972_1:100:762:+[Lack 3'-end]"</p>
<p>"rumen554_GL0085145_1 [gene] locus=scaffold1234497_1:3:797:-[Lack both ends]"</p>
<p>"rumen554_GL0100604_1 [gene] locus=scaffold1392860_1:2:520:+[Lack both ends]"</p>
<p>"rumen554_GL0125272_1 [gene] locus=scaffold13977_1:381:944:+[Lack 3'-end]"</p>
<p>"rumen554_GL0182616_1 [gene] locus=scaffold39392_1:29403:30608:+[Complete]",</p> <p>"rumen554_GL0850290_1 [gene] locus=scaffold492265_1:1435:2640:-[Complete]",</p> <p>"rumen100058_GL0954979_1 [gene] locus=scaffold1877489_1:1440:2645:-[Complete]",</p> <p>"rumen7049_GL1761271_1 [gene] locus=scaffold2267949_1:415:1620:+[Complete]"</p>
<p>"rumen554_GL0240059_1 [gene] locus=scaffold1824264_2:250:699:+[Lack 3'-end]"</p>
<p>"rumen554_GL0292759_1 [gene] locus=scaffold683178_1:83:1333:+[Complete]"</p>
<p>"rumen554_GL0300352_1 [gene] locus=scaffold1652984_1:2:745:-[Lack 3'-end]"</p>
<p>"rumen554_GL0332523_1 [gene] locus=scaffold1493107_1:603:1754:-[Complete]",</p> <p>"rumen554_GL2352802_1 [gene] locus=scaffold1127205_3:5530:6681:+[Complete]",</p> <p>"rumen0081_GL2416988_1 [gene] locus=scaffold845286_7:645:1796:+[Complete]",</p> <p>"rumen2009040_GL2887569_1 [gene] locus=scaffold60859_4:5530:6681:+[Complete]"</p>
<p>"rumen554_GL0346167_1 [gene] locus=scaffold2052939_1:2:469:-[Lack 3'-end]"</p>
<p>"rumen554_GL0354756_1 [gene] locus=C40912160_1:3:980:+[Lack both ends]"</p>
<p>"rumen554_GL0396792_1 [gene] locus=scaffold162544_1:3309:4517:+[Complete]"</p>
<p>"rumen554_GL0401470_1 [gene] locus=scaffold919471_1:2:691:-[Lack 3'-end]"</p>
<p>"rumen554_GL0500642_1 [gene] locus=scaffold1202093_1:3:695:+[Lack 5'-end]"</p>
<p>"rumen554_GL0572441_1 [gene] locus=scaffold1666900_4:3:959:-[Lack 3'-end]",</p> <p>"rumen0081_GL0118621_1 [gene] locus=scaffold2020316_1:3:959:-[Lack 3'-end]",</p> <p>"rumen2009040_GL1577303_1 [gene] locus=scaffold1931446_5:1354:2310:+[Lack 3'-end]"</p>
<p>"rumen554_GL0573574_1 [gene] locus=scaffold2141052_1:1:1023:+[Lack 5'-end]"</p>
<p>"rumen554_GL0645103_1 [gene] locus=scaffold1346050_1:3:569:+[Lack both ends]",</p> <p>"rumen2009040_GL3553905_1 [gene] locus=scaffold2776935_3:3:569:+[Lack both ends]"</p>
<p>"rumen554_GL0657441_1 [gene] locus=scaffold334047_1:3:851:+[Lack 5'-end]",</p> <p>"rumen554_GL1500979_1 [gene] locus=scaffold1433067_1:2:850:+[Lack 5'-end]"</p>
<p>"rumen554_GL0672460_1 [gene] locus=scaffold208804_1:3:500:+[Lack 5'-end]",</p> <p>"rumen0081_GL2431247_1 [gene] locus=scaffold341010_2:124:621:-[Lack 5'-end]"</p>
<p>"rumen554_GL0708177_1 [gene] locus=scaffold2154111_1:2:754:-[Lack 3'-end]"</p>
<p>"rumen554_GL0727547_1 [gene] locus=scaffold193632_3:3230:4390:-[Complete]",</p> <p>"rumen555_GL1401098_1 [gene] locus=scaffold783584_1:26596:27756:+[Complete]",</p> <p>"rumen7049_GL1553500_1 [gene] locus=scaffold983776_2:7381:8541:-[Complete]"</p>

["rumen554_GL0758983_1 [gene] locus=scaffold1120851_1:1455:2231:-[Lack 5'-end]", "rumen555_GL1872305_1 [gene] locus=C28685599_1:347:1123:-[Lack 5'-end]"]
["rumen554_GL0778519_1 [gene] locus=scaffold2116913_2:3:896:+[Lack both ends]", "rumen0081_GL1264715_1 [gene] locus=scaffold125895_1:436:1329:+[Lack 3'-end]"]
["rumen554_GL0806989_1 [gene] locus=scaffold1758895_1:2:634:-[Lack both ends]"]
["rumen554_GL0836579_1 [gene] locus=scaffold755456_1:546:1154:+[Lack 3'-end]"]
["rumen554_GL0851428_1 [gene] locus=scaffold1896722_1:1583:2515:-[Lack 5'-end]"]
["rumen554_GL0890659_1 [gene] locus=scaffold749086_3:328:1029:-[Lack 5'-end]"]
["rumen554_GL0911586_1 [gene] locus=scaffold462637_7:778:1446:-[Lack 5'-end]"]
["rumen554_GL0958608_1 [gene] locus=scaffold787818_2:1473:2315:+[Lack 3'-end]", "rumen0081_GL2325519_1 [gene] locus=scaffold1988499_1:149:991:+[Lack 3'-end]", "rumen100058_GL1509214_1 [gene] locus=scaffold79783_1:3:845:-[Lack both ends]", "rumen2009040_GL1742284_1 [gene] locus=scaffold661798_1:3:845:-[Lack both ends]", "rumen7049_GL1224206_1 [gene] locus=scaffold2079380_2:1:843:-[Lack 3'-end]"]
["rumen554_GL1022914_1 [gene] locus=scaffold3793_1:206:610:+[Lack 3'-end]"]
["rumen554_GL1061123_1 [gene] locus=scaffold2134084_2:1:675:+[Lack both ends]"]
["rumen554_GL1074776_1 [gene] locus=scaffold311408_3:3:869:+[Lack 5'-end]"]
["rumen554_GL1096009_1 [gene] locus=scaffold174776_5:1625:2503:+[Lack 3'-end]"]
["rumen554_GL1132063_1 [gene] locus=scaffold657036_2:2:523:-[Lack 3'-end]", "rumen7049_GL1194147_1 [gene] locus=scaffold857149_2:4142:4663:+[Lack 3'-end]"]
["rumen554_GL1135522_1 [gene] locus=scaffold61351_3:3:974:+[Lack 5'-end]", "rumen554_GL2325817_1 [gene] locus=scaffold2114121_1:1:969:+[Lack both ends]"]
["rumen554_GL1155624_1 [gene] locus=scaffold387244_1:2037:2528:+[Lack 3'-end]"]
["rumen554_GL1171239_1 [gene] locus=C40964752_1:2:679:-[Lack 3'-end]"]
["rumen554_GL1208580_1 [gene] locus=scaffold1415190_1:3:839:+[Lack 5'-end]"]
["rumen554_GL1280624_1 [gene] locus=scaffold1336613_1:18447:19637:-[Complete]"]
["rumen554_GL1300648_1 [gene] locus=scaffold619368_3:1944:2609:+[Lack 3'-end]", "rumen100058_GL1913305_1 [gene] locus=scaffold675000_2:184:849:+[Lack 3'-end]"]
["rumen554_GL1368563_1 [gene] locus=scaffold1146150_1:71:697:+[Lack 3'-end]"]
["rumen554_GL1412696_1 [gene] locus=C40619984_1:441:830:+[Lack 3'-end]"]
["rumen554_GL1421284_1 [gene] locus=scaffold426545_1:2:553:-[Lack both ends]"]
["rumen554_GL1650053_1 [gene] locus=scaffold937640_1:2:481:-[Lack 3'-end]"]
["rumen554_GL1663424_1 [gene] locus=scaffold1797843_1:3:1043:+[Lack 5'-end]"]
["rumen554_GL1697992_1 [gene] locus=scaffold33533_1:2:1036:-[Lack 3'-end]"]
["rumen554_GL1781224_1 [gene] locus=scaffold702412_4:875:1741:+[Complete]"]
["rumen554_GL1805054_1 [gene] locus=scaffold792886_2:129:506:+[Lack 3'-end]"]
["rumen554_GL1861872_1 [gene] locus=scaffold57384_2:835:1902:-[Lack 5'-end]"]
["rumen554_GL1911309_1 [gene] locus=scaffold971075_1:1645:2085:-[Lack 5'-end]", "rumen100058_GL0463803_1 [gene] locus=scaffold55392_3:499:939:-[Lack 5'-end]"]
["rumen554_GL1924440_1 [gene] locus=scaffold502985_2:2:607:+[Lack 5'-end]"]
["rumen554_GL1957605_1 [gene] locus=scaffold267550_10:3:632:+[Lack both ends]"]
["rumen554_GL2085541_1 [gene] locus=scaffold2042893_7:872:1465:+[Lack 3'-end]"]
["rumen554_GL2092833_1 [gene] locus=scaffold3184_1:1:648:+[Lack both ends]"]

"rumen554_GL2119682_1 [gene] locus=scaffold1385282_1:1:585:-[Lack both ends]"
"rumen554_GL2218541_1 [gene] locus=scaffold59206_4:1:414:+[Lack 5'-end]"
"rumen554_GL2219709_1 [gene] locus=scaffold546825_3:457:1224:+[Lack 3'-end]", "rumen554_GL2227990_1 [gene] locus=scaffold1191787_1:3:770:+[Lack both ends]"
"rumen554_GL2270870_1 [gene] locus=scaffold981268_5:38:706:-[Lack 5'-end]", "rumen100058_GL0745214_1 [gene] locus=scaffold412313_7:1547:2215:-[Lack 5'-end]"
"rumen554_GL2293751_1 [gene] locus=scaffold1981977_2:1:609:+[Lack both ends]"
"rumen554_GL2404831_1 [gene] locus=scaffold8458_1:3:641:+[Lack 5'-end]", "rumen555_GL1808978_1 [gene] locus=scaffold1488613_1:6603:7241:-[Lack 5'-end]", "rumen2009040_GL1927750_1 [gene] locus=scaffold1063027_4:72:710:-[Lack 5'-end]"
"rumen554_GL2519626_1 [gene] locus=C41442967_1:833:1621:-[Lack 5'-end]"
"rumen554_GL2531083_1 [gene] locus=scaffold921667_1:2:592:+[Lack both ends]"
"rumen554_GL2591305_1 [gene] locus=scaffold39542_1:3:899:+[Lack 5'-end]"
"rumen554_GL2591323_1 [gene] locus=scaffold115202_1:3:785:+[Lack both ends]"
"rumen554_GL2686984_1 [gene] locus=scaffold1713000_4:3:620:-[Lack 3'-end]"
"rumen554_GL2776916_1 [gene] locus=C39348879_1:3:488:+[Lack 5'-end]", "rumen0081_GL2388531_1 [gene] locus=scaffold789850_4:213:698:-[Lack 5'-end]"
"rumen554_GL2796675_1 [gene] locus=scaffold728367_1:2:1075:-[Lack 3'-end]"
"rumen554_GL2848765_1 [gene] locus=scaffold115438_6:10680:11390:+[Lack 3'-end]"
"rumen554_GL2884883_1 [gene] locus=scaffold633_1:1:621:+[Lack both ends]", "rumen3042_GL1065810_1 [gene] locus=scaffold1435381_1:1:621:-[Lack 3'-end]"
"rumen554_GL3132768_1 [gene] locus=scaffold1277686_1:3:857:-[Lack 3'-end]"
"rumen555_GL0080071_1 [gene] locus=scaffold666065_2:2:1123:-[Lack 3'-end]"
"rumen555_GL0104764_1 [gene] locus=scaffold935166_1:3:923:+[Lack both ends]"
"rumen555_GL0134205_1 [gene] locus=scaffold510840_2:1:561:+[Lack both ends]"
"rumen555_GL0170867_1 [gene] locus=scaffold731622_1:2:505:-[Lack both ends]"
"rumen555_GL0314564_1 [gene] locus=scaffold1305566_2:1:789:-[Lack 3'-end]"
"rumen555_GL0374273_1 [gene] locus=scaffold506691_1:55:1278:-[Complete]", "rumen2009040_GL2389521_1 [gene] locus=scaffold685648_3:51423:52646:-[Complete]"
"rumen555_GL0380294_1 [gene] locus=scaffold392642_1:1:828:+[Lack 5'-end]"
"rumen555_GL0410025_1 [gene] locus=C27283631_1:86:535:+[Lack 3'-end]"
"rumen555_GL0424271_1 [gene] locus=scaffold1136221_1:2439:3473:-[Lack 5'-end]"
"rumen555_GL0468659_1 [gene] locus=scaffold797069_3:2:514:+[Lack 5'-end]"
"rumen555_GL0498161_1 [gene] locus=scaffold373179_18:2731:3744:+[Complete]"
"rumen555_GL0517816_1 [gene] locus=C27940816_1:289:687:+[Lack 3'-end]"
"rumen555_GL0543964_1 [gene] locus=scaffold516737_1:2:448:-[Lack 3'-end]"
"rumen555_GL0590856_1 [gene] locus=C27343339_1:1:546:+[Lack both ends]"
"rumen555_GL0608207_1 [gene] locus=scaffold851016_3:1:651:+[Lack both ends]", "rumen3042_GL1063357_1 [gene] locus=scaffold256792_2:3:653:+[Lack both ends]"
"rumen555_GL0616059_1 [gene] locus=scaffold549975_1:2285:3433:-[Complete]"
"rumen555_GL0793359_1 [gene] locus=scaffold1234583_1:2038:3219:+[Complete]"
"rumen555_GL0858113_1 [gene] locus=scaffold709998_1:575:1765:-[Complete]"
"rumen555_GL0884194_1 [gene] locus=scaffold547954_4:2:1042:-[Lack 3'-end]"

["rumen555_GL0886278_1 [gene] locus=scaffold893410_2:2:397:+[Lack 5'-end]"]
["rumen555_GL0914457_1 [gene] locus=scaffold459220_5:304:753:+[Lack 3'-end]", "rumen2009040_GL0313435_1 [gene] locus=scaffold1369777_1:3:452:-[Lack 3'-end]"]
["rumen555_GL0969156_1 [gene] locus=scaffold591525_1:25703:26947:+[Complete]"]
["rumen555_GL1050486_1 [gene] locus=scaffold1305566_1:3890:4465:-[Lack 5'-end]"]
["rumen555_GL1111884_1 [gene] locus=scaffold1572667_1:3:1151:+[Lack 5'-end]"]
["rumen555_GL1158001_1 [gene] locus=scaffold1516884_1:2:505:-[Lack 3'-end]"]
["rumen555_GL1215771_1 [gene] locus=scaffold1328731_1:2781:4022:+[Complete]"]
["rumen555_GL1224500_1 [gene] locus=scaffold1462285_1:30:569:+[Complete]"]
["rumen555_GL1231214_1 [gene] locus=scaffold199175_2:1:1470:+[Lack 5'-end]"]
["rumen555_GL1231597_1 [gene] locus=scaffold797069_2:171:761:+[Lack 3'-end]"]
["rumen555_GL1245918_1 [gene] locus=scaffold985819_3:1:564:-[Lack both ends]"]
["rumen555_GL1293304_1 [gene] locus=scaffold818338_1:469:1542:-[Lack 5'-end]"]
["rumen555_GL1307302_1 [gene] locus=scaffold1428946_1:2:1210:-[Lack 3'-end]"]
["rumen555_GL1334155_1 [gene] locus=scaffold32475_4:267:914:-[Lack 5'-end]"]
["rumen555_GL1367432_1 [gene] locus=scaffold1293417_3:153:953:-[Lack 5'-end]"]
["rumen555_GL1418540_1 [gene] locus=scaffold41798_2:1:693:-[Lack 3'-end]"]
["rumen555_GL1584984_1 [gene] locus=scaffold622151_1:60:887:-[Lack 5'-end]", "rumen100058_GL0418175_1 [gene] locus=scaffold3166935_3:3:827:-[Lack both ends]"]
["rumen555_GL1625263_1 [gene] locus=scaffold1471599_1:1:1044:+[Lack 5'-end]"]
["rumen555_GL1655219_1 [gene] locus=scaffold840906_1:1:996:+[Lack 5'-end]"]
["rumen555_GL1691522_1 [gene] locus=scaffold1028955_1:294:1319:+[Lack 3'-end]"]
["rumen555_GL1918429_1 [gene] locus=scaffold748424_1:374:925:-[Lack 5'-end]"]
["rumen555_GL1982210_1 [gene] locus=scaffold895244_1:123:1037:-[Lack 5'-end]"]
["rumen555_GL2151353_1 [gene] locus=scaffold1167006_4:2:1108:+[Lack 5'-end]", "rumen100058_GL3483883_1 [gene] locus=scaffold433089_4:65:1171:-[Lack 5'-end]"]
["rumen555_GL2243424_1 [gene] locus=scaffold803255_2:3:494:+[Lack 5'-end]"]
["rumen555_GL2319609_1 [gene] locus=scaffold1260338_1:3:557:-[Lack 3'-end]"]
["rumen583_GL0030501_1 [gene] locus=scaffold40597_2:1:777:-[Lack 3'-end]"]
["rumen583_GL0055845_1 [gene] locus=scaffold100224_1:1133:1585:+[Lack 3'-end]"]
["rumen583_GL0145131_1 [gene] locus=scaffold66916_3:28768:30021:+[Complete]"]
["rumen583_GL0167007_1 [gene] locus=scaffold322842_1:1388:2209:+[Lack 3'-end]"]
["rumen583_GL0252536_1 [gene] locus=scaffold276320_6:1:1017:+[Lack 5'-end]"]
["rumen583_GL0354459_1 [gene] locus=scaffold293415_1:1:519:+[Lack both ends]"]
["rumen583_GL0431108_1 [gene] locus=scaffold119251_4:2:517:+[Lack 5'-end]"]
["rumen583_GL0461410_1 [gene] locus=C5270796_1:1:714:+[Lack both ends]", "rumen7049_GL0846476_1 [gene] locus=scaffold24484_5:264:980:-[Lack 5'-end]"]
["rumen583_GL0579141_1 [gene] locus=scaffold234249_1:197:1411:+[Complete]"]
["rumen583_GL0593259_1 [gene] locus=scaffold225231_3:2:721:+[Lack 5'-end]", "rumen100058_GL0607858_1 [gene] locus=scaffold1877422_1:2:718:-[Lack both ends]", "rumen100058_GL1451096_1 [gene] locus=scaffold1746242_2:257:976:-[Lack 5'-end]"]
["rumen583_GL0597670_1 [gene] locus=scaffold154057_1:374:1330:-[Lack 5'-end]", "rumen100058_GL2039320_1 [gene] locus=scaffold1180521_2:2:958:+[Lack 5'-end]"]

"rumen583_GL0636884_1 [gene] locus=scaffold26514_5:882:1427:-[Lack 5'-end]", "rumen2009040_GL0487544_1 [gene] locus=scaffold2722183_1:223:768:-[Complete]", "rumen2009040_GL1346976_1 [gene] locus=scaffold626730_2:3:548:+[Lack 5'-end]"
"rumen583_GL0656802_1 [gene] locus=scaffold59857_3:1739:2713:+[Complete]", "rumen100058_GL2886937_1 [gene] locus=scaffold2331360_3:1:972:-[Lack 3'-end]"
"rumen583_GL0767689_1 [gene] locus=scaffold100224_2:3:638:+[Lack both ends]"
"rumen583_GL0812118_1 [gene] locus=scaffold266994_3:1:651:-[Lack 3'-end]", "rumen3042_GL0081189_1 [gene] locus=scaffold1626490_7:1:651:-[Lack 3'-end]"
"rumen583_GL0813063_1 [gene] locus=scaffold312526_2:2:682:+[Lack both ends]"
"rumen7049_GL0001507_1 [gene] locus=scaffold915750_2:1:939:-[Lack 3'-end]"
"rumen7049_GL0635957_1 [gene] locus=scaffold722081_2:1257:1841:-[Lack 5'-end]"
"rumen7049_GL0750973_1 [gene] locus=scaffold2063222_2:1:732:-[Lack both ends]"
"rumen7049_GL0773160_1 [gene] locus=scaffold1064_2:2:550:+[Lack both ends]"
"rumen7049_GL0819564_1 [gene] locus=scaffold670055_1:1:981:+[Lack both ends]"
"rumen7049_GL0824516_1 [gene] locus=scaffold1783065_1:1:576:+[Lack both ends]"
"rumen7049_GL0874726_1 [gene] locus=scaffold883397_2:1830:2708:+[Lack 3'-end]"
"rumen7049_GL0991234_1 [gene] locus=scaffold66671_4:242:1267:-[Lack 5'-end]"
"rumen7049_GL1119867_1 [gene] locus=scaffold941244_4:386:916:-[Lack 5'-end]"
"rumen7049_GL1221953_1 [gene] locus=scaffold504049_3:264:716:+[Lack 3'-end]"
"rumen7049_GL1261530_1 [gene] locus=scaffold374494_1:1:1098:+[Lack both ends]"
"rumen7049_GL1342434_1 [gene] locus=scaffold1452838_3:2:823:+[Lack both ends]"
"rumen7049_GL1413700_1 [gene] locus=scaffold908729_2:1207:1842:-[Lack 5'-end]", "rumen7049_GL1873633_1 [gene] locus=scaffold1229850_4:1:636:+[Lack 5'-end]"
"rumen7049_GL1419103_1 [gene] locus=scaffold868215_1:3:461:-[Lack 3'-end]"
"rumen7049_GL1433169_1 [gene] locus=scaffold10855_1:1347:1850:-[Lack 5'-end]"
"rumen7049_GL1449797_1 [gene] locus=C51701869_1:130:588:-[Lack 5'-end]"
"rumen7049_GL1453544_1 [gene] locus=scaffold101548_2:1:531:-[Lack 3'-end]"
"rumen7049_GL1497820_1 [gene] locus=scaffold493989_1:4930:5994:-[Lack 5'-end]"
"rumen7049_GL1500999_1 [gene] locus=scaffold62117_3:195:1394:+[Complete]"
"rumen7049_GL1521773_1 [gene] locus=scaffold1170887_1:622:999:-[Lack 5'-end]"
"rumen7049_GL1574378_1 [gene] locus=C53010378_1:1:696:-[Lack 3'-end]"
"rumen7049_GL1590078_1 [gene] locus=scaffold908729_3:3:488:-[Lack 3'-end]"
"rumen7049_GL1679621_1 [gene] locus=scaffold2270630_1:1549:1947:+[Lack 3'-end]"
"rumen7049_GL1693159_1 [gene] locus=scaffold1907593_1:1:648:+[Lack both ends]"
"rumen7049_GL1716120_1 [gene] locus=scaffold941244_5:3:635:-[Lack both ends]"
"rumen7049_GL1762123_1 [gene] locus=scaffold1969850_1:1:864:+[Lack 5'-end]"
"rumen7049_GL1787872_1 [gene] locus=scaffold1367840_2:675:1865:-[Lack 5'-end]"
"rumen7049_GL1899143_1 [gene] locus=scaffold1590_1:3:848:-[Lack 3'-end]"
"rumen7049_GL2019771_1 [gene] locus=scaffold1894819_1:1:564:+[Lack both ends]"
"rumen7049_GL2123004_1 [gene] locus=scaffold738795_1:3:551:-[Lack 3'-end]"
"rumen7049_GL2128689_1 [gene] locus=C51355634_1:3:533:+[Lack both ends]"
"rumen7049_GL2182956_1 [gene] locus=scaffold289278_3:2:595:+[Lack both ends]"
"rumen7049_GL2213947_1 [gene] locus=scaffold752687_1:1:1125:+[Lack 5'-end]"

["rumen7049_GL2255690_1 [gene] locus=scaffold794849_1:1:558:+[Lack both ends]"]
["rumen7049_GL2506635_1 [gene] locus=scaffold2227300_1:3:932:-[Lack 3'-end]"]
["rumen7049_GL2742621_1 [gene] locus=scaffold355448_2:3:719:-[Lack both ends]"]
["rumen7049_GL2804323_1 [gene] locus=scaffold872623_1:760:1713:+[Lack 3'-end]"]

## C2

<p>["Ncazy AOC96454.1 Beta-1", "4-mannooligosaccharide phosphorylase [Flavobacterium anhuiense]",</p> <p>"cazy APA00252.1 glycosidase [Flavobacterium commune]",</p> <p>"cazy APY11541.1 glycosidase [Seonamhaeicola sp. S2-3]",</p> <p>"cazy ASO06391.1 1", "4-beta-mannosyl-N-acetylglucosamine phosphorylase [Arenibacter algicola]",</p> <p>"cazy AUC86603.1 glycosidase [Polaribacter sp. ALD11]",</p> <p>"cazy AWK06410.1 glycosidase [Flavobacterium sp. HYN0056]",</p> <p>"cazy AXB58136.1 glycosidase [Flavobacterium sp. HYN0086]",</p> <p>"cazy AXP81458.1 Beta-1-2C4-mannooligosaccharide phosphorylase [Mariniflexile sp. TRM1-10]",</p> <p>"cazy SNV15478.1 Domain of uncharacterised function (DUF377) [Capnocytophaga haemolytica]",</p> <p>"mouseMH-6-5_GL0077448 [gene] locus=scaffold46635_4:2:967:+ [Lack 5'-end] codon-table.11",</p> <p>"pigPIG-035_GL0077892 [gene] locus=scaffold14328_3:1498:2463:+ [Complete] codon-table.11",</p> <p>"pigPIG-108_GL0039825 [gene] locus=scaffold57191_1:13352:14317:+ [Complete] codon-table.11",</p> <p>"pigBMZ-3B_GL0032359 [gene] locus=scaffold6698_1:4687:5652:- [Complete] codon-table.11",</p> <p>"cazy 987450434 gb AMD85874.1  glycosidase [Capnocytophaga haemolytica]",</p> <p>"cazy 1042791627 gb ANQ52194.1  Glycosidase", "PH1107-related protein [Flammeovirga sp. MY04]",</p> <p>"cazy 146299793 ref ABQ05065.1 protein of unknown function [Flavobacterium johnsoniae UW101]",</p> <p>"cazy 295136005 ref YP_003586681.1  glycosidase", "PH1107-related protein [Zunongwangia profunda SM-A87]"</p>
<p>["Ncazy AOE12712.1 glycoside hydrolase family GH130 [uncultured bacterium]",</p> <p>"humangutV1.CD49-0_GL0178648 [gene] locus=C1383269_1:2:985:+ [Lack 5'-end] codon-table.11",</p> <p>"mouse7-1_GL0006877 [gene] locus=scaffold28884_1:13416:14399:+ [Complete] codon-table.11"]</p>
<p>["cazy CCg 29338339 gb AAO76140.1 β-1", "4-mannosyl-N-acetyl-glucosamine phosphorylase_Glycosidase",</p> <p>"PH117-related [Bacteroides thetaiotaomicron VPI-5482]",</p> <p>"cazy AQW92214.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy AQW95541.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy AQW99395.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy AQX03135.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy AQX05903.1 glycosidase [Elizabethkingia meningoseptica]",</p> <p>"cazy AQX07161.1 glycosidase [Elizabethkingia ursingii]",</p> <p>"cazy AQX13441.1 glycosidase [Elizabethkingia meningoseptica]",</p> <p>"cazy AQX47946.1 glycosidase [Elizabethkingia meningoseptica]",</p> <p>"cazy AQX51719.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy AQX84796.1 glycosidase [Elizabethkingia bruuniana]",</p> <p>"cazy AQX89941.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy ASF42136.1 glycosidase [Capnocytophaga sp. ChDC OS43]",</p> <p>"cazy ASM66972.1 glycosidase [Bacteroides caccae]",</p> <p>"cazy ASV79260.1 glycosidase [Elizabethkingia anophelis]",</p> <p>"cazy ATA1779.1 glycosidase [Capnocytophaga sputigena]",</p> <p>"cazy ATA73462.1 glycosidase [Capnocytophaga sp. H4358]"</p>



"cazy|ATA75602.1 glycosidase [Capnocytophaga sp. H2931]",

"cazy|ATA79533.1 glycosidase [Capnocytophaga sputigena]",

"cazy|ATA81942.1 glycosidase [Capnocytophaga leadbetteri]",

"cazy|ATA84218.1 glycosidase [Capnocytophaga sputigena]",

"cazy|ATC35103.1 glycosidase [Elizabethkingia anophelis R26]",

"cazy|ATC38743.1 glycosidase [Elizabethkingia anophelis Ag1]",

"cazy|ATC42423.1 glycosidase [Elizabethkingia anophelis]",

"cazy|ATC46099.1 glycosidase [Elizabethkingia anophelis]",

"cazy|ATL42797.1 glycosidase [Elizabethkingia miricola]",

"cazy|AVF48974.1 glycosidase [Elizabethkingia anophelis]",

"cazy|AVF52970.1 glycosidase [Elizabethkingia anophelis]",

"cazy|AVM50848.1 glycosidase [Capnocytophaga sp. oral taxon 878]",

"cazy|AVM52247.1 glycosidase [Bacteroides zoogloeiformans]",

"cazy|AVM55807.1 glycosidase [Capnocytophaga sp. oral taxon 864]",

"cazy|AVM57240.1 glycosidase [Bacteroides heparinolyticus]",

"cazy|AXT60144.1 glycosidase [Aquimarina sp. AD10]",

"cazy|BAX82697.1 glycosidase [Marinifilaceae bacterium SPP2]",

"cazy|SQG05129.1 Domain of uncharacterised function (DUF377) [Elizabethkingia meningoseptica]",

"humangutMH0057\_GL0025508 [gene] locus=scaffold20903\_2:8407:9375:+ [Complete] codon-table.11",

"humangutMH0094\_GL0075083 [gene] locus=scaffold20371\_4:10147:11115:- [Complete] codon-table.11",

"humangutMH0180\_GL0060341 [gene] locus=scaffold40469\_3:2382:3350:- [Complete] codon-table.11",

"humangutMH0192\_GL0125589 [gene] locus=scaffold34340\_4:2230:3198:+ [Complete] codon-table.11",

"humangutMH0195\_GL0063025 [gene] locus=scaffold81533\_1:535:1503:- [Complete] codon-table.11",

"humangutMH0265\_GL0056765 [gene] locus=scaffold21250\_3:6389:7357:- [Complete] codon-table.11",

"humangutMH0267\_GL0071113 [gene] locus=scaffold55979\_12:1266:2234:+ [Complete] codon-table.11",

"humangutV1\_CD38-0\_GL0037456 [gene] locus=scaffold62129\_1:8666:9634:+ [Complete] codon-table.11",

"humangutNOF010\_GL0024541 [gene] locus=scaffold35262\_1:25950:26918:- [Complete] codon-table.11",

"humangut667015.Bacsa\_0833 [Complete]:- codon-table.11",

"mouseS-Fe11\_GL0049040 [gene] locus=scaffold17840\_1:11592:12560:+ [Complete] codon-table.11",

"mouseMC-0-3\_GL0054853 [gene] locus=scaffold40460\_5:1928:2896:+ [Complete] codon-table.11",

"mouseMH-6-2\_GL0126099 [gene] locus=C1058985\_1:441:1409:+ [Complete] codon-table.11",

"mouse1A-dyr2-07\_GL0039762 [gene] locus=scaffold31161\_8:3072:4040:- [Complete] codon-table.11",

"mouse1A-dyr3-06\_GL0049008 [gene] locus=scaffold27804\_1:49829:50797:- [Complete] codon-table.11",

"pigPIG-012\_GL0107830 [gene] locus=scaffold39655\_5:3:971:+ [Lack 5'-end] codon-table.11",

"cazy|937962574|gb|ALJ04189.1| glycosidase [Algibacter alginolytica]",

"cazy|938481019|gb|ALJ45250.1| Beta-1",

"4-mannooligosaccharide phosphorylase [Bacteroides ovatus]",

"cazy|324317535|gb|ADY35426.1| glycosidase related protein [Bacteroides salanitronis DSM 18170]",

"cazy|1045272850|gb|ANU57541.1| glycosidase [Bacteroides sp. I48]",

"cazy|938477956|gb|ALJ42188.1| Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides thetaiotaomicron]",

"cazy|925194212|gb|ALC97496.1| glycosidase [Capnocytophaga sp. oral taxon 323]",

"cazy|1016605761|gb|AMX50831.1| glycosidase [Elizabethkingia anophelis]",

"cazy|1008914301|gb|AMR40735.1| glycosidase [Elizabethkingia anophelis]",

"cazy|1016609433|gb|AMX54223.1| glycosidase [Elizabethkingia anophelis]",

<p>"cazygi 1016602074 gb AMX47371.1  glycosidase [Elizabethkingia anophelis]",</p> <p>"cazygi 822827313 gb AKH94537.1  glycosidase [Elizabethkingia anophelis FMS-007]",</p> <p>"cazygi 675104695 gb AIL45988.1  putative glycoside hydrolase [Elizabethkingia anophelis NUHP1]",</p> <p>"cazygi 769869730 gb AJW61972.1  Beta-1", "4-mannooligosaccharide phosphorylase [Elizabethkingia miricola"]</p>
<p><b>["cazyCCgi 315447097 gb ADU20661.1 β-1", "4-mannooligosaccharide phosphorylase_glycosidase related protein [Ruminococcus albus 7 = DSM 20455]",</b></p> <p>"humangutMH0031_GL0006535 [gene] locus=scaffold3940_2:1147:2154:+ [Complete] codon-table.11",</p> <p>"humangutMH0150_GL0052407 [gene] locus=scaffold31033_23:1372:2379:- [Complete] codon-table.11",</p> <p>"humangutMH0181_GL0015422 [gene] locus=scaffold27717_21:1:1008:+ [Lack 5'-end] codon-table.11",</p> <p>"humangutMH0309_GL0012678 [gene] locus=scaffold72956_5:115:1122:+ [Complete] codon-table.11",</p> <p>"humangutMH0454_GL0213341 [gene] locus=scaffold65847_2:10038:11045:- [Complete] codon-table.11",</p> <p>"humangutV1_UC28-0_GL0123124 [gene] locus=scaffold14894_6:2515:3522:- [Complete] codon-table.11",</p> <p>"pigPIG-035_GL0150811 [gene] locus=scaffold77973_1:143:1150:- [Complete] codon-table.11",</p> <p>"pigDB-510B_GL0109450 [gene] locus=scaffold4200_5:4485:5492:+ [Complete] codon-table.11",</p> <p>"rumen554_GL2190451_1 [gene] locus=scaffold172783_2:11618:12625:-[Complete]",</p> <p>"rumen555_GL2013701_1 [gene] locus=scaffold871485_2:30014:31021:-[Complete]",</p> <p>"rumen0081_GL0613719_1 [gene] locus=scaffold142497_1:5484:6491:+[Complete]"</p>
<p><b>["cazyCCgi 651373346 ref WP_026486574.1 β-1", "4-mannooligosaccharide phosphorylase_glycosidase [Caldanaerobius polysaccharolyticus]",</b></p> <p>"cazy SYX87324.1 Beta-1", "4-mannooligosaccharide phosphorylase [Paenibacillus alvei]",</p> <p>"humangutSZEY-10A_GL0075713 [gene] locus=scaffold7737_2:779:1768:- [Complete] codon-table.11",</p> <p>"pigPIG-025_GL0011031 [gene] locus=scaffold97882_7:54798:55787:- [Complete] codon-table.11",</p> <p>"pigBMZ-2B_GL0067583 [gene] locus=scaffold34040_5:693:1682:- [Complete] codon-table.11"]</p>
<p><b>["cazyCCgi 651374303 ref WP_026486530.1 β-1", "4-mannooligosaccharide phosphorylase_glycosidase [Caldanaerobius polysaccharolyticus]",</b></p> <p><b>"cazyCCgi 290769685 gb ADD61463.1 β-1", "4-mannopyranosyl-chitobiose phosphorylase_putative protein [uncultured organism]",</b></p> <p>"humangutMH0262_GL0010724 [gene] locus=scaffold78173_1:3824:4807:+ [Complete] codon-table.11",</p> <p>"humangutMH0409_GL0042854 [gene] locus=scaffold25953_9:34462:35445:+ [Complete] codon-table.11",</p> <p>"rumen0081_GL0258022_1 [gene] locus=scaffold711522_2:1072:2055:+[Complete]",</p> <p>"rumen0081_GL2439589_1 [gene] locus=scaffold395692_2:368:1351:-[Complete]"</p>
<p><b>["cazyCCgi VCV21229.1 Beta-1", "4-mannooligosaccharide phosphorylase [Roseburia intestinalis L1-82]",</b></p> <p>"cazy AOZ96975.1 glycoside hydrolase GH130 family [Butyrivibrio hungatei]",</p> <p>"cazy ASU28438.1 glycosylase [Blautia coccooides]",</p> <p>"cazy AVM41763.1 glycosylase [Fastidiosipila sanguinis]",</p> <p>"humangutMH0001_GL0012726 [gene] locus=scaffold3748_3:819:1841:- [Complete] codon-table.11",</p> <p>"humangutMH0006_GL0069640 [gene] locus=scaffold5771_4:3021:4043:+ [Complete] codon-table.11",</p> <p>"humangutMH0014_GL0030038 [gene] locus=scaffold35967_1:870:1892:- [Complete] codon-table.11",</p> <p>"humangutMH0016_GL0060919 [gene] locus=scaffold9428_5:8292:9314:+ [Complete] codon-table.11",</p> <p>"humangutMH0100_GL0160312 [gene] locus=scaffold5389_46:50:1072:- [Complete] codon-table.11",</p> <p>"humangutMH0113_GL0020570 [gene] locus=scaffold17102_3:3989:5011:- [Complete] codon-table.11",</p> <p>"humangutMH0161_GL0096554 [gene] locus=scaffold96080_1:27178:28200:+ [Complete] codon-table.11",</p> <p>"humangutMH0200_GL0131567 [gene] locus=scaffold17224_1:5843:6865:- [Complete] codon-table.11",</p> <p>"humangutMH0206_GL0049502 [gene] locus=scaffold17212_7:15:1037:- [Complete] codon-table.11",</p> <p>"humangutMH0260_GL0146482 [gene] locus=scaffold13264_11:14013:15035:+ [Complete] codon-table.11",</p> <p>"humangutMH0355_GL0026988 [gene] locus=scaffold59455_8:4866:5888:- [Complete] codon-table.11",</p> <p>"humangutMH0385_GL0153945 [gene] locus=scaffold37197_11:1272:2294:- [Complete] codon-table.11",</p> <p>"humangutMH0457_GL0198107 [gene] locus=scaffold43943_6:397:1419:+ [Complete] codon-table.11",</p>

"humangutN006A\_GL0085957 [gene] locus=scaffold41619\_8:1261:2283:- [Complete] codon-table.11",

"humangutSZEY-79A\_GL0037345 [gene] locus=scaffold32900\_1:485:1507:- [Complete] codon-table.11",

"mouseS-Fe2\_GL0205548 [gene] locus=scaffold57199\_1:713:1735:+ [Complete] codon-table.11",

"mouseS-Fe2\_GL0160681 [gene] locus=scaffold84515\_1:47520:48542:+ [Complete] codon-table.11",

"mouseS-Fe8\_GL0202731 [gene] locus=scaffold84136\_4:27806:28828:+ [Complete] codon-table.11",

"mouseMC-6-1\_GL0102368 [gene] locus=scaffold72393\_2:2860:3882:+ [Complete] codon-table.11",

"mouseG1-6A\_GL0054348 [gene] locus=scaffold28780\_5:666:1688:- [Complete] codon-table.11",

"mouseGroup2-2A\_GL0001769 [gene] locus=scaffold194\_1:17837:18859:+ [Complete] codon-table.11",

"mouseGroup2-3A\_GL0134533 [gene] locus=scaffold80199\_2:5686:6708:- [Complete] codon-table.11",

"mouseGroup2-8A\_GL0147180 [gene] locus=scaffold121907\_8:187:1209:- [Complete] codon-table.11",

"mouse1-2\_GL0016004 [gene] locus=scaffold39337\_1:2456:3478:- [Complete] codon-table.11",

"mouse1-5\_GL0036818 [gene] locus=scaffold26302\_1:432:1454:+ [Complete] codon-table.11",

"mouse2-2\_GL0045689 [gene] locus=scaffold54323\_1:17172:18194:+ [Complete] codon-table.11",

"mouse2-2\_GL0076416 [gene] locus=scaffold14974\_4:38683:39705:+ [Complete] codon-table.11",

"mouse2-8\_GL0082818 [gene] locus=scaffold10824\_2:7864:8886:- [Complete] codon-table.11",

"mouse29\_GL0004046 [gene] locus=scaffold98111\_2:4515:5537:- [Complete] codon-table.11",

"mouse35\_GL0008205 [gene] locus=scaffold1654\_3:3:1025:+ [Lack 5'-end] codon-table.11",

"mouse3-6\_GL0009577 [gene] locus=scaffold63212\_1:5348:6370:- [Complete] codon-table.11",

"mouse4-8\_GL00099500 [gene] locus=scaffold61328\_1:16433:17455:+ [Complete] codon-table.11",

"mouse5-1\_GL0032036 [gene] locus=scaffold24858\_2:6076:7098:- [Complete] codon-table.11",

"mouse54\_GL0098345 [gene] locus=scaffold38839\_3:2141:3163:+ [Complete] codon-table.11",

"mouse6-1\_GL0086336 [gene] locus=scaffold3735\_1:19621:20643:+ [Complete] codon-table.11",

"mouse6-2\_GL0056583 [gene] locus=scaffold27523\_9:5660:6682:- [Complete] codon-table.11",

"mouse6-7\_GL0056546 [gene] locus=scaffold18483\_2:3407:4429:+ [Complete] codon-table.11",

"pigPIG\_111\_GL0242587 [gene] locus=scaffold89853\_4:107:1129:- [Complete] codon-table.11",

"pigPIG\_144\_GL0102691 [gene] locus=scaffold2700\_5:26267:27289:- [Complete] codon-table.11",

"pigPIG\_154\_GL0044208 [gene] locus=scaffold38224\_2:2109:3131:+ [Complete] codon-table.11",

"pigPIG\_200\_GL0062716 [gene] locus=scaffold108665\_2:246:1268:+ [Complete] codon-table.11",

"pigPIG\_203\_GL0064463 [gene] locus=scaffold62405\_17:956:1978:- [Complete] codon-table.11",

"pigPIG-001\_GL0136661 [gene] locus=scaffold53466\_8:426:1448:- [Complete] codon-table.11",

"pigPIG-001\_GL0159825 [gene] locus=scaffold36090\_4:86:1108:- [Complete] codon-table.11",

"pigPIG-017\_GL0131674 [gene] locus=scaffold766\_5:2554:3576:+ [Complete] codon-table.11",

"pigPIG-017\_GL0236531 [gene] locus=scaffold70193\_4:1219:2241:- [Complete] codon-table.11",

"pigPIG-022\_GL0089756 [gene] locus=scaffold1106\_5:6704:7726:- [Complete] codon-table.11",

"pigPIG-023\_GL0120565 [gene] locus=scaffold148282\_1:76406:77428:+ [Complete] codon-table.11",

"pigPIG-033\_GL0092555 [gene] locus=scaffold78260\_5:2658:3680:- [Complete] codon-table.11",

"pigPIG-033\_GL0102692 [gene] locus=scaffold73245\_1:1720:2742:- [Complete] codon-table.11",

"pigPIG-044\_GL0139261 [gene] locus=scaffold51992\_17:1438:2460:- [Complete] codon-table.11",

"pigPIG-062\_GL0130920 [gene] locus=scaffold91288\_2:9032:10054:+ [Complete] codon-table.11",

"pigPIG-101\_GL0023440 [gene] locus=scaffold56096\_1:2464:3486:- [Complete] codon-table.11",

"pigPIG-106\_GL0046631 [gene] locus=scaffold17851\_9:6645:7667:- [Complete] codon-table.11",

"pigBHZ-10B\_GL0009433 [gene] locus=scaffold124559\_4:1863:2885:- [Complete] codon-table.11",

"pigDB-537B\_GL0144100 [gene] locus=scaffold128039\_1:995:2017:- [Complete] codon-table.11",

"pigZXZ-4B\_GL0116412 [gene] locus=scaffold118720\_2:639:1661:+ [Complete] codon-table.11",

"rumen553_GL0055107_1 [gene] locus=scaffold382495_2:1147:2169:-[Complete]",
"rumen553_GL0598340_1 [gene] locus=scaffold368919_2:79:1101:-[Complete]",
"rumen553_GL0620791_1 [gene] locus=scaffold430590_1:63846:64868:+[Complete]",
"rumen553_GL0811323_1 [gene] locus=scaffold250358_2:5650:6672:-[Complete]",
"rumen552_GL0864442_1 [gene] locus=scaffold148924_1:2:1024:-[Complete]",
"rumen552_GL1341759_1 [gene] locus=scaffold137436_3:150:1172:-[Complete]",
"rumen583_GL0067054_1 [gene] locus=scaffold295777_3:45:1067:-[Complete]",
"rumen583_GL0091770_1 [gene] locus=scaffold324703_1:59880:60902:+[Complete]",
"rumen583_GL0159580_1 [gene] locus=scaffold172591_7:10669:11691:-[Complete]",
"rumen583_GL0325327_1 [gene] locus=scaffold76910_2:7448:8470:-[Complete]",
"rumen583_GL0385135_1 [gene] locus=scaffold19862_2:43:1065:-[Complete]",
"rumen554_GL1823485_1 [gene] locus=scaffold1579573_1:191:1213:-[Complete]",
"rumen554_GL2137295_1 [gene] locus=scaffold640047_1:47573:48595:+[Complete]",
"rumen0081_GL1932850_1 [gene] locus=scaffold808879_5:5307:6329:-[Complete]",
"rumen100058_GL0302441_1 [gene] locus=scaffold915010_2:1165:2187:-[Complete]",
"rumen100058_GL0492646_1 [gene] locus=scaffold317403_3:2586:3608:-[Complete]",
"rumen100058_GL2403505_1 [gene] locus=scaffold276030_2:11:1033:-[Complete]",
"rumen2009040_GL3471506_1 [gene] locus=scaffold135228_1:761:1783:-[Complete]",
"cazygi 1045290885 gb ANU75635.1  glycosylase [Blautia sp. YL58]",
"cazygi 326543194 gb ADZ85053.1  glycosidase related protein [Clostridium lentocellum DSM 5427]",
"cazygi 326543232 gb ADZ85091.1  glycosidase related protein [Clostridium lentocellum DSM 5427]",
"cazygi 160429064 gb ABX42627.1  glycosidase PH1107-related [Lachnoclostridium phytofermentans ISDg]",
"cazygi 345502713 gb AEN97396.1  glycosidase related protein [Roseburia hominis A2-183]",
"cazygi 291537318 emb CBL10430.1  Predicted glycosylase [Roseburia intestinalis M50/1]",
"cazygi 291539264 emb CBL12375.1  Predicted glycosylase [Roseburia intestinalis XB6B4]",
"cazygi 663097292 gb AIF25950.1  putative glycosidase related protein [uncultured bacterium Ad_091_F22_contig1]",
"cazygi 663097607 gb AIF26243.1  putative glycosidase related protein [uncultured bacterium Lq_007_G03]"
["cazygi 1003108889 gb AMO13191.1  glycoside hydrolase [uncultured bacterium]"]
["cazygi 1015666995 gb AMW33356.1  glycosidase [Fervidobacterium islandicum]"]
["cazygi 1027790250 emb CUS05925.1  Beta-1", "4-mannooligosaccharide phosphorylase [Ardenticatena]"]
["cazygi 1033477965 dbj BAV13072.1  glycosidase PH1107-related [Clostridium cellulovorans]"]
["cazygi 1049076866 gb ANX01044.1  glycosylase [[Clostridium] stercorarium subsp. leptospartum DSM 9219]",
"cazygi 472398958 gb AGI39157.1  mannosylglucose phosphorylase [[Clostridium] stercorarium subsp. stercorarium DSM 8532]",
"cazygi 1049074312 gb ANW98510.1  glycosylase [[Clostridium] stercorarium subsp. thermolacticum DSM 2910]"
["cazygi 160428527 gb ABX42090.1  glycosidase PH1107-related [Lachnoclostridium phytofermentans ISDg]"]
["cazygi 217337279 gb ACK43072.1  glycosidase PH1107-related [Dictyoglomus turgidum DSM 6724]"
["cazygi 220000694 gb ACL77295.1  glycosidase PH1107-related [[Clostridium] cellulolyticum H10]",
"cazygi 373946951 gb AEY67872.1  putative glycosylase [Clostridium sp. BNL1100]"
["cazygi 221572710 gb ACM23522.1  Glycosidase [Thermotoga neapolitana DSM 4359]",
"cazygi 752580911 gb AJG41424.1  glycosylase [Thermotoga sp. RQ7]"
["cazygi 222457361 gb ACM61623.1  glycosidase PH1107-related [Caldicellulosiruptor bescii DSM 6725]",
"cazygi 311776547 gb ADQ06033.1  glycosidase related protein [Caldicellulosiruptor hydrothermalis 108]",
"cazygi 312181485 gb ADQ41655.1  glycosidase related protein [Caldicellulosiruptor kristjanssonii 177R1B]",
"cazygi 312201880 gb ADQ45207.1  glycosidase related protein [Caldicellulosiruptor kronotskyensis 2002]",

"cazygi 343963799 gb AEM72946.1  glycosidase related protein [Caldicellulosiruptor lactoaceticus 6A]", "cazygi 302575635 gb ADL43426.1  glycosidase related protein [Caldicellulosiruptor obsidiansis OB47]", "cazygi 145408938 gb ABP65942.1  glycosidase", " PH1107-related protein [Caldicellulosiruptor saccharolyticus DSM 8903]"
["cazygi 256581110 gb ACU92245.1  glycosidase PH1107-related [Capnocytophaga ochracea DSM 7271]"
["cazygi 290770046 gb ADD61810.1  putative protein [uncultured organism]", "rumen553_GL0441395_1 [gene] locus=scaffold84340_2:101227:102339:+[Complete]", "cazygi 291541075 emb CBL14186.1  Predicted glycosylase [Roseburia intestinalis XB6B4]"
["cazygi 302578870 gb ADL52882.1  glycosidase related protein [Clostridium cellulovorans 743B]"
["cazygi 306531529 gb ADN01063.1  putative glycosylase [Spirochaeta thermophila DSM 6192]"
["cazygi 315473032 gb ADU29635.1  glycosidase related protein [Bacillus cellulosilyticus DSM 2522]", "cazygi 1000297352 gb AML27054.1  putative glycosidase [Bacillus sp. N16-5]"
["cazygi 332181648 gb AEE17336.1  glycosidase related protein [Treponema brennaborense DSM 12168]"
["cazygi 332699916 gb AEE96857.1  glycosidase related protein [Mahella australiensis 50-1 BON]"
["cazygi 339410796 gb AEJ60361.1  glycosidase related protein [Spirochaeta thermophila DSM 6578]"
["cazygi 339903322 gb AEK24401.1  Hypothetical protein Ccan_22860 [Capnocytophaga canimorsus Cc5]"
["cazygi 374843357 emb CCF12061.1  hypothetical protein [Paenibacillus sp. Q8]"
["cazygi 383110288 gb AFG35891.1  putative glycosylase [Fervidobacterium pennivorans DSM 9078]", "cazygi 1028458698 gb ANE41631.1  glycosidase [Fervidobacterium pennivorans]", "cazygi 217036715 gb ACJ75237.1  conserved hypothetical protein [Thermosiphon africanus TCF52B]"
["cazygi 395812581 gb AFN75330.1  glycosidase PH1107-related protein [Melioribacter roseus P3M-2]"
["cazygi 407728372 dbj BAM48370.1  hypothetical protein AXY_22380 [Amphibacillus xylanus NBRC 15112]", "cazygi 686549368 gb AIQ60064.1  glycosylase [Paenibacillus borealis]", "cazygi 686557139 gb AIQ67833.1  glycosylase [Paenibacillus graminis]", "cazygi 806911815 emb CQR54423.1  Beta-1", "4-mannooligosaccharide phosphorylase [Paenibacillus riograndensis SBR5]", "cazygi 686520597 gb AIQ31298.1  glycosylase [Paenibacillus sp. FSL P4-0081]"
["cazygi 430024079 gb AGA35561.1  glycoside hydrolase family 43", " partial [Caldanaerobius polysaccharolyticus]"
["cazygi 663097319 gb AIF25974.1  putative glycosidase related protein [uncultured bacterium Ad_095_K16_contig2]"
["cazygi 673067760 emb CD225115.1  Beta-1", "4-mannooligosaccharide phosphorylase [[Clostridium] cellulosi]"
["cazygi 686549812 gb AIQ60508.1  glycosylase [Paenibacillus borealis]"
["cazygi 744796446 gb AJC74022.1  glycosylase [Pseudothromotoga hypogea DSM 11164 = NBRC 106472]", "cazygi 157314894 gb ABV33993.1  glycosidase PH1107-related [Pseudothromotoga lettingae TMO]", "cazygi 4981779 gb AAD36300.1 AE001779_2 conserved hypothetical protein [Thermotoga maritima MSB8]", "cazygi 811642464 gb AKE30873.1  glycosylase [Thermotoga maritima]", "cazygi 811630537 gb AKE27136.1  glycosylase [Thermotoga maritima]", "cazygi 281374081 gb ADA67643.1  glycosidase PH1107-related protein [Thermotoga naphthophila RKU-10]", "cazygi 147736211 gb ABQ47551.1  glycosidase", " PH1107-related [Thermotoga petrophila RKU-1]", "cazygi 728865928 gb AIY87108.1  glycosidase PH1107-related protein [Thermotoga sp. 2812B]", "cazygi 728867658 gb AIY88837.1  glycosidase PH1107-related protein [Thermotoga sp. Cell2]", "cazygi 170176877 gb ACB09929.1  glycosidase PH1107-related [Thermotoga sp. RQ2]"
["cazygi 991824681 gb AMF93030.1  glycosylase [Vibrio fluvialis]", "cazygi 1042390254 gb ANQ24661.1  glycosylase [Vibrio natriegens]"
["cazy AOK90367.1 glycosylase [Paenibacillus polymyxa]", "cazy APB69117.1 glycosylase [Paenibacillus polymyxa]",

<p>"cazy APB73775.1 glycosylase [Paenibacillus polymyxa]",</p> <p>"cazy APQ61721.1 glycosylase [Paenibacillus polymyxa]",</p> <p>"cazy ASR45398.1 glycosylase [Paenibacillus kribbensis]",</p> <p>"cazy AUO06681.1 glycosylase [Paenibacillus sp. lzh-N1]",</p> <p>"cazy AUS29142.1 glycosylase [Paenibacillus polymyxa]",</p> <p>"cazygi 920791914 gb ALA44433.1  glycosylase [Paenibacillus peoriae]",</p> <p>"cazygi 723615828 gb AIY09201.1  glycosylase [Paenibacillus polymyxa]",</p> <p>"cazygi 565677752 gb AHC22322.1  glycosylase [Paenibacillus polymyxa CR1]",</p> <p>"cazygi 305860619 gb ADM72407.1  glycosylase [Paenibacillus polymyxa E681]",</p> <p>"cazygi 392305246 emb CCI71609.1  glycosidase [Paenibacillus polymyxa M1]",</p> <p>"cazygi 748408394 gb AJE51910.1  glycosylase [Paenibacillus polymyxa]",</p> <p>"cazygi 309249531 gb ADO59098.1  glycosylase [Paenibacillus polymyxa SC2]",</p> <p>"cazygi 595636226 gb AHM68484.1  glycosidase like protein [Paenibacillus polymyxa SQR-21]",</p> <p>"cazygi 954043275 gb ALP37040.1  glycosylase [Paenibacillus sp. IHB B 3084]",</p> <p>"cazygi 357200019 gb AET57916.1  glycosidase like protein [Paenibacillus terrae HPL-003]"</p>
<p>["cazy AOR95091.1 glycosylase [Clostridium butyricum]",</p> <p>"cazy APF24412.1 hypothetical protein NPD4_1003 [Clostridium butyricum]",</p> <p>"cazy AQR97693.1 beta-1", "4-mannooligosaccharide phosphorylase [Clostridium saccharoperbutylacetonicum]",</p> <p>"cazy AXB83879.1 glycosylase [Clostridium butyricum]",</p> <p>"cazy SNX53913.1 beta-1", "4-mannooligosaccharide/beta-1", "4-mannosyl-N-acetylglucosamine phosphorylase [Thermoanaerobacterium sp. RBITD]",</p> <p>"humangutMH0277_GL0042744 [gene] locus=scaffold19815_1:40231:41247:- [Complete] codon-table.11",</p> <p>"cazygi 961431628 gb ALS17957.1  glycosylase [Clostridium butyricum]",</p> <p>"cazygi 959156843 gb ALP91461.1  glycosylase [Clostridium butyricum]",</p> <p>"cazygi 1028925582 gb ANF15082.1  glycosylase [Clostridium butyricum]",</p> <p>"cazygi 451788055 gb AGF59023.1  putative glycosylase [Clostridium saccharoperbutylacetonicum N1-4(HMT)]",</p> <p>"cazygi 389569314 gb AFK85719.1  glycosidase related protein [Thermoanaerobacterium saccharolyticum JW/SL-YS485]",</p> <p>"cazygi 302777167 gb ADL67726.1  glycosidase-related [Thermoanaerobacterium thermosaccharolyticum DSM 571]"</p>
<p>["cazy AOS43555.1 Beta-1", "4-mannooligosaccharide phosphorylase [Lacunisphaera limnophila]",</p> <p>"cazygi 177841343 gb ACB75595.1  glycosidase PH1107-related [Opitutus terrae PB90-1]"</p>
<p>["cazy AOZ94170.1 glycosylase [Paenibacillus crassostreae]",</p> <p>"cazy ASA19960.1 glycosylase [Paenibacillus donghaensis]",</p> <p>"cazy AWB46380.1 glycosylase [Paenibacillus sp. CAA11]",</p> <p>"cazygi 686546540 gb AIQ57236.1  glycosylase [Paenibacillus borealis]",</p> <p>"cazygi 690615652 gb AIQ16865.1  glycosylase [Paenibacillus sp. FSL H7-0357]",</p> <p>"cazygi 690616322 gb AIQ17535.1  glycosylase [Paenibacillus sp. FSL H7-0357]",</p> <p>"cazygi 686517733 gb AIQ28434.1  glycosylase [Paenibacillus sp. FSL P4-0081]",</p> <p>"cazygi 686536688 gb AIQ47386.1  glycosylase [Paenibacillus sp. FSL R7-0273]",</p> <p>"cazygi 686542219 gb AIQ52916.1  glycosylase [Paenibacillus sp. FSL R7-0331]",</p> <p>"cazygi 686552475 gb AIQ63170.1  glycosylase [Paenibacillus stellifer]"</p>
<p>["cazy APC39750.1 glycosylase [Clostridium estertheticum subsp. estertheticum]",</p> <p>"cazygi 82523802 emb CAI78545.1  hypothetical protein [uncultured Chloroflexi bacterium]"</p>
<p>["cazy APO42885.1 glycosylase [Paenibacillus xylanexedens]"</p>
<p>["cazy APS39188.1 glycosidase [Salegentibacter sp. T436]",</p> <p>"cazy ASE18319.1 glycosidase [Prevotella melaninogenica]",</p>

<p>"cazy ATA77353.1 glycosidase [Capnocytophaga canimorsus]",</p> <p>"cazy ATA91837.1 glycosidase [Capnocytophaga canimorsus]",</p> <p>"cazy ATA94100.1 glycosidase [Capnocytophaga canimorsus]",</p> <p>"cazy AU156627.1 glycosidase [Prevotella jejuni]",</p> <p>"cazy AWL78816.1 glycosidase [Capnocytophaga canimorsus]",</p> <p>"cazy AXV49873.1 glycosidase [Prevotella denticola]",</p> <p>"cazy BBA29964.1 1","4-beta-mannosyl-N-acetylglucosamine phosphorylase [Prevotella melaninogenica]",</p> <p>"humangutMH0166_GL0018134 [gene] locus=scaffold11391_1:34077:35051:+ [Complete] codon-table.11",</p> <p>"humangut158924089-stool1_revised_scaffold16799_1_gene36849 strand:- start:4086 stop:5060 length:975 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11",</p> <p>"humangut553171.HMPREF0648_0792 [Complete]:- codon-table.11",</p> <p>"mouseMH-0-3_GL0040838 [gene] locus=scaffold24246_3:1738:2712:- [Complete] codon-table.11",</p> <p>"mouseG1-4A_GL0001880 [gene] locus=scaffold99_2:27529:28503:+ [Complete] codon-table.11",</p> <p>"mouse20_GL0104310 [gene] locus=scaffold95191_23:188:1162:+ [Complete] codon-table.11",</p> <p>"cazy 610422242 gb AHW59446.1  glycosidase [Draconibacterium orientale]",</p> <p>"cazy 326944893 gb AEA20778.1  hypothetical protein HMPREF9137_2294 [Prevotella denticola F0289]",</p> <p>"cazy 913019237 gb AKU70190.1  glycosidase [Prevotella fusca JCM 17724]",</p> <p>"cazy 302150791 gb ADK97052.1  hypothetical protein HMPREF0659_A6441 [Prevotella melaninogenica ATCC 25845]",</p> <p>"cazy 1043184170 gb ANR73902.1  glycosidase [Prevotella scopos JCM 17725]",</p> <p>"cazy 288332494 gb EFC70974.1  hypothetical protein HMPREF0669_00679 (plasmid) [Prevotella sp. oral taxon 299 str. F0039]"</p>
<p>"cazy APT73993.1 glycosidase [Thermosipho melanesiensis]",</p> <p>"cazy 217037215 gb ACJ75737.1  unknwon conserved protein [Thermosipho africanus TCF52B]",</p> <p>"cazy 149793426 gb ABR30874.1  glycosidase"," PH1107-related [Thermosipho melanesiensis BI429]"</p>
<p>"cazy APT76001.1 glycosidase [Marinitoga sp. 1137]"</p>
<p>"cazy AQO69862.1 Beta-1","4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium SM-Chi-D1]"</p>
<p>"cazy AQO71744.1 Beta-1","4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium SM-Chi-D1]"</p>
<p>"cazy AQT68108.1 Beta-1","4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium ST-NAGAB-D1]"</p>
<p>"cazy ASB38139.1 glycosidase [Muribaculum intestinale]",</p> <p>"mouseS-Fe10_GL0132028 [gene] locus=C955776_1:29603:30559:+ [Complete] codon-table.11",</p> <p>"pigPIG-001_GL0217556 [gene] locus=scaffold20914_2:432:1388:+ [Complete] codon-table.11",</p> <p>"pigPIG-011_GL0085855 [gene] locus=scaffold12435_3:133:1089:+ [Complete] codon-table.11",</p> <p>"cazy 1045279095 gb ANU63776.1  glycosidase [Parabacteroides sp. YL27]"</p>
<p>"cazy ASB41841.1 glycosidase [Acutalibacter muris]",</p> <p>"humangutV1.UC13-0_GL0061527 [gene] locus=scaffold24550_2:9491:10492:- [Complete] codon-table.11",</p> <p>"mouseS-Fe1_GL0086041 [gene] locus=scaffold9659_1:241:1242:+ [Complete] codon-table.11",</p> <p>"mouseS-Fe9_GL0239525 [gene] locus=scaffold7813_4:3386:4387:- [Lack 5'-end] codon-table.11",</p> <p>"mouse2-2_GL0055864 [gene] locus=scaffold122201_1:1830:2831:- [Complete] codon-table.11",</p> <p>"rumen583_GL0273127_1 [gene] locus=scaffold51578_2:12391:13392:-[Complete]",</p> <p>"cazy 1045270240 gb ANU54932.1  glycosidase [Ruminiclostridium sp. KB18]"</p>
<p>"cazy ASE63461.1 glycosidase [Chryseobacterium indologenes]",</p> <p>"cazy ASK31449.1 glycosidase [Chryseobacterium sp. T16E-39]",</p> <p>"cazy ASW75147.1 glycosidase [Chryseobacterium piperi]",</p> <p>"cazy ATA68024.1 glycosidase [Capnocytophaga cynodegmi]",</p> <p>"cazy ATA89573.1 glycosidase [Capnocytophaga stomatis]",</p>

"cazy|ATN07456.1 glycosidase [Chryseobacterium indologenes]",

"humangutMH0003\_GL0075746 [gene] locus=scaffold17037\_1:3556:4527:- [Complete] codon-table.11",

"humangutMH0004\_GL0033557 [gene] locus=scaffold48841\_2:72:1043:+ [Complete] codon-table.11",

"humangutMH0006\_GL0073708 [gene] locus=scaffold102740\_1:9518:10489:+ [Complete] codon-table.11",

"humangutMH0011\_GL0031624 [gene] locus=scaffold6982\_4:53:1024:+ [Complete] codon-table.11",

"humangutMH0038\_GL0023413 [gene] locus=scaffold14633\_3:21944:22915:+ [Complete] codon-table.11",

"humangutMH0046\_GL0032276 [gene] locus=scaffold45316\_2:186:1157:- [Complete] codon-table.11",

"humangutMH0047\_GL0000100 [gene] locus=scaffold9606\_1:7600:8571:- [Complete] codon-table.11",

"humangutMH0052\_GL0052339 [gene] locus=scaffold24048\_2:334:1305:- [Complete] codon-table.11",

"humangutMH0055\_GL0020468 [gene] locus=scaffold43568\_1:105:1076:- [Complete] codon-table.11",

"humangutMH0055\_GL0034072 [gene] locus=scaffold2797\_1:618:1589:- [Complete] codon-table.11",

"humangutMH0101\_GL0081430 [gene] locus=scaffold26934\_4:197:1168:- [Complete] codon-table.11",

"humangutMH0116\_GL0138390 [gene] locus=scaffold93220\_1:8256:9227:- [Complete] codon-table.11",

"humangutMH0126\_GL0121407 [gene] locus=scaffold133197\_1:12424:13395:+ [Complete] codon-table.11",

"humangutMH0140\_GL0083856 [gene] locus=scaffold94387\_1:12435:13406:+ [Complete] codon-table.11",

"humangutMH0281\_GL0165041 [gene] locus=scaffold38155\_1:2892:3863:- [Complete] codon-table.11",

"humangutMH0302\_GL0082303 [gene] locus=scaffold34643\_9:5730:6701:+ [Complete] codon-table.11",

"humangutMH0314\_GL0108231 [gene] locus=scaffold62845\_1:286:1257:- [Complete] codon-table.11",

"humangutMH0321\_GL0007378 [gene] locus=scaffold101808\_6:542:1513:- [Complete] codon-table.11",

"humangutMH0333\_GL0010365 [gene] locus=scaffold26160\_1:79693:80664:+ [Complete] codon-table.11",

"humangutMH0381\_GL0169932 [gene] locus=scaffold63368\_5:715:1686:- [Complete] codon-table.11",

"humangutMH0402\_GL0171617 [gene] locus=scaffold82462\_1:600:1571:+ [Complete] codon-table.11",

"humangutMH0435\_GL0062501 [gene] locus=scaffold79199\_1:19153:20124:+ [Complete] codon-table.11",

"humangutO2\_UC24-1\_GL0121919 [gene] locus=scaffold96768\_1:596:1567:- [Complete] codon-table.11",

"humangutO2\_UC31-1\_GL0148553 [gene] locus=scaffold47996\_1:8964:9935:- [Complete] codon-table.11",

"humangutN001A\_GL0039907 [gene] locus=scaffold52055\_1:11991:12962:+ [Complete] codon-table.11",

"humangutN085A\_GL0030918 [gene] locus=C534392\_1:50:1021:- [Complete] codon-table.11",

"humangut158256496-stool1\_revised\_C965981\_1\_gene88806 strand:- start:1110 stop:2081 length:972 start\_codon:yes stop\_codon:yes gene\_type:complete [Complete] codon-table.11",

"humangut765560005-stool1\_revised\_scaffold23582\_1\_gene63099 strand:+ start:17288 stop:18259 length:972 start\_codon:yes stop\_codon:yes gene\_type:complete [Complete] codon-table.11",

"mouseGroup2-5A\_GL0021665 [gene] locus=scaffold9730\_7:244:1215:- [Complete] codon-table.11",

"mouse10\_GL0099266 [gene] locus=scaffold30593\_1:26097:27068:- [Complete] codon-table.11",

"mouse2B-dyr19-06\_GL0008674 [gene] locus=scaffold6602\_8:2261:3232:- [Complete] codon-table.11",

"pigPIG\_119\_GL0347395 [gene] locus=scaffold142087\_9:19322:20293:- [Complete] codon-table.11",

"rumen555\_GL0373485\_1 [gene] locus=scaffold156620\_7:3306:4277:+[Complete]",

"cazy|g|939203325|gb|ALJ61498.1| Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides cellulosilyticus]",

"cazy|g|319416378|gb|ADV43489.1| glycosidase related protein [Bacteroides helcogenes P 36-108]",

"cazy|g|570741375|gb|AHF12135.1| glycosidase [Barnesiella viscericola DSM 18177]",

"cazy|g|828458824|gb|AKK72745.1| glycosidase [Chryseobacterium gallinarum]",

"cazy|g|674269942|db|BAP29335.1| glycosidase [Chryseobacterium sp. STRB126]"

---

"cazy|ASM70687.1 glycosidase [Blautia hansenii DSM 20583]",

"humangutMH0010\_GL0000927 [gene] locus=scaffold579\_12:2396:3382:+ [Complete] codon-table.11",

"humangutMH0372\_GL0052869 [gene] locus=scaffold80648\_1:8151:9137:- [Complete] codon-table.11",



"humangutMH0373\_GL0083014 [gene] locus=scaffold4398\_14:1479:2465:- [Complete] codon-table.11",

"humangutV1.CD12-3\_GL0040072 [gene] locus=scaffold26822\_2:25571:26557:+ [Complete] codon-table.11",

"humangutDLM013\_GL0046706 [gene] locus=scaffold3678\_7:1871:2857:+ [Complete] codon-table.11",

"mouseMC-0-3\_GL0005804 [gene] locus=scaffold2810\_2:2716:3702:- [Complete] codon-table.11",

"mouseG1-5A\_GL0007008 [gene] locus=scaffold1620\_3:9842:10828:- [Complete] codon-table.11",

"mouse1-1\_GL0058502 [gene] locus=scaffold63511\_9:1433:2419:+ [Complete] codon-table.11",

"mouse1-1\_GL0105382 [gene] locus=scaffold33983\_1:9839:10825:+ [Complete] codon-table.11",

"mouse1-1\_GL0143778 [gene] locus=scaffold320\_1:568:1554:- [Complete] codon-table.11",

"mouse1-2\_GL0060243 [gene] locus=scaffold42352\_1:11675:12661:+ [Complete] codon-table.11",

"mouse13\_GL0004655 [gene] locus=scaffold51777\_1:888:1874:- [Complete] codon-table.11",

"mouse2-3\_GL0096850 [gene] locus=scaffold59790\_1:64775:65761:+ [Complete] codon-table.11",

"mouse4-1\_GL0051115 [gene] locus=scaffold40970\_1:1024:2010:- [Complete] codon-table.11",

"mouse6-2\_GL0024360 [gene] locus=scaffold14875\_2:46984:47970:- [Complete] codon-table.11",

"pigPIG\_119\_GL0171139 [gene] locus=scaffold190017\_2:160:1146:+ [Complete] codon-table.11",

"pigDB-512B\_GL0151230 [gene] locus=scaffold208408\_1:239:1225:- [Complete] codon-table.11",

"pigDB-517B\_GL0133330 [gene] locus=scaffold7355\_1:53:1039:+ [Complete] codon-table.11",

"pigSYZ-448B\_GL0114656 [gene] locus=scaffold56409\_1:565:1551:- [Complete] codon-table.11",

"pigZXZ-8B\_GL0242426 [gene] locus=scaffold182904\_1:899:1885:+ [Complete] codon-table.11",

"rumen555\_GL1091079\_1 [gene] locus=scaffold730046\_1:2368:3354:+ [Complete]",

"cazygijl291541206|emb|CBL14317.1| Predicted glycosylase [Roseburia intestinalis XB6B4]"

---

["cazy|AST53133.1 glycosidase [Parabacteroides sp. CT06]",

"cazy|AUJ45968.1 glycosidase [Bacteroides fragilis]",

"cazy|BAD48081.1 conserved hypothetical protein [Bacteroides fragilis YCH46]",

"humangutMH0006\_GL0038257 [gene] locus=scaffold31109\_4:10469:11467:+ [Complete] codon-table.11",

"humangutMH0009\_GL0004248 [gene] locus=scaffold36082\_1:7444:8442:+ [Complete] codon-table.11",

"humangutMH0041\_GL0063443 [gene] locus=scaffold14739\_8:354:1352:+ [Complete] codon-table.11",

"humangutMH0090\_GL0006072 [gene] locus=scaffold32146\_4:2418:3416:- [Complete] codon-table.11",

"humangutMH0101\_GL0076321 [gene] locus=scaffold20113\_4:6408:7406:+ [Complete] codon-table.11",

"humangutMH0118\_GL0029001 [gene] locus=scaffold39394\_2:19067:20065:+ [Complete] codon-table.11",

"humangutMH0138\_GL0004080 [gene] locus=scaffold2292\_5:177:1175:+ [Complete] codon-table.11",

"humangutMH0158\_GL0053814 [gene] locus=scaffold49547\_5:7904:8902:+ [Complete] codon-table.11",

"humangutMH0229\_GL0055276 [gene] locus=scaffold569\_3:11097:12095:- [Complete] codon-table.11",

"humangutMH0309\_GL0132661 [gene] locus=scaffold411\_12:14013:15011:- [Complete] codon-table.11",

"humangutMH0374\_GL0074973 [gene] locus=scaffold6906\_4:765:1763:+ [Complete] codon-table.11",

"humangutMH0400\_GL0011364 [gene] locus=scaffold62787\_1:260:1258:- [Complete] codon-table.11",

"humangutO2.CD2-0\_GL0013926 [gene] locus=scaffold22628\_1:41883:42881:+ [Complete] codon-table.11",

"humangutT2D-109A\_GL0010527 [gene] locus=scaffold27792\_1:3383:4381:- [Complete] codon-table.11",

"humangut160765029-stool1\_revised\_scaffold20596\_1\_gene110346 strand:- start:1088 stop:2086 length:999 start\_codon:yes stop\_codon:yes gene\_type:complete [Complete] codon-table.11",

"humangut679189.HMPREF9019\_2256 [Complete]:- codon-table.11",

"mouseS-Fe1\_GL0016303 [gene] locus=scaffold1736\_1:85704:86702:- [Complete] codon-table.11",

"mouseGroup2-7A\_GL0107291 [gene] locus=scaffold63922\_9:525:1523:+ [Complete] codon-table.11",

"pigPIG-003\_GL0043079 [gene] locus=scaffold88790\_11:2555:3553:+ [Complete] codon-table.11",

"pigPIG-006\_GL0134772 [gene] locus=scaffold124202\_5:2132:3130:+ [Complete] codon-table.11",

<p>"pigPIG-007_GL0093565 [gene] locus=scaffold151718_2:575:1573:- [Complete] codon-table.11",</p> <p>"pigPIG-008_GL0134693 [gene] locus=scaffold118693_3:8735:9733:+ [Complete] codon-table.11",</p> <p>"pigPIG-014_GL0048635 [gene] locus=scaffold53272_1:79528:80526:- [Complete] codon-table.11",</p> <p>"pigPIG-031_GL0208473 [gene] locus=scaffold4037_1:606:1604:- [Complete] codon-table.11",</p> <p>"pigPIG-034_GL0166059 [gene] locus=scaffold145591_1:3384:4382:+ [Complete] codon-table.11",</p> <p>"pigPIG-067_GL0036307 [gene] locus=scaffold151267_1:93:1091:+ [Complete] codon-table.11",</p> <p>"pigBHZ-11B_GL0010546 [gene] locus=scaffold75456_1:206:1204:- [Complete] codon-table.11",</p> <p>"rumen553_GL0024980_1 [gene] locus=scaffold986_1:3966:4964:+[Complete]",</p> <p>"rumen553_GL0119108_1 [gene] locus=C7497718_1:60:1058:+[Complete]",</p> <p>"rumen553_GL0208890_1 [gene] locus=scaffold368380_1:10895:11893:+[Complete]",</p> <p>"rumen552_GL0523106_1 [gene] locus=scaffold127266_4:20569:21567:-[Complete]",</p> <p>"rumen552_GL0818245_1 [gene] locus=scaffold261788_5:3840:4838:-[Complete]",</p> <p>"rumen552_GL1282954_1 [gene] locus=scaffold481957_2:28:1026:-[Complete]",</p> <p>"rumen554_GL2994928_1 [gene] locus=scaffold1409865_1:12853:13851:-[Complete]",</p> <p>"rumen555_GL1179928_1 [gene] locus=scaffold1172364_12:9197:10195:-[Complete]",</p> <p>"rumen555_GL1208700_1 [gene] locus=scaffold25095_2:2304:3302:+[Complete]",</p> <p>"rumen555_GL1860074_1 [gene] locus=scaffold155906_2:32477:33475:+[Complete]",</p> <p>"rumen2009040_GL1348356_1 [gene] locus=scaffold574579_5:2330:3328:+[Complete]",</p> <p>"cazygi 922661194 emb CUA17878.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides fragilis]",</p> <p>"cazygi 794205266 gb AKA51257.1  glycosidase [Bacteroides fragilis]",</p> <p>"cazygi 1042800252 gb ANQ59899.1  glycosidase [Bacteroides fragilis]",</p> <p>"cazygi 159890459 gb ABX03539.1  glycosidase PH1107-related [Herpetosiphon aurantiacus DSM 785]",</p> <p>"cazygi 149935713 gb ABR42410.1  conserved hypothetical protein [Parabacteroides distasonis ATCC 8503]",</p> <p>"cazygi 433302576 gb AGB28392.1  putative glycosylase [Prevotella dentalis DSM 3688]",</p> <p>"cazygi 953019838 gb ALC049545.1  glycosidase [Prevotella enoece]",</p> <p>"cazygi 643431564 gb AIA99576.1  hypothetical protein [uncultured bacterium contig00010(2014)]"</p>
<p>["cazy AUP80075.1 glycosidase [Flavivirga eckloniae]",</p> <p>"cazygi 88707752 gb EAQ99992.1  hypothetical protein FB2170_01422 [Maribacter sp. HTCC2170]"</p>
<p>["cazy AUS96708.1 glycosidase [Pseudoclostridium thermosuccinogenes]",</p> <p>"mouseG1-3A_GL0026020 [gene] locus=scaffold13529_3:9003:9998:+ [Complete] codon-table.11",</p> <p>"mouse2-1_GL0075368 [gene] locus=scaffold5530_3:189:1184:+ [Complete] codon-table.11",</p> <p>"mouse2-1_GL0088592 [gene] locus=scaffold67877_1:8952:9947:- [Complete] codon-table.11",</p> <p>"rumen7049_GL2441192_1 [gene] locus=scaffold413534_6:2009:3004:+[Complete]"</p>
<p>["cazy AVM42902.1 glycosidase [Fastidiosipila sanguinis]",</p> <p>"pigPIG_144_GL0105367 [gene] locus=C3793824_1:63:1073:- [Complete] codon-table.11]"</p>
<p>["cazy AVM47165.1 glycosidase [Victivallales bacterium CCUG 44730]"</p>
<p>["cazy AVM69290.1 glycosidase [Lachnospiraceae bacterium oral taxon 500]",</p> <p>"humangutMH0211_GL0069392 [gene] locus=scaffold22191_7:9815:10804:+ [Complete] codon-table.11",</p> <p>"humangutO2_UC20-1_GL0005080 [gene] locus=scaffold8006_6:1167:2156:+ [Complete] codon-table.11",</p> <p>"humangutO2_UC38-1_GL0042109 [gene] locus=scaffold5461_3:58:1047:+ [Complete] codon-table.11",</p> <p>"humangutT2D-22A_GL0097388 [gene] locus=scaffold30195_1:14784:15773:+ [Complete] codon-table.11",</p> <p>"mouseS-Fe12_GL0116109 [gene] locus=scaffold79297_8:2528:3517:+ [Complete] codon-table.11",</p> <p>"mouseMC-0-1_GL0105636 [gene] locus=scaffold93524_1:280:1269:- [Complete] codon-table.11",</p> <p>"mouse1A-dyr4-07_GL0106525 [gene] locus=scaffold51198_3:410:1399:- [Complete] codon-table.11",</p>

"mouse2-3\_GL0005066 [gene] locus=scaffold46218\_4:52117:53106:- [Complete] codon-table.11",

"mouse35\_GL0122006 [gene] locus=scaffold47094\_5:7249:8238:+ [Complete] codon-table.11",

"mouse4-2\_GL0099480 [gene] locus=scaffold60900\_2:12283:13272:- [Complete] codon-table.11",

"mouse54\_GL0079445 [gene] locus=scaffold7983\_6:3156:4145:- [Complete] codon-table.11",

"pigPIG\_116\_GL0134633 [gene] locus=scaffold168385\_2:1338:2327:- [Complete] codon-table.11",

"rumen583\_GL0632373\_1 [gene] locus=scaffold100870\_2:3216:4205:-[Complete]",

"rumen100058\_GL3559996\_1 [gene] locus=scaffold448284\_8:2020:3009:-[Complete]"

---

["cazy|AWV32554.1 glycosylase [Paenibacillus odorifer]",

"cazy|686562517|gb|AIQ73210.1| glycosylase [Paenibacillus odorifer]",

"cazy|690621768|gb|AIQ22782.1| glycosylase [Paenibacillus sp. FSL H7-0737]",

"cazy|686523885|gb|AIQ34585.1| glycosylase [Paenibacillus sp. FSL R5-0345]"

---

["cazy|AXB29277.1 glycosylase [Faecalibacterium prausnitzii]",

"humangutMH0193\_GL0079555 [gene] locus=scaffold80193\_1:8807:9826:- [Complete] codon-table.11",

"humangutMH0434\_GL0140597 [gene] locus=scaffold83331\_17:877:1896:- [Complete] codon-table.11",

"humangutO2.UC21-2\_GL0102009 [gene] locus=scaffold17595\_1:33:1052:- [Complete] codon-table.11",

"humangut706846339-stool1\_revised\_scaffold23726\_3\_gene129109 strand:- start:3386 stop:4405 length:1020 start\_codon:yes stop\_codon:yes gene\_type:complete [Complete] codon-table.11",

"mouseMC-0-1\_GL0064823 [gene] locus=scaffold53168\_13:7491:8510:- [Complete] codon-table.11",

"mouseMC-0-1\_GL0086097 [gene] locus=scaffold75211\_4:225:1244:- [Complete] codon-table.11",

"mouseMC-6-1\_GL0107989 [gene] locus=scaffold75276\_1:7108:8127:- [Complete] codon-table.11",

"pigPIG\_144\_GL0061430 [gene] locus=scaffold282677\_1:886:1905:+ [Complete] codon-table.11",

"pigPIG-009\_GL0138986 [gene] locus=scaffold3128\_3:383:1402:+ [Complete] codon-table.11",

"pigPIG-017\_GL0190980 [gene] locus=scaffold105253\_2:863:1882:- [Complete] codon-table.11",

"pigPIG-034\_GL0075037 [gene] locus=scaffold145714\_2:6349:7368:+ [Complete] codon-table.11",

"pigPIG-059\_GL0145572 [gene] locus=scaffold21026\_6:1306:2325:- [Complete] codon-table.11",

"pigPIG-061\_GL0061185 [gene] locus=scaffold150548\_2:61:1080:+ [Complete] codon-table.11",

"pigBHZ-10B\_GL0178364 [gene] locus=scaffold94497\_9:2950:3969:- [Complete] codon-table.11",

"pigEYZ-592B\_GL0198908 [gene] locus=scaffold45536\_2:65969:66988:+ [Complete] codon-table.11",

"rumen553\_GL0062626\_1 [gene] locus=scaffold65877\_2:603:1622:+[Complete]",

"rumen553\_GL0289551\_1 [gene] locus=scaffold227037\_4:2407:3426:-[Complete]",

"rumen552\_GL0163252\_1 [gene] locus=scaffold156556\_4:634:1653:-[Complete]",

"rumen583\_GL0160972\_1 [gene] locus=scaffold139414\_1:2651:3670:+[Complete]",

"rumen583\_GL0709304\_1 [gene] locus=scaffold196890\_1:2693:3712:+[Complete]",

"rumen583\_GL0824088\_1 [gene] locus=scaffold316177\_1:142:1161:+[Complete]",

"rumen554\_GL0769507\_1 [gene] locus=scaffold1153488\_1:465:1484:+[Complete]",

"rumen554\_GL1748617\_1 [gene] locus=scaffold462637\_8:1625:2644:-[Complete]",

"rumen554\_GL2286209\_1 [gene] locus=scaffold407690\_3:118:1137:-[Complete]",

"rumen554\_GL2590785\_1 [gene] locus=scaffold94633\_5:3:1019:-[Lack both ends]",

"rumen555\_GL1294659\_1 [gene] locus=scaffold755112\_1:13012:14031:-[Complete]",

"rumen555\_GL1894784\_1 [gene] locus=scaffold1146238\_1:140:1159:+[Complete]",

"rumen555\_GL2262294\_1 [gene] locus=scaffold561072\_3:195:1214:-[Complete]",

"rumen100058\_GL0162288\_1 [gene] locus=scaffold1342822\_1:11998:13017:-[Complete]",

"rumen2009040\_GL1491257\_1 [gene] locus=scaffold36167\_4:443:1462:+[Complete]",

"rumen2009040\_GL1560257\_1 [gene] locus=scaffold3072615\_1:280:1299:-[Complete]",

"rumen3042\_GL1401775\_1 [gene] locus=scaffold1017850\_7:206:1225:+[Complete]",

"cazy|295104428|emb|CBL01972.1| Predicted glycosylase [Faecalibacterium prausnitzii SL3/3"]

["cazy|AYF38257.1 glycosylase [Ethanoligenens harbinense]",

"cazy|AYF41003.1 glycosylase [Ethanoligenens harbinense]",

"humangutMH0053\_GL0075281 [gene] locus=scaffold7906\_13:8322:9347:+[Complete] codon-table.11",

"humangutMH0143\_GL0066611 [gene] locus=scaffold10045\_5:68901:69926:-[Complete] codon-table.11",

"humangutMH0239\_GL0155109 [gene] locus=scaffold10725\_5:1010:2035:+[Complete] codon-table.11",

"humangutMH0431\_GL0109397 [gene] locus=scaffold114921\_1:80419:81444:-[Complete] codon-table.11",

"humangutO2\_UC12-1\_GL0066556 [gene] locus=scaffold50205\_3:28:1053:-[Complete] codon-table.11",

"humangutO2\_UC8-0\_GL0078900 [gene] locus=scaffold39947\_3:125:1150:+[Complete] codon-table.11",

"humangutT2D-108A\_GL0038945 [gene] locus=scaffold102521\_1:17645:18670:+[Complete] codon-table.11",

"humangutT2D-11A\_GL0038543 [gene] locus=scaffold59242\_6:13368:14393:-[Complete] codon-table.11",

"mouseS-Fe10\_GL0047342 [gene] locus=scaffold35905\_2:487:1512:+[Complete] codon-table.11",

"mouse2-2\_GL0057369 [gene] locus=scaffold117963\_5:20591:21616:+[Complete] codon-table.11",

"mouse7-1\_GL0080165 [gene] locus=scaffold575\_1:1575:2600:+[Complete] codon-table.11",

"mouse7-5\_GL0135179 [gene] locus=scaffold49132\_1:3791:4816:+[Complete] codon-table.11",

"mouse8-3\_GL0003503 [gene] locus=scaffold64522\_1:3462:4487:+[Complete] codon-table.11",

"pigPIG-001\_GL0131189 [gene] locus=scaffold52084\_1:16361:17386:+[Complete] codon-table.11",

"pigPIG-025\_GL0024354 [gene] locus=scaffold56563\_3:642:1667:-[Complete] codon-table.11",

"pigPIG-037\_GL0164496 [gene] locus=scaffold32231\_1:46604:47629:+[Complete] codon-table.11",

"pigPIG-054\_GL0165254 [gene] locus=scaffold157312\_1:13377:14402:+[Complete] codon-table.11",

"pigPIG-060\_GL0078259 [gene] locus=scaffold108689\_2:901:1926:+[Complete] codon-table.11",

"pigPIG-107\_GL0030546 [gene] locus=scaffold130215\_1:57358:58383:+[Complete] codon-table.11",

"pigPIG-109\_GL0153660 [gene] locus=scaffold15355\_2:1398:2423:+[Complete] codon-table.11",

"pigSYZ-481B\_GL0077449 [gene] locus=scaffold73765\_3:2:1027:+[Lack 5'-end] codon-table.11",

"rumen552\_GL0212503\_1 [gene] locus=scaffold34627\_1:17573:18598:+[Complete]",

"rumen552\_GL0260102\_1 [gene] locus=scaffold870516\_2:503:1528:+[Complete]",

"rumen552\_GL0699264\_1 [gene] locus=scaffold586952\_1:15165:16190:-[Complete]",

"rumen583\_GL0042904\_1 [gene] locus=scaffold225231\_1:5042:6067:+[Complete]",

"rumen583\_GL0063682\_1 [gene] locus=scaffold268085\_3:56557:57582:+[Complete]",

"rumen583\_GL0754105\_1 [gene] locus=scaffold195983\_1:22689:23714:+[Complete]",

"rumen554\_GL0695329\_1 [gene] locus=scaffold2141897\_1:676:1701:-[Complete]",

"rumen554\_GL2664813\_1 [gene] locus=scaffold150755\_1:1588:2613:-[Complete]",

"rumen555\_GL0962278\_1 [gene] locus=scaffold903670\_6:4081:5106:+[Complete]",

"rumen555\_GL1563354\_1 [gene] locus=scaffold12362\_1:1157:2182:-[Complete]",

"rumen0081\_GL0221277\_1 [gene] locus=scaffold713930\_3:15667:16692:-[Complete]",

"rumen0081\_GL2192118\_1 [gene] locus=C39822215\_1:922:1947:+[Complete]",

"rumen0081\_GL2239602\_1 [gene] locus=scaffold792061\_4:521:1546:-[Complete]",

"rumen100058\_GL0658159\_1 [gene] locus=scaffold219057\_1:4551:5576:-[Complete]",

"rumen100058\_GL1286058\_1 [gene] locus=scaffold901462\_10:2321:3346:+[Complete]",

"rumen100058\_GL2613818\_1 [gene] locus=scaffold2582560\_3:167:1192:-[Complete]",

"rumen100058\_GL3613107\_1 [gene] locus=scaffold1858877\_1:1:1026:+[Lack 5'-end]",

"rumen2009040\_GL0506093\_1 [gene] locus=scaffold2066715\_2:622:1647:+[Complete]",

"rumen2009040\_GL0767965\_1 [gene] locus=scaffold1487504\_2:915:1940:+[Complete]",

<p>"rumen2009040_GL1136740_1 [gene] locus=scaffold543396_1:197:1222:+[Complete]",</p> <p>"rumen2009040_GL1916699_1 [gene] locus=scaffold1597861_1:916:1941:-[Complete]",</p> <p>"rumen2009040_GL2361668_1 [gene] locus=scaffold2277265_2:1780:2805:+[Complete]",</p> <p>"rumen2009040_GL3557692_1 [gene] locus=scaffold872905_4:3590:4615:-[Complete]",</p> <p>"rumen7049_GL0522168_1 [gene] locus=scaffold426564_3:399:1424:-[Complete]",</p> <p>"rumen7049_GL0810742_1 [gene] locus=scaffold1432378_1:203:1228:+[Complete]",</p> <p>"rumen7049_GL1850379_1 [gene] locus=scaffold1085425_2:2462:3487:+[Complete]",</p> <p>"rumen7049_GL2607885_1 [gene] locus=scaffold34287_6:2306:3331:-[Complete]",</p> <p>"cazygi 295094606 emb CBK83697.1  Predicted glycosylase [Coproccoccus sp. ART55/1]",</p> <p>"cazygi 315469860 gb ADU26464.1  glycosidase related protein [Ethanolgenens harbinense YUAN-3]"</p>
<p>["cazy SCV09583.1 hypothetical protein BACOV975_03377 [Bacteroides ovatus V975]",</p> <p>"humangutMH0003_GL0007967 [gene] locus=scaffold40843_2:227:1234:- [Complete] codon-table.11",</p> <p>"humangutMH0180_GL0015791 [gene] locus=scaffold4132_7:2616:3623:- [Complete] codon-table.11",</p> <p>"humangut159551223-stool1_revised_scaffold18547_1_gene104513 strand:+ start:1324 stop:2331 length:1008 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"mouse28_GL0101701 [gene] locus=scaffold63073_4:20538:21545:- [Complete] codon-table.11",</p> <p>"pigPIG_191_GL0230098 [gene] locus=scaffold75479_1:3:1010:+ [Lack 5'-end] codon-table.11"]</p>
<p>["cazy SMF88250.1 beta-1", "4-mannooligosaccharide/beta-1", "4-mannosyl-N-acetylglucosamine phosphorylase [Paenibacillus uliginis N3/975]",</p> <p>"mouse1-1_GL0045549 [gene] locus=scaffold87940_1:27786:28784:- [Complete] codon-table.11",</p> <p>"mouse14_GL0003911 [gene] locus=scaffold6104_5:488:1486:- [Complete] codon-table.11",</p> <p>"mouse2-2_GL0059722 [gene] locus=scaffold52241_3:1:999:+ [Lack 5'-end] codon-table.11",</p> <p>"mouse5-8_GL0044701 [gene] locus=scaffold54091_13:882:1880:- [Complete] codon-table.11",</p> <p>"mouse7-8_GL0036592 [gene] locus=scaffold4684_2:4628:5626:+ [Complete] codon-table.11",</p> <p>"rumen100058_GL3852657_1 [gene] locus=scaffold336949_4:988:1986:+[Complete]",</p> <p>"rumen2009040_GL3580840_1 [gene] locus=scaffold2454716_1:117:1115:+[Complete]",</p> <p>"cazygi 309390304 gb ADO78184.1  glycosidase related protein [Halanaerobium praevalens DSM 2228]",</p> <p>"cazygi 686549305 gb AIQ60001.1  glycosidase [Paenibacillus borealis]",</p> <p>"cazygi 686520539 gb AIQ31240.1  glycosidase [Paenibacillus sp. FSL P4-0081]",</p> <p>"cazygi 686532065 gb AIQ42764.1  glycosidase [Paenibacillus sp. FSL R5-0912]",</p> <p>"cazygi 766900956 gb AJS57688.1  glycosidase [Paenibacillus sp. IHBB 10380]"</p>
<p>["cazy SSC11544.1 Beta-1", "4-mannooligosaccharide phosphorylase [Mesotoga infera]",</p> <p>"cazygi 387859209 gb AFK07300.1  putative glycosylase [Mesotoga prima MesG1.Ag.4.2]",</p> <p>"cazygi 387859280 gb AFK07371.1  putative glycosylase [Mesotoga prima MesG1.Ag.4.2]"</p>
<p>["humangut158256496-stool1_revised_C835833_1_gene174095 strand:- start:3 stop:542 length:540 start_codon:no stop_codon:no gene_type:incomplete [Lack both ends] codon-table.11"]</p>
<p>["humangut158458797-stool1_revised_scaffold28805_1_gene79507 strand:- start:264 stop:896 length:633 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut158479027-stool1_revised_scaffold30056_1_gene47194 strand:+ start:3 stop:989 length:987 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut158499257-stool2_revised_C1279497_1_gene58504 strand:- start:59 stop:1018 length:960 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"mouseS-Fe10_GL0133378 [gene] locus=scaffold53511_1:8190:9149:+ [Complete] codon-table.11",</p> <p>"mouseS-Fe4_GL0042600 [gene] locus=scaffold73848_2:23173:24132:+ [Complete] codon-table.11"]</p>

<p>["humangut158499257-stool2_revised_scaffold72386_1_gene163327 strand:- start:342 stop:1319 length:978 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "humangut340101.Vvad_PD0761 [Complete]:- codon-table.11"]</p>
<p>["humangut158499257-stool2_revised_scaffold72531_1_gene159875 strand:- start:4341 stop:5312 length:972 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut158802708-stool1_revised_C1008059_1_gene86467 strand:- start:3134 stop:4063 length:930 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut159227541-stool2_revised_C945178_1_gene16611 strand:+ start:843 stop:1808 length:966 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut159571453-stool1_revised_scaffold14955_1_gene41830 strand:- start:2 stop:499 length:498 start_codon:no stop_codon:no gene_type:incomplete [Lack both ends] codon-table.11"]</p>
<p>["humangut159571453-stool2_revised_C1173406_1_gene60413 strand:- start:527 stop:1723 length:1197 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut159733294-stool1_revised_scaffold14067_1_gene118451 strand:+ start:3 stop:1031 length:1029 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut160704339-stool1_revised_C1402643_1_gene146236 strand:+ start:2157 stop:3194 length:1038 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut160704339-stool1_revised_scaffold30429_2_gene61233 strand:- start:44 stop:1027 length:984 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut160765029-stool1_revised_scaffold5378_2_gene125289 strand:- start:886 stop:1713 length:828 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut508703490-stool1_revised_scaffold18895_1_gene4490 strand:+ start:153 stop:929 length:777 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut604812005-stool2_revised_C648904_1_gene64050 strand:+ start:115 stop:678 length:564 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut763678604-stool1_revised_scaffold63435_2_gene111067 strand:+ start:3 stop:1016 length:1014 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "mouse1-1_GL0007446 [gene] locus=scaffold21897_2:2716:3729:+ [Complete] codon-table.11"]</p>
<p>["humangut763759525-stool1_revised_scaffold7590_1_gene57992 strand:- start:1004 stop:1987 length:984 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut764062976-stool1_revised_scaffold42844_1_gene85098 strand:+ start:3778 stop:4797 length:1020 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut764325968-stool1_revised_C587037_1_gene57487 strand:+ start:2 stop:1138 length:1137 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "mouse10_GL0002655 [gene] locus=scaffold8820_1:23230:24366:- [Complete] codon-table.11"]</p>
<p>["humangut764487809-stool1_revised_scaffold41314_1_gene32942 strand:+ start:830 stop:1630 length:801 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut764588959-stool1_revised_C809727_1_gene161960 strand:- start:629 stop:1474 length:846 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangutDLF006_GL0019934 [gene] locus=scaffold11533_10:432:1037:+ [Lack 3'-end] codon-table.11", "pigPIG_196_GL0235344 [gene] locus=scaffold40058_2:409:1014:+ [Lack 3'-end] codon-table.11"]</p>
<p>["humangutDLM015_GL0024411 [gene] locus=scaffold32325_4:31:618:- [Lack 5'-end] codon-table.11"]</p>

["humangutDLM019_GL0089165 [gene] locus=C792839_1:838:1386:+ [Lack 3'-end] codon-table.11"]
["humangutDOF008_GL0075713 [gene] locus=scaffold5558_22:2304:2819:+ [Complete] codon-table.11"]
["humangutDOM005_GL0030995 [gene] locus=scaffold13634_4:2297:3319:- [Complete] codon-table.11"]
["humangutDOM015_GL0044842 [gene] locus=scaffold20149_2:60:1133:- [Complete] codon-table.11"]
["humangutHT14A_GL0112810 [gene] locus=scaffold12911_2:3:737:- [Lack 3'-end] codon-table.11"]
["humangutHT25A_GL0012985 [gene] locus=scaffold13608_1:1:555:- [Lack both ends] codon-table.11"]
["humangutMH0001_GL0006833 [gene] locus=scaffold20375_1:360:1361:- [Complete] codon-table.11", "humangutMH0002_GL0050993 [gene] locus=scaffold21434_2:5265:6266:- [Complete] codon-table.11", "humangutMH0284_GL0164857 [gene] locus=scaffold227_2:11462:12463:- [Complete] codon-table.11", "humangutNOF013_GL0042668 [gene] locus=scaffold16252_2:37056:38057:+ [Complete] codon-table.11", "humangutT2D-135A_GL0108516 [gene] locus=scaffold4791_1:58343:59344:- [Complete] codon-table.11", "mouseMC-6-2_GL0049587 [gene] locus=scaffold33069_1:833:1834:+ [Complete] codon-table.11", "mouseG1-1A_GL0117276 [gene] locus=scaffold86222_1:11338:12339:+ [Complete] codon-table.11", "mouse10_GL0009130 [gene] locus=scaffold65698_1:30989:31990:+ [Complete] codon-table.11", "mouse10_GL0040594 [gene] locus=scaffold31213_3:486:1487:- [Complete] codon-table.11", "rumen553_GL0152112_1 [gene] locus=scaffold435106_1:22873:23874:+[Complete]", "rumen555_GL0767286_1 [gene] locus=scaffold869588_1:31827:32828:-[Complete]", "rumen7049_GL0427735_1 [gene] locus=scaffold336103_8:1493:2494:-[Complete]", "cazygi 922838593 gb ALA72633.1  glycosidase [Bacteroides dorei]", "cazygi 671713472 gb All65745.1  glycosidase [Bacteroides dorei]", "cazygi 671714526 gb All66798.1  glycosidase [Bacteroides dorei]", "cazygi 1026627367 gb AND18573.1  glycosidase [Bacteroides dorei CL03T12C01]", "cazygi 149931622 gb ABR38320.1  conserved hypothetical protein [Bacteroides vulgatus ATCC 8482]", "cazygi 941509161 gb ALK82696.1  putative glycoside hydrolase [Bacteroides vulgatus]"]
["humangutMH0002_GL0074276 [gene] locus=scaffold25860_7:11505:12485:+ [Complete] codon-table.11", "humangutMH0175_GL0056294 [gene] locus=scaffold21715_11:2532:3512:- [Complete] codon-table.11", "humangutMH0200_GL0090971 [gene] locus=scaffold107042_3:412:1392:- [Lack 5'-end] codon-table.11", "humangutMH0369_GL0104891 [gene] locus=scaffold115450_2:41781:42761:+ [Complete] codon-table.11", "pigPIG_125_GL0035608 [gene] locus=scaffold233897_3:294:1274:- [Complete] codon-table.11", "pigPIG-035_GL0065099 [gene] locus=scaffold74040_2:21474:22454:+ [Complete] codon-table.11", "pigPIG-058_GL0059068 [gene] locus=scaffold16066_1:770:1750:+ [Complete] codon-table.11", "pigBHZ-10B_GL0263822 [gene] locus=scaffold195385_2:211:1191:- [Complete] codon-table.11"]
["humangutMH0003_GL0070288 [gene] locus=scaffold22546_4:2110:3174:- [Complete] codon-table.11", "mouseMC-6-4_GL0100222 [gene] locus=scaffold71050_1:176952:178016:+ [Complete] codon-table.11", "mouseG1-3A_GL0132082 [gene] locus=scaffold84469_1:6217:7281:+ [Complete] codon-table.11", "pigPIG-001_GL0017370 [gene] locus=scaffold135436_1:3032:4096:- [Complete] codon-table.11"]
["humangutMH0006_GL0073173 [gene] locus=scaffold44109_4:3285:4316:- [Complete] codon-table.11", "rumen554_GL0351222_1 [gene] locus=scaffold1306023_1:537:1568:-[Complete]", "rumen554_GL1022066_1 [gene] locus=scaffold952786_2:1533:2564:+[Complete]", "rumen554_GL3107611_1 [gene] locus=scaffold491579_2:801:1832:-[Complete]", "rumen555_GL2221633_1 [gene] locus=scaffold391993_1:1454:2485:-[Complete]", "rumen0081_GL0339967_1 [gene] locus=scaffold8278_2:105:1136:-[Complete]", "rumen0081_GL0510561_1 [gene] locus=scaffold200904_3:934:1965:+[Complete]", "rumen100058_GL0159733_1 [gene] locus=scaffold80811_4:718:1749:+[Complete]",

<p>"rumen100058_GL1341543_1 [gene] locus=scaffold965193_2:1013:2044:-[Complete]",</p> <p>"rumen100058_GL2877558_1 [gene] locus=scaffold15954_1:3782:4813:+[Complete]",</p> <p>"rumen100058_GL3324878_1 [gene] locus=scaffold1542797_3:1022:2053:+[Complete]",</p> <p>"rumen2009040_GL0605756_1 [gene] locus=scaffold785353_2:4431:5462:-[Complete]",</p> <p>"rumen2009040_GL1454879_1 [gene] locus=scaffold1374058_2:5810:6841:-[Complete]",</p> <p>"rumen2009040_GL2494979_1 [gene] locus=scaffold785460_1:3:1034:+[Lack 5'-end]",</p> <p>"rumen3042_GL1617281_1 [gene] locus=scaffold334575_1:195:1226:-[Complete]",</p> <p>"rumen7049_GL1194146_1 [gene] locus=scaffold857149_2:2902:3933:+[Complete]"</p>
<p>["humangutMH0006_GL0079366 [gene] locus=scaffold37415_1:14309:15319:- [Complete] codon-table.11",</p> <p>"humangutMH0066_GL0062751 [gene] locus=scaffold42541_1:20708:21718:+ [Complete] codon-table.11",</p> <p>"humangutMH0153_GL0014600 [gene] locus=scaffold9405_52:4828:5838:+ [Complete] codon-table.11",</p> <p>"humangutV1_UC32-0_GL0004308 [gene] locus=scaffold73750_5:1328:2338:+ [Complete] codon-table.11",</p> <p>"humangutNLM003_GL0025011 [gene] locus=scaffold4615_5:1:1011:+ [Lack 5'-end] codon-table.11",</p> <p>"humangutED16A_GL0084421 [gene] locus=scaffold56845_10:3:1013:+ [Lack 5'-end] codon-table.11",</p> <p>"humangut160765029-stool1_revised_scaffold20279_1_gene36266 strand:- start:3221 stop:4231 length:1011 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"humangut765135172-stool1_revised_scaffold5747_1_gene85184 strand:- start:671 stop:1681 length:1011 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"mouseMC-6-1_GL0021356 [gene] locus=scaffold11166_1:6050:7060:+ [Complete] codon-table.11",</p> <p>"mouse1-1_GL0044908 [gene] locus=scaffold74334_1:62839:63849:- [Complete] codon-table.11",</p> <p>"pigPIG_122_GL0032378 [gene] locus=scaffold213557_2:1:1011:+ [Lack 5'-end] codon-table.11",</p> <p>"cazygi 390424090(gb) AFL78596.1  putative glycosylase [Alistipes finegoldii DSM 17242]"</p>
<p>["humangutMH0012_GL007633 [gene] locus=scaffold5089_1:34892:35926:- [Complete] codon-table.11",</p> <p>"humangutMH0086_GL0046571 [gene] locus=scaffold33385_5:36023:37057:+ [Complete] codon-table.11",</p> <p>"humangutMH0143_GL0096593 [gene] locus=scaffold18775_3:3:1037:+ [Lack 5'-end] codon-table.11",</p> <p>"humangutMH0247_GL0061712 [gene] locus=scaffold8399_21:1823:2857:- [Complete] codon-table.11",</p> <p>"humangutT2D-133A_GL0022420 [gene] locus=scaffold11867_33:3:1037:+ [Lack 5'-end] codon-table.11",</p> <p>"mouseS-Fe3_GL0078026 [gene] locus=scaffold9711_7:434:1468:- [Complete] codon-table.11",</p> <p>"mouseG1-1A_GL0008998 [gene] locus=scaffold3859_1:50223:51257:+ [Complete] codon-table.11",</p> <p>"mouseG1-5A_GL0080408 [gene] locus=scaffold51540_3:5228:6262:+ [Complete] codon-table.11",</p> <p>"mouseG1-5A_GL0112859 [gene] locus=scaffold77446_3:50345:51379:- [Complete] codon-table.11",</p> <p>"mouse1-1_GL0015202 [gene] locus=scaffold14214_14:1328:2362:- [Complete] codon-table.11",</p> <p>"mouse2-1_GL0026530 [gene] locus=scaffold83145_2:17848:18882:- [Complete] codon-table.11",</p> <p>"mouse2-3_GL0035306 [gene] locus=scaffold59252_3:14398:15432:- [Complete] codon-table.11",</p> <p>"mouse2-5_GL0068667 [gene] locus=scaffold23663_4:4599:5633:- [Complete] codon-table.11",</p> <p>"mouse6-2_GL0021672 [gene] locus=scaffold52589_2:21989:23023:+ [Complete] codon-table.11",</p> <p>"pigPIG-034_GL0052637 [gene] locus=scaffold42231_2:4221:5255:- [Complete] codon-table.11",</p> <p>"pigPIG-044_GL0183933 [gene] locus=scaffold106266_1:1:1035:+ [Lack 5'-end] codon-table.11",</p> <p>"pigPIG-077_GL0171451 [gene] locus=scaffold28563_6:20172:21206:+ [Complete] codon-table.11",</p> <p>"rumen552_GL0500597_1 [gene] locus=scaffold214801_2:6581:7615:-[Complete]",</p> <p>"rumen552_GL1374890_1 [gene] locus=scaffold1084712_1:2632:3666:-[Complete]",</p> <p>"rumen583_GL0572358_1 [gene] locus=scaffold335058_1:123985:125019:-[Complete]",</p> <p>"rumen0081_GL1164626_1 [gene] locus=scaffold2012364_1:291:1325:+[Complete]",</p> <p>"rumen7049_GL1801325_1 [gene] locus=scaffold477292_6:11863:12897:-[Complete]"</p>



<p>"humangutMH0012_GL0162861 [gene] locus=scaffold99774_3:7903:8856:- [Complete] codon-table.11",</p> <p>"pigPIG_137_GL0139699 [gene] locus=scaffold30657_11:3:956:- [Complete] codon-table.11"]</p>
<p>"humangutMH0013_GL0037620 [gene] locus=scaffold110_1:673:1623:- [Complete] codon-table.11",</p> <p>"humangutMH0053_GL0068920 [gene] locus=scaffold626_4:1802:2752:- [Complete] codon-table.11",</p> <p>"humangutMH0096_GL0116454 [gene] locus=scaffold2538_23:2068:3018:- [Complete] codon-table.11",</p> <p>"humangutMH0124_GL0124320 [gene] locus=scaffold477_9:3873:4823:- [Complete] codon-table.11",</p> <p>"humangutMH0262_GL0043670 [gene] locus=scaffold20731_13:199:1149:- [Complete] codon-table.11",</p> <p>"pigPIG_116_GL0215284 [gene] locus=scaffold191671_1:11165:12115:+ [Complete] codon-table.11",</p> <p>"pigPIG-012_GL0140313 [gene] locus=scaffold106884_1:1608:2558:- [Complete] codon-table.11",</p> <p>"pigPIG-025_GL0054893 [gene] locus=scaffold36974_1:10841:11791:- [Complete] codon-table.11",</p> <p>"pigPIG-090_GL0059069 [gene] locus=scaffold32602_5:42:992:- [Complete] codon-table.11",</p> <p>"pigBHZ-7B_GL0139024 [gene] locus=scaffold13472_1:11996:12946:- [Complete] codon-table.11",</p> <p>"pigEYZ-120B_GL0317062 [gene] locus=scaffold25512_11:1726:2676:+ [Complete] codon-table.11",</p> <p>"rumen100058_GL3096331_1 [gene] locus=scaffold38791_2:649:1599:-[Complete]",</p> <p>"rumen2009040_GL0441176_1 [gene] locus=scaffold2048064_4:8118:9068:+[Complete]",</p> <p>"rumen2009040_GL2810383_1 [gene] locus=scaffold675163_2:701:1651:+[Complete]"</p>
<p>"humangutMH0017_GL0009327 [gene] locus=scaffold30260_19:291:1316:+ [Complete] codon-table.11"]</p>
<p>"humangutMH0030_GL0005166 [gene] locus=scaffold11561_2:3462:4541:- [Complete] codon-table.11",</p> <p>"humangutMH0308_GL0161116 [gene] locus=scaffold89184_2:1904:2983:+ [Complete] codon-table.11"]</p>
<p>"humangutMH0037_GL0017616 [gene] locus=scaffold455_20:3:869:- [Lack 3'-end] codon-table.11"]</p>
<p>"humangutMH0045_GL0029867 [gene] locus=scaffold19450_1:11569:12354:- [Complete] codon-table.11",</p> <p>"rumen555_GL2328202_1 [gene] locus=scaffold210456_1:2698:3483:+[Complete]"</p>
<p>"humangutMH0046_GL0024529 [gene] locus=scaffold45167_3:1:723:- [Lack 3'-end] codon-table.11"]</p>
<p>"humangutMH0048_GL0000259 [gene] locus=scaffold5871_5:2:685:- [Lack 3'-end] codon-table.11"]</p>
<p>"humangutMH0054_GL0021605 [gene] locus=scaffold4199_1:5393:6364:+ [Complete] codon-table.11",</p> <p>"humangutMH0130_GL0002707 [gene] locus=scaffold9609_4:1742:2713:+ [Complete] codon-table.11",</p> <p>"pigPIG-046_GL0086195 [gene] locus=scaffold121955_1:7422:8393:+ [Complete] codon-table.11"]</p>
<p>"humangutMH0054_GL0061333 [gene] locus=scaffold2139_1:9118:10125:+ [Complete] codon-table.11",</p> <p>"humangutMH0074_GL0033152 [gene] locus=scaffold11828_3:5629:6636:- [Complete] codon-table.11",</p> <p>"humangutMH0108_GL0051486 [gene] locus=scaffold20039_1:1751:2758:- [Complete] codon-table.11",</p> <p>"humangutMH0161_GL0092587 [gene] locus=scaffold22931_19:976:1983:+ [Complete] codon-table.11",</p> <p>"humangutMH0198_GL0004874 [gene] locus=scaffold10037_3:28908:29915:- [Complete] codon-table.11",</p> <p>"humangutMH0230_GL0094142 [gene] locus=scaffold12339_1:207:1214:- [Complete] codon-table.11",</p> <p>"humangutMH0262_GL0144422 [gene] locus=scaffold52175_4:7243:8250:+ [Complete] codon-table.11",</p> <p>"humangutMH0266_GL0143819 [gene] locus=scaffold11364_6:5967:6974:+ [Complete] codon-table.11",</p> <p>"humangutMH0302_GL0090532 [gene] locus=scaffold18882_3:3640:4647:- [Complete] codon-table.11",</p> <p>"humangutMH0319_GL0103473 [gene] locus=scaffold51083_1:2038:3045:- [Complete] codon-table.11",</p> <p>"humangutMH0443_GL0062302 [gene] locus=scaffold41370_3:685:1692:- [Complete] codon-table.11",</p> <p>"humangutO2.CD1-0_GL0163366 [gene] locus=scaffold71766_1:2173:3180:- [Complete] codon-table.11",</p> <p>"humangutO2.UC22-1_GL0037024 [gene] locus=scaffold63429_1:1363:2370:+ [Complete] codon-table.11",</p> <p>"humangutO2.UC41-1_GL0201289 [gene] locus=scaffold117952_1:9172:10179:- [Complete] codon-table.11",</p> <p>"humangutV1.CD44-0_GL0031209 [gene] locus=scaffold58205_2:3053:4060:- [Complete] codon-table.11",</p> <p>"humangutV1.UC35-0_GL0004173 [gene] locus=scaffold3407_10:2948:3955:- [Complete] codon-table.11",</p> <p>"humangutN084A_GL0036398 [gene] locus=C703110_1:2353:3360:- [Complete] codon-table.11",</p>

"humangutT2D-102A_GL0023114 [gene] locus=scaffold75873_1:11748:12755:+ [Complete] codon-table.11",
"humangutT2D-26A_GL0009503 [gene] locus=scaffold61396_3:3667:4674:- [Complete] codon-table.11",
"humangut158337416-stool1_revised_scaffold3342_1_gene86922 strand:+ start:1305 stop:2312 length:1008 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",
"humangut158499257-stool2_revised_scaffold65358_1_gene61956 strand:- start:1947 stop:2954 length:1008 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",
"humangut638754422-stool1_revised_scaffold3920_1_gene57956 strand:+ start:50352 stop:51359 length:1008 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",
"mouseS-Fe10_GL0143739 [gene] locus=scaffold225_2:92194:93201:+ [Complete] codon-table.11",
"mouseMC-6-3_GL0005908 [gene] locus=scaffold1945_2:39217:40224:- [Complete] codon-table.11",
"mouse13_GL0077551 [gene] locus=scaffold22877_5:279:1286:- [Complete] codon-table.11",
"mouse1B-dyr12-07_GL0031314 [gene] locus=scaffold7349_1:1957:2964:- [Complete] codon-table.11",
"mouse20_GL0163161 [gene] locus=scaffold113299_1:18879:19886:+ [Complete] codon-table.11",
"mouse31_GL0048804 [gene] locus=scaffold122_4:3:1010:- [Complete] codon-table.11",
"pigPIG-022_GL0151450 [gene] locus=scaffold29824_1:1050:2057:+ [Complete] codon-table.11",
"cazygij 291515082 emb CBK64292.1  Predicted glycosylase [Alistipes shahii WAL 8301]"
["humangutMH0056_GL0032889 [gene] locus=scaffold15457_2:3:626:- [Lack both ends] codon-table.11"]
["humangutMH0062_GL0052144 [gene] locus=scaffold11559_1:467:1039:+ [Lack 3'-end] codon-table.11"]
["humangutMH0062_GL0073614 [gene] locus=scaffold7351_1:214:1296:- [Complete] codon-table.11"]
["humangutMH0069_GL0038472 [gene] locus=scaffold61521_1:3346:4335:- [Complete] codon-table.11", "pigEYZ-362B_GL0018425 [gene] locus=scaffold177282_1:1379:2368:- [Complete] codon-table.11", "rumen554_GL0544849_1 [gene] locus=scaffold1148971_4:4608:5597:+[Complete]", "rumen100058_GL2223164_1 [gene] locus=scaffold374389_2:568:1557:-[Complete]", "rumen2009040_GL0511168_1 [gene] locus=scaffold1187221_7:2589:3578:+[Complete]", "rumen2009040_GL0855763_1 [gene] locus=scaffold1884549_2:1:990:-[Complete]", "rumen2009040_GL1256803_1 [gene] locus=scaffold565906_6:7292:8281:-[Complete]"
["humangutMH0070_GL0022753 [gene] locus=scaffold14051_3:586:1587:- [Complete] codon-table.11"]
["humangutMH0077_GL0062682 [gene] locus=scaffold13129_1:2:718:+ [Lack 5'-end] codon-table.11"]
["humangutMH0077_GL0064107 [gene] locus=scaffold30884_2:4060:5295:+ [Complete] codon-table.11"]
["humangutMH0091_GL0103697 [gene] locus=scaffold41416_11:207:1037:- [Lack 5'-end] codon-table.11"]
["humangutMH0113_GL0096944 [gene] locus=scaffold39885_3:27249:28211:+ [Complete] codon-table.11", "mouse10_GL0047205 [gene] locus=scaffold56474_1:14525:15487:+ [Complete] codon-table.11"]
["humangutMH0116_GL0149865 [gene] locus=scaffold78008_1:1:954:+ [Lack 5'-end] codon-table.11"]
["humangutMH0125_GL0107874 [gene] locus=scaffold9295_9:1331:2371:- [Complete] codon-table.11"]
["humangutMH0131_GL0124864 [gene] locus=scaffold52942_5:5191:6336:+ [Complete] codon-table.11"]
["humangutMH0141_GL0105826 [gene] locus=scaffold50519_7:2:856:- [Lack 3'-end] codon-table.11", "rumen552_GL1031059_1 [gene] locus=C22050106_1:212:1066:+[Lack 3'-end]", "rumen3042_GL1593958_1 [gene] locus=scaffold1149001_1:5221:6075:+[Lack 3'-end]"
["humangutMH0144_GL0085137 [gene] locus=scaffold33826_7:1081:2079:+ [Complete] codon-table.11", "mouseGroup2-3A_GL0037234 [gene] locus=scaffold15184_2:2801:3799:+ [Complete] codon-table.11", "rumen553_GL0333566_1 [gene] locus=scaffold4789_3:231:1229:-[Complete]", "rumen553_GL0724914_1 [gene] locus=scaffold109429_2:65133:66131:+[Complete]", "rumen553_GL0803416_1 [gene] locus=scaffold433819_1:3652:4650:+[Complete]", "rumen553_GL0877558_1 [gene] locus=scaffold218042_2:402:1400:+[Complete]"

<p>"rumen552_GL0168191_1 [gene] locus=scaffold16320_9:190:1188:+[Complete]",</p> <p>"rumen552_GL0331847_1 [gene] locus=C22507414_1:6988:7986:-[Complete]",</p> <p>"rumen583_GL0091630_1 [gene] locus=scaffold310069_1:8390:9388:+[Complete]",</p> <p>"rumen554_GL0668499_1 [gene] locus=C41165291_1:140:1138:+[Complete]",</p> <p>"rumen555_GL0499302_1 [gene] locus=scaffold755544_2:1509:2507:-[Complete]",</p> <p>"rumen555_GL1686954_1 [gene] locus=scaffold1131879_2:7001:7999:+[Complete]",</p> <p>"rumen0081_GL1720882_1 [gene] locus=scaffold76176_13:863:1861:+[Complete]",</p> <p>"rumen2009040_GL3655194_1 [gene] locus=scaffold1232779_3:57:1055:-[Complete]",</p> <p>"rumen7049_GL0409848_1 [gene] locus=scaffold1618727_1:230:1228:+[Complete]",</p> <p>"cazygi 571257543 emb CCO03868.1  Glycoside Hydrolase Family 130 protein [Ruminococcus bicirculans]"</p>
<p>["humangutMH0147_GL0058267 [gene] locus=scaffold34624_4:1454:2605:- [Complete] codon-table.11"]</p>
<p>["humangutMH0149_GL0065606 [gene] locus=scaffold3870_10:11473:12516:+ [Complete] codon-table.11",</p> <p>"humangutT2D-140A_GL0072840 [gene] locus=scaffold30211_2:293:1336:- [Complete] codon-table.11",</p> <p>"mouseMC-0-1_GL0081617 [gene] locus=scaffold70529_1:7132:8175:- [Complete] codon-table.11",</p> <p>"mouseGroup2-5A_GL0067020 [gene] locus=scaffold39731_17:2777:3820:- [Complete] codon-table.11",</p> <p>"mouse2B-dyr23-07_GL0027859 [gene] locus=C454172_1:1632:2675:+ [Complete] codon-table.11",</p> <p>"rumen554_GL1095844_1 [gene] locus=scaffold247511_2:47:1090:+[Complete]",</p> <p>"rumen100058_GL0662624_1 [gene] locus=scaffold1264265_3:4856:5899:-[Complete]"</p>
<p>["humangutMH0149_GL0135257 [gene] locus=scaffold77841_3:14376:15386:- [Complete] codon-table.11"]</p>
<p>["humangutMH0168_GL0097676 [gene] locus=scaffold917_5:195:773:- [Lack 5'-end] codon-table.11"]</p>
<p>["humangutMH0170_GL0071387 [gene] locus=scaffold10595_4:127:999:+ [Lack 3'-end] codon-table.11"]</p>
<p>["humangutMH0186_GL0082655 [gene] locus=scaffold21459_11:4293:5051:+ [Lack 3'-end] codon-table.11",</p> <p>"pigBHZ-4B_GL0100091 [gene] locus=scaffold145523_2:2:760:- [Lack 3'-end] codon-table.11"]</p>
<p>["humangutMH0189_GL0040812 [gene] locus=scaffold645_6:2271:3248:+ [Complete] codon-table.11",</p> <p>"humangutO2.UC47-0_GL0056011 [gene] locus=scaffold73615_7:2:979:+ [Lack 5'-end] codon-table.11",</p> <p>"pigPIG-049_GL0071696 [gene] locus=scaffold23465_2:12:989:+ [Complete] codon-table.11",</p> <p>"pigPIG-052_GL0054588 [gene] locus=scaffold129083_2:3793:4770:- [Complete] codon-table.11",</p> <p>"pigBHZ-8B_GL0117323 [gene] locus=scaffold67234_2:1249:2226:- [Complete] codon-table.11",</p> <p>"pigDB-510B_GL0002338 [gene] locus=scaffold165928_2:313:1290:+ [Complete] codon-table.11",</p> <p>"pigEYZ-381B_GL0030405 [gene] locus=scaffold229025_1:2041:3018:- [Complete] codon-table.11",</p> <p>"rumen553_GL0593875_1 [gene] locus=scaffold381191_2:1174:2151:-[Complete]",</p> <p>"cazygi 390522395 gb AFL98126.1  putative glycosylase [Ornithobacterium rhinotracheale DSM 15997]",</p> <p>"cazygi 686513339 gb AIP99884.1  glycosidase [Ornithobacterium rhinotracheale ORT-UMN 88]"</p>
<p>["humangutMH0189_GL0046548 [gene] locus=scaffold7166_7:2:871:+ [Lack both ends] codon-table.11"]</p>
<p>["humangutMH0193_GL0151567 [gene] locus=scaffold48753_8:32579:33607:+ [Complete] codon-table.11",</p> <p>"mouse1-2_GL0101011 [gene] locus=scaffold7366_22:5101:6129:- [Complete] codon-table.11",</p> <p>"pigPIG-039_GL0006794 [gene] locus=scaffold172054_1:2742:3770:+ [Complete] codon-table.11",</p> <p>"pigBMZ-17B_GL0086225 [gene] locus=scaffold116002_6:360:1388:+ [Complete] codon-table.11",</p> <p>"rumen554_GL1338143_1 [gene] locus=scaffold1192500_2:1327:2355:+[Complete]",</p> <p>"rumen554_GL2517352_1 [gene] locus=scaffold5297_1:2844:3872:+[Complete]",</p> <p>"rumen555_GL0884603_1 [gene] locus=scaffold199175_1:6769:7797:+[Complete]",</p> <p>"rumen555_GL0998754_1 [gene] locus=scaffold721890_1:29:1057:-[Complete]",</p> <p>"rumen555_GL1367176_1 [gene] locus=scaffold1160883_1:665:1693:+[Complete]",</p> <p>"rumen0081_GL1251027_1 [gene] locus=scaffold1087847_1:2155:3183:+[Complete]",</p>

"rumen100058_GL1134211_1 [gene] locus=scaffold505029_1:124:1152:-[Complete]", "rumen100058_GL1945834_1 [gene] locus=scaffold659282_1:2299:3327:+[Complete]"
["humangutMH0197_GL0162843 [gene] locus=scaffold136207_2:1:846:- [Lack 3'-end] codon-table.11"]
["humangutMH0197_GL0177559 [gene] locus=scaffold131358_1:737:1219:- [Lack 5'-end] codon-table.11"]
["humangutMH0212_GL0074415 [gene] locus=scaffold1862_18:1404:2384:+ [Complete] codon-table.11", "mouseS-Fe12_GL0196102 [gene] locus=scaffold7461_11:4473:5453:- [Complete] codon-table.11", "mouseMC-0-1_GL0003086 [gene] locus=scaffold1174_4:278:1258:+ [Complete] codon-table.11", "mouseG1-1A_GL0037566 [gene] locus=scaffold25365_1:33399:34379:- [Complete] codon-table.11", "mouseG1-1A_GL0037586 [gene] locus=scaffold25365_1:64275:65255:- [Complete] codon-table.11", "mouseGroup2-3A_GL0165413 [gene] locus=scaffold107419_1:18570:19550:+ [Complete] codon-table.11", "mouse10_GL0047421 [gene] locus=scaffold62640_2:18278:19258:+ [Complete] codon-table.11", "mouse1_GL0094620 [gene] locus=scaffold11473_4:2802:3782:- [Complete] codon-table.11", "mouse1-2_GL0057476 [gene] locus=scaffold72407_6:6926:7906:+ [Complete] codon-table.11", "mouse2-2_GL0051309 [gene] locus=C1485145_1:93:1073:+ [Complete] codon-table.11", "mouse2-3_GL0096831 [gene] locus=scaffold59790_1:35136:36116:+ [Complete] codon-table.11", "mouse3-6_GL0068398 [gene] locus=scaffold10_2:15787:16767:- [Complete] codon-table.11", "mouse4-8_GL0049572 [gene] locus=scaffold504_4:43675:44655:+ [Complete] codon-table.11", "mouse4-8_GL0076624 [gene] locus=scaffold11068_2:1384:2364:+ [Complete] codon-table.11"]
["humangutMH0220_GL0164069 [gene] locus=scaffold17526_1:58:1047:+ [Complete] codon-table.11", "pigPIG_153_GL0036422 [gene] locus=scaffold32198_1:543:1532:- [Complete] codon-table.11"]
["humangutMH0245_GL0146682 [gene] locus=scaffold28855_5:2:430:- [Lack 3'-end] codon-table.11"]
["humangutMH0250_GL0223774 [gene] locus=scaffold13892_12:155:1108:- [Complete] codon-table.11"]
["humangutMH0260_GL0147700 [gene] locus=scaffold41047_1:82:663:+ [Lack 3'-end] codon-table.11"]
["humangutMH0262_GL0030555 [gene] locus=scaffold6436_5:1:759:- [Lack 3'-end] codon-table.11"]
["humangutMH0270_GL0044430 [gene] locus=scaffold20929_2:1244:2299:+ [Complete] codon-table.11"]
["humangutMH0277_GL0039787 [gene] locus=scaffold19094_1:344:1375:+ [Complete] codon-table.11"]
["humangutMH0281_GL0131783 [gene] locus=scaffold81319_1:3469:4038:- [Lack 5'-end] codon-table.11", "humangut508703490-stool1_revised_scaffold3467_3_gene28638 strand:- start:12408 stop:12977 length:570 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangutMH0287_GL0094017 [gene] locus=scaffold40373_6:109:1140:+ [Complete] codon-table.11", "rumen553_GL0374569_1 [gene] locus=scaffold192374_1:95638:96669:+[Complete]", "rumen554_GL1628264_1 [gene] locus=scaffold2194842_1:215:1246:+[Complete]"
["humangutMH0303_GL0035338 [gene] locus=scaffold35829_14:1:567:- [Lack 3'-end] codon-table.11"]
["humangutMH0303_GL0118055 [gene] locus=scaffold42008_3:84:1145:- [Complete] codon-table.11", "humangutN038A_GL0019547 [gene] locus=scaffold20313_7:490:1551:- [Lack 5'-end] codon-table.11", "pigPIG-039_GL0000916 [gene] locus=scaffold91017_9:5030:6091:+ [Complete] codon-table.11"]
["humangutMH0303_GL0199969 [gene] locus=scaffold70592_2:219:1190:- [Complete] codon-table.11"]
["humangutMH0309_GL0028253 [gene] locus=scaffold6046_3:2:688:+ [Lack 5'-end] codon-table.11"]
["humangutMH0355_GL0016053 [gene] locus=scaffold148089_2:22:978:- [Complete] codon-table.11", "humangutO2_UC29-1_GL0037523 [gene] locus=scaffold55840_5:1011:1967:- [Complete] codon-table.11"]
["humangutMH0357_GL0045195 [gene] locus=scaffold18423_10:3:1067:+ [Lack 5'-end] codon-table.11"]
["humangutMH0369_GL0155294 [gene] locus=scaffold5680_2:3:854:+ [Lack 5'-end] codon-table.11"]
["humangutMH0381_GL0168056 [gene] locus=scaffold45574_11:1:681:+ [Lack both ends] codon-table.11",

"rumen554_GL2592698_1 [gene] locus=scaffold1255305_1:2:682:-[Lack 3'-end]",
"rumen0081_GL2387199_1 [gene] locus=scaffold1888956_1:3:683:+[Lack both ends]"
["humangutMH0382_GL0091523 [gene] locus=scaffold7953_8:1:663:+ [Lack 5'-end] codon-table.11", "mouseMC-6-5_GL0123570 [gene] locus=scaffold95762_1:1:663:+ [Lack 5'-end] codon-table.11"]
["humangutMH0382_GL0154334 [gene] locus=scaffold35103_1:3:716:+ [Lack both ends] codon-table.11"]
["humangutMH0387_GL0029039 [gene] locus=scaffold12283_5:6659:7738:- [Complete] codon-table.11"]
["humangutMH0397_GL0116910 [gene] locus=scaffold2829_39:1:1077:+ [Lack 5'-end] codon-table.11"]
["humangutMH0399_GL0023075 [gene] locus=scaffold120460_2:3:515:+ [Lack both ends] codon-table.11"]
["humangutMH0400_GL0110506 [gene] locus=scaffold25753_1:195:1136:- [Lack 5'-end] codon-table.11"]
["humangutMH0402_GL0139858 [gene] locus=scaffold153726_2:3:548:- [Lack both ends] codon-table.11"]
["humangutMH0407_GL0183292 [gene] locus=scaffold23718_13:1:1041:+ [Lack 5'-end] codon-table.11", "mouse11_GL0083170 [gene] locus=scaffold90279_4:69:1109:- [Lack 5'-end] codon-table.11", "mouse26_GL0143939 [gene] locus=scaffold53671_2:3494:4534:- [Complete] codon-table.11", "mouse4-1_GL0031569 [gene] locus=scaffold29527_1:22919:23959:+ [Complete] codon-table.11", "mouse5-5_GL0084385 [gene] locus=scaffold64478_2:41991:43031:+ [Complete] codon-table.11", "mouse7-5_GL0099091 [gene] locus=scaffold62478_1:4353:5393:- [Complete] codon-table.11", "pigPIG-027_GL0027327 [gene] locus=scaffold49328_8:413:1453:- [Complete] codon-table.11", "rumen552_GL0517601_1 [gene] locus=scaffold11542_8:6907:7947:+[Complete]", "rumen552_GL0987052_1 [gene] locus=scaffold1115340_1:3566:4606:-[Complete]", "rumen100058_GL2046874_1 [gene] locus=scaffold136438_4:162:1202:-[Complete]"
["humangutMH0408_GL0118706 [gene] locus=scaffold127104_3:1542:2570:- [Complete] codon-table.11"]
["humangutMH0421_GL0035274 [gene] locus=scaffold54804_5:3:1028:+ [Lack 5'-end] codon-table.11"]
["humangutMH0426_GL0018631 [gene] locus=scaffold58191_1:1153:1920:- [Lack 5'-end] codon-table.11"]
["humangutMH0428_GL0117452 [gene] locus=scaffold126494_3:20986:22113:- [Complete] codon-table.11"]
["humangutMH0429_GL0034838 [gene] locus=scaffold52026_6:723:1685:- [Complete] codon-table.11", "humangut158499257-stool2_revised_scaffold12674_2_gene215003 strand:- start:8453 stop:9415 length:963 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "mouseS-Fe8_GL0093162 [gene] locus=scaffold56129_1:824:1786:- [Lack 5'-end] codon-table.11"]
["humangutMH0431_GL0078633 [gene] locus=scaffold30057_3:617:1462:+ [Lack 3'-end] codon-table.11"]
["humangutMH0433_GL0186557 [gene] locus=scaffold28903_3:603:1043:- [Lack 5'-end] codon-table.11"]
["humangutMH0437_GL0054517 [gene] locus=scaffold9441_16:2:709:+ [Lack 5'-end] codon-table.11"]
["humangutMH0437_GL0254245 [gene] locus=scaffold102268_1:3:722:- [Lack both ends] codon-table.11"]
["humangutMH0457_GL0165653 [gene] locus=C2199620_1:3:599:- [Lack 3'-end] codon-table.11"]
["humangutN038A_GL0048650 [gene] locus=C772186_1:1:429:+ [Lack 5'-end] codon-table.11"]
["humangutN038A_GL0106061 [gene] locus=scaffold4397_10:62:679:+ [Lack 3'-end] codon-table.11"]
["humangutN051A_GL0044481 [gene] locus=scaffold18856_3:110:532:- [Complete] codon-table.11"]
["humangutN066A_GL0107416 [gene] locus=scaffold49167_2:2:640:- [Lack both ends] codon-table.11"]
["humangutNLM027_GL0039233 [gene] locus=scaffold31637_3:1001:2026:- [Complete] codon-table.11", "mouseMC-0-1_GL0067499 [gene] locus=scaffold55912_2:86:1111:+ [Complete] codon-table.11", "pigPIG-083_GL0081509 [gene] locus=scaffold168547_2:261:1286:+ [Complete] codon-table.11", "pigEYZ-381B_GL0016318 [gene] locus=scaffold65333_1:521:1546:- [Complete] codon-table.11"]
["humangutNOF008_GL0089493 [gene] locus=scaffold4840_1:146:1087:+ [Lack 3'-end] codon-table.11"]
["humangutNOM004_GL0020231 [gene] locus=scaffold632_9:3:617:+ [Lack both ends] codon-table.11"]

["humangutO2.UC11-1_GL0089924 [gene] locus=scaffold10588_4:3:536:- [Lack 3'-end] codon-table.11"]
["humangutO2.UC18-1_GL0073107 [gene] locus=scaffold50456_1:32410:33462:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC18-1_GL0097081 [gene] locus=C1517119_1:3:509:+ [Lack both ends] codon-table.11"]
["humangutO2.UC18-1_GL0191078 [gene] locus=scaffold112581_1:3530:4207:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC19-2_GL0032028 [gene] locus=scaffold42319_8:879:1490:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC20-1_GL0102030 [gene] locus=scaffold57915_1:3920:4432:+ [Complete] codon-table.11", "rumen2009040_GL2485921_1 [gene] locus=scaffold48956_3:2:514:+ [Lack 5'-end]"]
["humangutO2.UC21-2_GL0080310 [gene] locus=scaffold12179_16:456:956:- [Lack 5'-end] codon-table.11", "pigPIG-007_GL0029642 [gene] locus=scaffold30699_1:3:500:- [Lack both ends] codon-table.11"]
["humangutO2.UC29-0_GL0026334 [gene] locus=scaffold373_4:2:1090:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC32-1_GL0154626 [gene] locus=scaffold89918_3:1:1059:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC35-1_GL0065883 [gene] locus=scaffold10493_1:3:641:+ [Lack 5'-end] codon-table.11", "humangutV1.UC50-1_GL0145932 [gene] locus=scaffold94632_3:1:636:+ [Lack both ends] codon-table.11"]
["humangutO2.UC35-1_GL0064221 [gene] locus=scaffold35660_15:3:608:- [Lack 3'-end] codon-table.11"]
["humangutO2.UC41-0_GL0021867 [gene] locus=scaffold52570_3:2:727:+ [Lack both ends] codon-table.11"]
["humangutO2.UC41-0_GL0099349 [gene] locus=scaffold35913_2:1:537:- [Lack both ends] codon-table.11"]
["humangutO2.UC47-1_GL0002152 [gene] locus=scaffold52285_1:1032:1538:+ [Lack 3'-end] codon-table.11"]
["humangutO2.UC51-0_GL0092079 [gene] locus=scaffold16611_18:4537:5577:- [Complete] codon-table.11"]
["humangutO2.UC52-0_GL0088588 [gene] locus=C1307293_1:1261:2283:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC60-0_GL0087539 [gene] locus=scaffold43748_3:1:582:- [Lack 3'-end] codon-table.11"]
["humangutO2.UC7-1_GL0177132 [gene] locus=scaffold59965_3:32045:33076:+ [Complete] codon-table.11", "mouse5-7_GL0130853 [gene] locus=scaffold79670_1:2:1033:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC8-2_GL0064491 [gene] locus=scaffold40685_6:40603:41538:+ [Complete] codon-table.11"]
["humangutSZEY-26A_GL0007821 [gene] locus=scaffold23789_1:37311:38363:- [Complete] codon-table.11", "rumen554_GL2352801_1 [gene] locus=scaffold1127205_3:4361:5413:+ [Complete]"]
["humangutSZEY-29A_GL0042375 [gene] locus=scaffold917_4:1149:1712:- [Lack 5'-end] codon-table.11"]
["humangutSZEY-69A_GL0007593 [gene] locus=scaffold5091_7:372:986:- [Lack 5'-end] codon-table.11"]
["humangutT2D-157A_GL0045181 [gene] locus=scaffold3295_8:1:807:- [Lack 3'-end] codon-table.11"]
["humangutT2D-33A_GL0105813 [gene] locus=scaffold35838_1:16531:17295:+ [Lack 3'-end] codon-table.11"]
["humangutT2D-35A_GL0004763 [gene] locus=scaffold1796_1:13:1059:- [Complete] codon-table.11", "humangutT2D-41A_GL0104862 [gene] locus=scaffold3972_8:3:1049:+ [Lack 5'-end] codon-table.11", "mouse1-4_GL0037745 [gene] locus=scaffold12922_3:135:1181:+ [Complete] codon-table.11", "mouse5-1_GL0045110 [gene] locus=scaffold12825_7:621:1667:- [Complete] codon-table.11"]
["humangutT2D-48A_GL0079777 [gene] locus=scaffold15415_7:9925:10509:+ [Lack 3'-end] codon-table.11"]
["humangutT2D-51A_GL0027405 [gene] locus=scaffold61679_1:1:429:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-51A_GL0062678 [gene] locus=scaffold91752_1:1:756:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-52A_GL0017199 [gene] locus=scaffold3660_3:3:773:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-62A_GL0022311 [gene] locus=scaffold1006_8:1837:2844:+ [Complete] codon-table.11", "pigPIG-007_GL0212626 [gene] locus=scaffold32192_3:47:1054:- [Complete] codon-table.11"]
["humangutT2D-62A_GL0057777 [gene] locus=scaffold2778_13:3257:4228:+ [Complete] codon-table.11"]
["humangutT2D-76A_GL0073077 [gene] locus=scaffold26895_1:3:620:+ [Lack both ends] codon-table.11"]
["humangutV1.CD15-3_GL0085774 [gene] locus=scaffold15479_34:9712:10683:- [Complete] codon-table.11"]
["humangutV1.CD25-4_GL0009661 [gene] locus=scaffold7865_2:408:902:- [Lack 5'-end] codon-table.11"]

["humangutV1.CD3-0-PN_GL0015918 [gene] locus=scaffold6292_3:3:611:- [Lack 3'-end] codon-table.11"]
["humangutV1.CD30-0_GL0021637 [gene] locus=scaffold43682_3:3:617:- [Lack both ends] codon-table.11"]
["humangutV1.CD42-0_GL0076323 [gene] locus=scaffold3497_11:15799:16815:+ [Complete] codon-table.11"]
["humangutV1.CD55-0_GL0211473 [gene] locus=scaffold70538_3:2:562:+ [Lack both ends] codon-table.11", "rumen554_GL3158057_1 [gene] locus=scaffold1529397_1:1:561:+[Lack both ends]"]
["humangutV1.FI17_GL0042880 [gene] locus=scaffold78622_5:16482:17477:- [Complete] codon-table.11", "rumen552_GL0555913_1 [gene] locus=scaffold391812_2:2921:3916:-[Complete]"]
["humangutV1.FI17_GL0215038 [gene] locus=scaffold67174_3:3:758:- [Lack both ends] codon-table.11"]
["humangutV1.FI17_GL0221942 [gene] locus=scaffold8131_3:3:881:+ [Lack 5'-end] codon-table.11"]
["humangutV1.FI28_GL0086913 [gene] locus=scaffold70262_3:1:181:+ [Lack 5'-end] codon-table.11"]
["humangutV1.UC11-5_GL0014111 [gene] locus=scaffold14897_18:201:1238:+ [Complete] codon-table.11", "humangut159753524-stool1_revised_scaffold17260_2_gene39433 strand:+ start:1 stop:1038 length:1038 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "humangutMH0364_GL0058645 [gene] locus=scaffold51576_25:140:1174:+ [Lack 3'-end] codon-table.11", "mouseGroup2-6A_GL0009990 [gene] locus=scaffold5386_5:1097:2134:- [Lack 5'-end] codon-table.11", "mouse20_GL0137763 [gene] locus=scaffold37707_1:7070:8107:- [Complete] codon-table.11", "mouse7-1_GL0034864 [gene] locus=scaffold72_16:6021:7058:+ [Complete] codon-table.11"]
["humangutV1.UC11-5_GL0123810 [gene] locus=scaffold5864_2:2:505:+ [Lack both ends] codon-table.11", "pigPIG_151_GL0280216 [gene] locus=scaffold280443_1:2:505:- [Lack both ends] codon-table.11"]
["humangutV1.UC11-5_GL0195187 [gene] locus=scaffold85150_3:2:739:+ [Lack 5'-end] codon-table.11", "mouse7-2_GL0041940 [gene] locus=scaffold35517_6:81:818:- [Complete] codon-table.11"]
["humangutV1.UC16-0_GL0069329 [gene] locus=scaffold16876_1:2:670:- [Lack 3'-end] codon-table.11"]
["humangutV1.UC17-2_GL0015894 [gene] locus=scaffold28094_1:1:660:+ [Lack both ends] codon-table.11"]
["humangutV1.UC17-2_GL0083726 [gene] locus=scaffold41122_4:2:649:- [Lack 3'-end] codon-table.11", "rumen3042_GL0504186_1 [gene] locus=scaffold223018_2:3:650:+[Lack both ends]"]
["humangutV1.UC38-4_GL0166133 [gene] locus=scaffold21280_8:12277:13332:- [Complete] codon-table.11", "mouse2-3_GL0031396 [gene] locus=scaffold235_3:6008:7063:- [Complete] codon-table.11", "pigPIG-065_GL0007788 [gene] locus=scaffold15243_8:454:1509:+ [Complete] codon-table.11", "rumen553_GL0553273_1 [gene] locus=C7637698_1:538:1593:-[Complete]", "rumen100058_GL3245499_1 [gene] locus=scaffold608862_5:1049:2104:+[Complete]"]
["humangutV1.UC40-1_GL0067979 [gene] locus=scaffold56606_4:2:427:+ [Lack 5'-end] codon-table.11"]
["humangutV1.UC51-0_GL0038735 [gene] locus=scaffold18193_46:8332:8898:- [Lack 5'-end] codon-table.11"]
["humangutV1.UC54-0_GL0149599 [gene] locus=scaffold7166_6:3402:4475:+ [Complete] codon-table.11", "humangut160765029-stool1_revised_C1097260_1_gene98143 strand:- start:1314 stop:2387 length:1074 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11", "rumen583_GL0668725_1 [gene] locus=scaffold85441_1:1:1071:+[Lack both ends]"]
["humangutV1.UC6-0_GL0083590 [gene] locus=scaffold85180_1:82:786:- [Lack 5'-end] codon-table.11"]
["mouse1-1_GL0013755 [gene] locus=scaffold85905_2:3182:4222:- [Complete] codon-table.11"]
["mouse1-1_GL0124139 [gene] locus=scaffold12413_10:656:1843:- [Lack 5'-end] codon-table.11"]
["mouse1-6_GL0082804 [gene] locus=scaffold37174_4:1031:2068:- [Complete] codon-table.11"]
["mouse11_GL0028995 [gene] locus=scaffold80892_2:3:602:+ [Lack both ends] codon-table.11"]
["mouse11_GL0063366 [gene] locus=scaffold67069_1:2766:3758:+ [Complete] codon-table.11", "mouse1-2_GL0086073 [gene] locus=scaffold17958_3:18710:19702:+ [Complete] codon-table.11",

"mouse1-7_GL0031690 [gene] locus=scaffold77452_1:314:1306:+ [Complete] codon-table.11",
"mouse1A-dyr4-07_GL0101500 [gene] locus=scaffold13481_1:1287:2279:+ [Complete] codon-table.11",
"mouse8-1_GL0054971 [gene] locus=scaffold2906_5:2179:3171:- [Complete] codon-table.11",
"cazygii690621879 gb AIQ22893.1  glycosidase [Paenibacillus sp. FSL H7-0737]",
"cazygii686524044 gb AIQ34744.1  glycosidase [Paenibacillus sp. FSL R5-0345]"
["mouse13_GL0064072 [gene] locus=scaffold51821_1:22792:23754:+ [Complete] codon-table.11"]
["mouse14_GL0107550 [gene] locus=scaffold6028_2:1017:2039:- [Complete] codon-table.11"]
["mouse17_GL0087175 [gene] locus=scaffold73438_2:156:1256:- [Complete] codon-table.11"]
["mouse1A-dyr4-07_GL0070334 [gene] locus=scaffold24038_1:2442:2900:- [Lack 5'-end] codon-table.11",
"pigBHZ-5B_GL0086327 [gene] locus=scaffold167485_1:49:507:- [Lack 5'-end] codon-table.11"]
["mouse2-2_GL0079470 [gene] locus=scaffold81255_3:3302:4174:+ [Lack 3'-end] codon-table.11",
"pigPIG_155_GL0209038 [gene] locus=scaffold258678_1:3:875:- [Lack 3'-end] codon-table.11"]
["mouse2-2_GL0122780 [gene] locus=scaffold34208_4:2:757:+ [Lack both ends] codon-table.11"]
["mouse20_GL0026050 [gene] locus=scaffold37937_1:3648:4634:- [Complete] codon-table.11"]
["mouse20_GL0131442 [gene] locus=scaffold21671_4:3:599:- [Lack both ends] codon-table.11"]
["mouse23_GL0035436 [gene] locus=scaffold62600_1:458:1582:- [Lack 5'-end] codon-table.11"]
["mouse26_GL0130784 [gene] locus=scaffold14459_3:153:1250:- [Complete] codon-table.11"]
["mouse28_GL0074759 [gene] locus=scaffold13983_10:1:546:+ [Lack 5'-end] codon-table.11"]
["mouse2A-dyr16-07_GL0072185 [gene] locus=scaffold23927_13:1555:2616:- [Complete] codon-table.11"]
["mouse38_GL0056566 [gene] locus=scaffold16483_4:837:1883:- [Complete] codon-table.11"]
["mouse40_GL0009374 [gene] locus=scaffold1596_9:2465:3433:+ [Complete] codon-table.11"]
["mouse40_GL0036592 [gene] locus=scaffold17608_2:3:938:- [Lack 3'-end] codon-table.11"]
["mouse47_GL0008624 [gene] locus=scaffold12137_4:1:591:- [Lack both ends] codon-table.11"]
["mouse5-2_GL0036463 [gene] locus=scaffold16925_6:2:643:- [Lack both ends] codon-table.11"]
["mouse5-4_GL0061663 [gene] locus=scaffold47002_2:1:795:- [Lack both ends] codon-table.11"]
["mouse5-7_GL0065173 [gene] locus=scaffold105587_1:3:479:+ [Lack 5'-end] codon-table.11"]
["mouse5-8_GL0077583 [gene] locus=scaffold31802_12:3:470:+ [Lack 5'-end] codon-table.11",
"rumen0081_GL0373187_1 [gene] locus=scaffold1486689_1:292:759:-[Lack 5'-end]"
["mouse5-8_GL0080354 [gene] locus=scaffold38327_13:1995:2663:+ [Complete] codon-table.11"]
["mouse6-1_GL0098890 [gene] locus=scaffold1798_5:24648:25709:- [Complete] codon-table.11"]
["mouse6-3_GL0001548 [gene] locus=scaffold329_1:290:1285:- [Complete] codon-table.11"]
["mouse6-3_GL0021301 [gene] locus=scaffold89548_2:2:595:- [Lack 3'-end] codon-table.11"]
["mouse7-8_GL0159389 [gene] locus=scaffold22039_7:1225:2124:- [Lack 5'-end] codon-table.11"]
["mouse7_GL0111132 [gene] locus=scaffold6113_2:616:1116:+ [Lack 3'-end] codon-table.11"]
["mouse8-2_GL0132087 [gene] locus=scaffold59387_2:2:526:- [Lack 3'-end] codon-table.11"]
["mouse8-3_GL0115173 [gene] locus=scaffold18104_20:2364:3515:- [Complete] codon-table.11"]
["mouse8-5_GL0049588 [gene] locus=scaffold20343_6:934:1881:- [Lack 5'-end] codon-table.11"]
["mouse8-7_GL0086857 [gene] locus=scaffold38404_2:3:635:- [Lack both ends] codon-table.11"]
["mouseG1-1A_GL0083748 [gene] locus=scaffold66057_3:8:1012:- [Complete] codon-table.11",
"mouse2-1_GL0074983 [gene] locus=scaffold6325_1:94196:95200:+ [Complete] codon-table.11",
"mouse2-5_GL0040801 [gene] locus=scaffold43826_2:2876:3880:- [Complete] codon-table.11",
"mouse29_GL0069267 [gene] locus=scaffold57287_3:6072:7076:+ [Complete] codon-table.11",
"pigPIG_196_GL0134022 [gene] locus=scaffold117271_4_1:123:1127:+ [Complete] codon-table.11",



"pigPIG-006_GL0197673 [gene] locus=scaffold106067_7:3442:4446:- [Complete] codon-table.11"
"mouseG1-3A_GL0113050 [gene] locus=scaffold77102_3:277:1383:- [Complete] codon-table.11"
"mouseG1-4A_GL0100224 [gene] locus=C689339_1:2:538:- [Lack both ends] codon-table.11"
"mouseG1-5A_GL0021287 [gene] locus=scaffold10354_4:9023:10015:+ [Complete] codon-table.11"
"mouseG1-5A_GL0171673 [gene] locus=scaffold128990_1:3:500:- [Lack 3'-end] codon-table.11"
"mouseG1-6A_GL0009418 [gene] locus=scaffold1871_1:60:500:- [Lack 5'-end] codon-table.11", "pigPIG_122_GL0065820 [gene] locus=scaffold1943_2:737:1177:- [Lack 5'-end] codon-table.11"
"mouseG1-6A_GL0009419 [gene] locus=scaffold1871_2:1:477:- [Lack 3'-end] codon-table.11"
"mouseG1-6A_GL0023704 [gene] locus=scaffold9642_9:2458:3471:+ [Complete] codon-table.11", "mouseGroup2-3A_GL0194463 [gene] locus=scaffold125876_2:59483:60496:- [Complete] codon-table.11", "mouse2-2_GL0096018 [gene] locus=scaffold90474_7:388:1401:+ [Complete] codon-table.11", "mouse6-3_GL0066399 [gene] locus=scaffold85639_4:36:1049:+ [Complete] codon-table.11", "mouse7-5_GL0122105 [gene] locus=scaffold31774_1:31:1044:+ [Complete] codon-table.11", "pigPIG_142_GL0319933 [gene] locus=scaffold239052_8:2400:3413:- [Complete] codon-table.11", "rumen555_GL1093153_1 [gene] locus=C29059764_1:1:1014:+[Lack 5'-end]"
"mouseG1-7A_GL0109682 [gene] locus=scaffold79261_2:2:931:- [Lack 3'-end] codon-table.11"
"mouseG1-7A_GL0121857 [gene] locus=scaffold88864_13:2:901:+ [Lack 5'-end] codon-table.11"
"mouseGroup2-1A_GL0050661 [gene] locus=scaffold32594_1:1:729:- [Lack both ends] codon-table.11"
"mouseGroup2-2A_GL0066926 [gene] locus=scaffold43669_1:1:729:- [Lack 3'-end] codon-table.11"
"mouseGroup2-2A_GL0140754 [gene] locus=scaffold107841_2:3:560:- [Lack both ends] codon-table.11"
"mouseGroup2-3A_GL0026302 [gene] locus=scaffold9194_7:1780:2775:- [Lack 5'-end] codon-table.11"
"mouseGroup2-3A_GL0028504 [gene] locus=scaffold10358_2:1:972:- [Lack 3'-end] codon-table.11", "mouseGroup2-8A_GL0007280 [gene] locus=scaffold1536_16:1:972:- [Lack 3'-end] codon-table.11"
"mouseGroup2-3A_GL0155033 [gene] locus=scaffold97533_1:1:705:+ [Lack both ends] codon-table.11"
"mouseGroup2-8A_GL0028085 [gene] locus=scaffold15469_8:470:1015:+ [Lack 3'-end] codon-table.11"
"mouseGroup2-8A_GL0040043 [gene] locus=scaffold24786_2:2:571:+ [Lack both ends] codon-table.11"
"mouseMC-0-1_GL0020728 [gene] locus=scaffold15693_7:1:957:+ [Lack 5'-end] codon-table.11"
"mouseMC-0-1_GL0063972 [gene] locus=scaffold52426_6:1437:2447:- [Complete] codon-table.11", "rumen0081_GL1464453_1 [gene] locus=scaffold1139643_1:2:1012:+[Lack 5'-end]"
"mouseMC-0-1_GL0070811 [gene] locus=scaffold59537_2:3388:4452:+ [Complete] codon-table.11"
"mouseMC-0-1_GL0105217 [gene] locus=scaffold93234_4:2:940:+ [Lack 5'-end] codon-table.11"
"mouseMC-0-1_GL0126465 [gene] locus=C1203236_1:376:1380:- [Complete] codon-table.11", "rumen555_GL0706695_1 [gene] locus=scaffold1082947_1:604:1608:+[Complete]"
"mouseMC-0-3_GL0052777 [gene] locus=scaffold38783_2:179:1198:+ [Complete] codon-table.11"
"mouseMC-0-3_GL0063232 [gene] locus=scaffold48149_4:3475:4386:+ [Complete] codon-table.11", "pigPIG-006_GL0214877 [gene] locus=scaffold176505_2:493:1404:+ [Complete] codon-table.11"
"mouseMC-6-2_GL0114086 [gene] locus=scaffold89911_3:2230:2691:- [Lack 5'-end] codon-table.11"
"mouseMC-6-2_GL0145123 [gene] locus=scaffold117289_1:3:842:+ [Lack 5'-end] codon-table.11", "rumen100058_GL1632487_1 [gene] locus=scaffold2307440_2:366:1205:-[Lack 5'-end]", "rumen2009040_GL1107729_1 [gene] locus=scaffold1102455_2:1:840:+[Lack 5'-end]"
"mouseMC-6-2_GL0179822 [gene] locus=scaffold132865_1:10272:11327:+ [Complete] codon-table.11", "rumen554_GL3065378_1 [gene] locus=scaffold2055200_2:19498:20553:+[Complete]"
"mouseMC-6-2_GL0183036 [gene] locus=scaffold132992_1:101978:103096:+ [Complete] codon-table.11"

["mouseMC-6-3_GL0104116 [gene] locus=scaffold78176_1:1:513:+ [Lack both ends] codon-table.11"]
["mouseMH-6-3_GL0039014 [gene] locus=scaffold22789_5:1:1026:+ [Lack 5'-end] codon-table.11"]
["mouseMH-6-5_GL0037067 [gene] locus=scaffold21339_2:14:574:- [Lack 5'-end] codon-table.11"]
["mouseS-Fe10_GL0046194 [gene] locus=scaffold3537_5:349:1317:- [Complete] codon-table.11", "pigEYZ-120B_GL0303698 [gene] locus=scaffold14900_6:149:1117:- [Complete] codon-table.11"]
["mouseS-Fe12_GL0052729 [gene] locus=scaffold2727_5:484:1566:+ [Complete] codon-table.11", "rumen555_GL1460227_1 [gene] locus=scaffold1378456_1:15028:16110:+[Complete]"]
["mouseS-Fe12_GL0146061 [gene] locus=scaffold79297_6:336:1319:+ [Complete] codon-table.11"]
["mouseS-Fe12_GL0191054 [gene] locus=scaffold7461_20:1732:2280:- [Complete] codon-table.11"]
["mouseS-Fe20_GL0180053 [gene] locus=scaffold102347_1:25922:26662:- [Complete] codon-table.11"]
["mouseS-Fe3_GL0010927 [gene] locus=scaffold99806_5:1174:1887:+ [Lack 3'-end] codon-table.11"]
["mouseS-Fe6_GL0105173 [gene] locus=scaffold109628_5:2:685:- [Lack both ends] codon-table.11"]
["mouseS-Fe6_GL0106658 [gene] locus=scaffold60443_2:576:1382:+ [Lack 3'-end] codon-table.11", "rumen554_GL2325094_1 [gene] locus=scaffold1503866_3:1:807:-[Lack 3'-end]"]
["mouseS-Fe8_GL0203068 [gene] locus=scaffold59716_1:487:1332:- [Lack 5'-end] codon-table.11"]
["mouseS-Fe9_GL0153613 [gene] locus=scaffold46730_4:3:530:- [Lack both ends] codon-table.11"]
["mouseS-Fe9_GL0294675 [gene] locus=scaffold15614_7:2:487:- [Lack 3'-end] codon-table.11"]
["pigBHZ-11B_GL0083249 [gene] locus=scaffold60694_4:3219:4214:- [Lack 5'-end] codon-table.11"]
["pigBHZ-11B_GL0090194 [gene] locus=scaffold167910_1:1:477:- [Lack 3'-end] codon-table.11"]
["pigBHZ-4B_GL0090287 [gene] locus=scaffold91530_1:3532:3927:- [Lack 5'-end] codon-table.11"]
["pigBHZ-5B_GL0033276 [gene] locus=scaffold209243_3:253:777:- [Lack 5'-end] codon-table.11"]
["pigBHZ-5B_GL0222855 [gene] locus=scaffold171737_1:1:516:- [Lack both ends] codon-table.11"]
["pigBHZ-7B_GL0204072 [gene] locus=scaffold187695_2:622:1620:+ [Lack 3'-end] codon-table.11"]
["pigBHZ-8B_GL0096113 [gene] locus=scaffold33234_10:68:1132:- [Lack 5'-end] codon-table.11"]
["pigBHZ-9B_GL0066795 [gene] locus=scaffold53814_9:454:1419:+ [Complete] codon-table.11"]
["pigBMZ-10B_GL0005454 [gene] locus=scaffold66908_2:21139:22158:+ [Complete] codon-table.11", "rumen553_GL0321377_1 [gene] locus=scaffold253522_1:14226:15245:+[Complete]", "rumen553_GL0574790_1 [gene] locus=scaffold263575_1:107:1126:-[Complete]", "rumen552_GL0518438_1 [gene] locus=scaffold185440_2:1369:2388:-[Complete]", "rumen583_GL0485454_1 [gene] locus=scaffold13822_4:1175:2194:+[Complete]", "rumen554_GL1280625_1 [gene] locus=scaffold1336613_1:19824:20843:+[Complete]", "rumen554_GL1777955_1 [gene] locus=scaffold469779_2:1378:2397:-[Complete]", "rumen554_GL2189559_1 [gene] locus=scaffold1422874_1:106:1125:-[Complete]", "rumen555_GL1086794_1 [gene] locus=scaffold394634_1:2:1018:-[Lack 3'-end]", "rumen0081_GL1505816_1 [gene] locus=scaffold1429322_1:1721:2740:-[Complete]", "rumen100058_GL0992048_1 [gene] locus=scaffold502394_6:1940:2959:-[Complete]", "rumen100058_GL1184422_1 [gene] locus=scaffold2318530_1:319:1338:-[Complete]", "rumen2009040_GL0195154_1 [gene] locus=scaffold2145838_6:498:1517:-[Complete]", "rumen3042_GL0591221_1 [gene] locus=scaffold537693_2:1578:2597:+[Complete]", "rumen7049_GL2859710_1 [gene] locus=scaffold1193541_1:296:1315:-[Complete]"]
["pigBMZ-17B_GL0041107 [gene] locus=scaffold170850_1:1:696:+ [Lack 5'-end] codon-table.11"]
["pigBMZ-17B_GL0114194 [gene] locus=scaffold32995_1:2:565:+ [Lack both ends] codon-table.11"]
["pigBMZ-17B_GL0171035 [gene] locus=scaffold102262_4:1:756:+ [Lack 5'-end] codon-table.11"]

["pigBMZ-7B_GL0005440 [gene] locus=scaffold27109_1:2:733:+ [Lack both ends] codon-table.11"]
["pigBMZ-9B_GL0017818 [gene] locus=scaffold6417_5:2:457:- [Lack 3'-end] codon-table.11"]
["pigDB-510B_GL0116829 [gene] locus=scaffold4072_1:460:1323:- [Lack 5'-end] codon-table.11"]
["pigDB-510B_GL0203636 [gene] locus=scaffold133867_4:1064:1780:+ [Lack 3'-end] codon-table.11"]
["pigDB-512B_GL0130519 [gene] locus=scaffold23936_1:1:717:+ [Lack 5'-end] codon-table.11"]
["pigDB-537B_GL0180315 [gene] locus=scaffold29432_7:468:1436:- [Complete] codon-table.11"]
["pigEYZ-120B_GL0313316 [gene] locus=scaffold188948_5:575:1540:- [Complete] codon-table.11"]
["pigEYZ-254B_GL0131965 [gene] locus=scaffold15125_3:2:730:- [Lack 3'-end] codon-table.11"]
["pigEYZ-353B_GL0258768 [gene] locus=scaffold172929_2:1:759:- [Lack both ends] codon-table.11"]
["pigEYZ-378B_GL0004433 [gene] locus=scaffold60190_1:2888:3583:+ [Lack 3'-end] codon-table.11", "rumen0081_GL1024715_1 [gene] locus=scaffold922929_2:3:698:-[Lack 3'-end]"]
["pigEYZ-381B_GL0306685 [gene] locus=scaffold205698_2:2:817:+ [Lack both ends] codon-table.11"]
["pigEYZ-468B_GL0069605 [gene] locus=scaffold76583_2:2:601:+ [Lack 5'-end] codon-table.11", "rumen0081_GL2416987_1 [gene] locus=scaffold845286_7:2:601:+[Lack 5'-end]"]
["pigPIG-001_GL0169555 [gene] locus=scaffold31187_9:3604:4605:+ [Lack 3'-end] codon-table.11", "rumen100058_GL0132315_1 [gene] locus=scaffold1516124_2:479:1483:-[Lack 5'-end]", "rumen100058_GL2269814_1 [gene] locus=scaffold4654_2:3:1004:-[Lack 3'-end]", "rumen3042_GL1490754_1 [gene] locus=scaffold542093_2:421:1422:+[Lack 3'-end]", "rumen3042_GL1972449_1 [gene] locus=scaffold470323_8:2140:3144:-[Complete]"]
["pigPIG-001_GL0228666 [gene] locus=scaffold122346_4:1:851:+ [Lack both ends] codon-table.11"]
["pigPIG-004_GL0019300 [gene] locus=scaffold96885_3:3242:4357:- [Lack 5'-end] codon-table.11"]
["pigPIG-005_GL0153503 [gene] locus=scaffold121017_1:313:954:+ [Lack 3'-end] codon-table.11"]
["pigPIG-006_GL0112184 [gene] locus=scaffold122780_1:3:542:+ [Lack both ends] codon-table.11", "rumen2009040_GL2275139_1 [gene] locus=scaffold1696944_1:1:540:-[Lack both ends]"]
["pigPIG-011_GL0150563 [gene] locus=scaffold44416_1:38:514:- [Lack 5'-end] codon-table.11"]
["pigPIG-017_GL0093868 [gene] locus=scaffold147351_9:1:645:+ [Lack 5'-end] codon-table.11"]
["pigPIG-018_GL0091264 [gene] locus=scaffold143363_11:586:1314:+ [Lack 3'-end] codon-table.11"]
["pigPIG-022_GL0080548 [gene] locus=scaffold59559_7:1:864:- [Lack 3'-end] codon-table.11"]
["pigPIG-023_GL0056374 [gene] locus=scaffold148285_1:3:668:- [Lack both ends] codon-table.11"]
["pigPIG-024_GL0218414 [gene] locus=scaffold117167_5:320:1414:- [Complete] codon-table.11"]
["pigPIG-026_GL0071880 [gene] locus=scaffold104889_1:6433:7443:+ [Complete] codon-table.11"]
["pigPIG-026_GL0116698 [gene] locus=scaffold1878_2:158:1339:+ [Complete] codon-table.11"]
["pigPIG-027_GL0261576 [gene] locus=scaffold178107_1:339:1322:- [Complete] codon-table.11"]
["pigPIG-031_GL0026806 [gene] locus=scaffold20325_4:2:745:- [Lack 3'-end] codon-table.11"]
["pigPIG-031_GL0070146 [gene] locus=scaffold12058_1:3:734:- [Lack 3'-end] codon-table.11"]
["pigPIG-031_GL0109326 [gene] locus=scaffold104274_1:11586:12590:- [Complete] codon-table.11"]
["pigPIG-031_GL0138975 [gene] locus=scaffold128840_1:1:875:- [Lack 3'-end] codon-table.11", "rumen552_GL0647860_1 [gene] locus=scaffold104244_2:3:677:+[Lack both ends]"]
["pigPIG-031_GL0158070 [gene] locus=scaffold30741_4:2:526:+ [Lack 5'-end] codon-table.11"]
["pigPIG-031_GL0183583 [gene] locus=scaffold35012_2:2:859:+ [Lack both ends] codon-table.11"]
["pigPIG-032_GL0156946 [gene] locus=scaffold51801_10:1609:2601:+ [Complete] codon-table.11"]
["pigPIG-033_GL0032022 [gene] locus=C1607875_1:3:629:- [Lack both ends] codon-table.11"]
["pigPIG-034_GL0056463 [gene] locus=scaffold67620_6:1476:2234:- [Lack 5'-end] codon-table.11"]

["pigPIG-034_GL0086619 [gene] locus=scaffold24268_6:1955:3046:- [Complete] codon-table.11"]
["pigPIG-034_GL0130359 [gene] locus=scaffold11643_2:587:1123:+ [Lack 3'-end] codon-table.11"]
["pigPIG-035_GL0001096 [gene] locus=scaffold90148_2:2:826:- [Lack 3'-end] codon-table.11"]
["pigPIG-035_GL0017485 [gene] locus=scaffold86648_2:137:775:- [Lack 5'-end] codon-table.11"]
["pigPIG-035_GL0022303 [gene] locus=scaffold79779_2:1:627:+ [Lack 5'-end] codon-table.11"]
["pigPIG-036_GL0020839 [gene] locus=scaffold127014_1:431:1129:+ [Lack 3'-end] codon-table.11"]
["pigPIG-038_GL0021185 [gene] locus=scaffold112665_2:2:613:- [Lack both ends] codon-table.11"]
["pigPIG-038_GL0131957 [gene] locus=scaffold87099_2:2:517:+ [Lack both ends] codon-table.11"]
["pigPIG-038_GL0228101 [gene] locus=scaffold51839_3:226:822:+ [Lack 3'-end] codon-table.11"]
["pigPIG-039_GL0020000 [gene] locus=scaffold109634_1:1335:2129:- [Complete] codon-table.11"]
["pigPIG-042_GL0146265 [gene] locus=scaffold15812_22:349:1347:+ [Complete] codon-table.11"]
["pigPIG-043_GL0176010 [gene] locus=scaffold125895_1:19:627:- [Lack 5'-end] codon-table.11"]
["pigPIG-045_GL0165943 [gene] locus=scaffold45985_4:3:674:- [Lack 3'-end] codon-table.11"]
["pigPIG-046_GL0121324 [gene] locus=scaffold124352_2:2:685:+ [Lack 5'-end] codon-table.11"]
["pigPIG-046_GL0162651 [gene] locus=scaffold147028_1:10280:11035:- [Complete] codon-table.11"]
["pigPIG-048_GL0106673 [gene] locus=scaffold88520_1:1:879:+ [Lack 5'-end] codon-table.11"]
["pigPIG-052_GL0033206 [gene] locus=scaffold77968_1:3:626:- [Lack both ends] codon-table.11"]
["pigPIG-053_GL0226587 [gene] locus=scaffold172312_1:3:653:+ [Lack both ends] codon-table.11"]
["pigPIG-076_GL0066297 [gene] locus=scaffold177549_2:2:835:- [Lack 3'-end] codon-table.11"]
["pigPIG-084_GL0078495 [gene] locus=scaffold145976_1:427:1179:+ [Lack 3'-end] codon-table.11"]
["pigPIG-086_GL0168234 [gene] locus=scaffold48952_1:3:530:+ [Lack 5'-end] codon-table.11"]
["pigPIG-086_GL0170780 [gene] locus=scaffold39925_2:428:940:+ [Lack 3'-end] codon-table.11"]
["pigPIG-094_GL0069997 [gene] locus=scaffold55492_3:127:744:- [Lack 5'-end] codon-table.11"]
["pigPIG-094_GL0107435 [gene] locus=scaffold16034_12:1:663:- [Lack 3'-end] codon-table.11"]
["pigPIG-103_GL0226005 [gene] locus=scaffold62430_1:266:757:- [Lack 5'-end] codon-table.11"]
["pigPIG-105_GL0105545 [gene] locus=scaffold22207_3:3:782:+ [Lack 5'-end] codon-table.11"]
["pigPIG-107_GL0188439 [gene] locus=scaffold18356_1:2:508:- [Lack 3'-end] codon-table.11"]
["pigPIG-108_GL0002701 [gene] locus=scaffold114361_1:231:1055:- [Lack 5'-end] codon-table.11"]
["pigPIG-110_GL0136177 [gene] locus=scaffold22146_5:2:418:+ [Lack 5'-end] codon-table.11"]
["pigPIG-110_GL0147214 [gene] locus=scaffold22146_4:780:1427:+ [Lack 3'-end] codon-table.11"]
["pigPIG-110_GL0176009 [gene] locus=scaffold92729_5:2:631:- [Lack both ends] codon-table.11", "rumen7049_GL1501887_1 [gene] locus=C51935206_1:1:630:- [Lack both ends]"]
["pigPIG_112_GL0043743 [gene] locus=scaffold180654_1:46:597:- [Lack 5'-end] codon-table.11"]
["pigPIG_112_GL0046752 [gene] locus=C2909405_1:155:688:+ [Lack 3'-end] codon-table.11"]
["pigPIG_113_GL0228033 [gene] locus=scaffold208174_1:43:690:- [Lack 5'-end] codon-table.11"]
["pigPIG_114_GL0139742 [gene] locus=scaffold107545_3:90:1073:- [Lack 5'-end] codon-table.11"]
["pigPIG_114_GL0184431 [gene] locus=scaffold149440_1:66:674:+ [Lack 3'-end] codon-table.11"]
["pigPIG_115_GL0148003 [gene] locus=scaffold168813_3:129:938:- [Lack 5'-end] codon-table.11"]
["pigPIG_117_GL0190473 [gene] locus=scaffold262986_1:9237:10058:+ [Lack 3'-end] codon-table.11"]
["pigPIG_120_GL0063343 [gene] locus=scaffold47651_1:3:578:- [Lack 3'-end] codon-table.11"]
["pigPIG_120_GL0202954 [gene] locus=C2021344_1:3:653:- [Lack both ends] codon-table.11"]
["pigPIG_121_GL0018361 [gene] locus=scaffold3077_1:3:557:- [Lack both ends] codon-table.11"]
["pigPIG_121_GL0340510 [gene] locus=scaffold238125_1:2:856:+ [Lack both ends] codon-table.11"]

["pigPIG_124_GL0162375 [gene] locus=C3077170_1:3:626:- [Lack both ends] codon-table.11"]
["pigPIG_124_GL0246913 [gene] locus=scaffold236658_1:493:1155:+ [Lack 3'-end] codon-table.11"]
["pigPIG_125_GL0120814 [gene] locus=scaffold71681_1:2:811:- [Lack 3'-end] codon-table.11"]
["pigPIG_134_GL0004942 [gene] locus=C3182390_1:63:770:- [Lack 5'-end] codon-table.11"]
["pigPIG_147_GL0060621 [gene] locus=scaffold5827_2:179:727:- [Lack 5'-end] codon-table.11"]
["pigPIG_147_GL0120521 [gene] locus=scaffold191187_3:3:569:+ [Lack both ends] codon-table.11"]
["pigPIG_151_GL0062620 [gene] locus=scaffold282726_3:2133:2702:+ [Lack 3'-end] codon-table.11", "pigPIG-019_GL0077816 [gene] locus=scaffold61368_1:3:572:- [Lack 3'-end] codon-table.11"]
["pigPIG_151_GL0235159 [gene] locus=scaffold160179_4:875:1855:- [Complete] codon-table.11", "rumen554_GL1214101_1 [gene] locus=scaffold210164_7:1586:2566:-[Complete]", "rumen3042_GL1252232_1 [gene] locus=scaffold1581218_3:655:1635:-[Complete]", "rumen7049_GL2016357_1 [gene] locus=scaffold547177_1:13771:14751:-[Complete]"]
["pigPIG_151_GL0296431 [gene] locus=scaffold15482_2:2083:3141:- [Complete] codon-table.11", "rumen552_GL0039217_1 [gene] locus=scaffold1080482_1:2078:3136:-[Complete]"]
["pigPIG_161_GL0112306 [gene] locus=scaffold75100_2:2:529:- [Lack 3'-end] codon-table.11", "rumen100058_GL0343992_1 [gene] locus=scaffold1850228_1:3:530:-[Lack 3'-end]"]
["pigPIG_161_GL0203859 [gene] locus=scaffold48755_4:7030:8076:- [Complete] codon-table.11", "pigPIG-004_GL0134388 [gene] locus=scaffold116127_3:6122:7168:+ [Complete] codon-table.11", "pigPIG-084_GL0029807 [gene] locus=scaffold3479_2:1353:2399:- [Complete] codon-table.11", "pigBHZ-2B_GL0168420 [gene] locus=scaffold108509_3:1719:2765:- [Complete] codon-table.11", "pigBHZ-8B_GL0156557 [gene] locus=scaffold121381_2:49:1095:- [Complete] codon-table.11", "pigDB-11B_GL0045004 [gene] locus=scaffold168309_1:22693:23739:+ [Complete] codon-table.11", "pigEYZ-120B_GL0231006 [gene] locus=scaffold227465_1:1931:2977:+ [Complete] codon-table.11", "rumen553_GL0221646_1 [gene] locus=scaffold33195_7:14679:15725:-[Complete]", "rumen583_GL0637373_1 [gene] locus=scaffold61989_5:9256:10302:-[Complete]"]
["pigPIG_173_GL0086508 [gene] locus=scaffold244695_1:1:1083:+ [Lack 5'-end] codon-table.11"]
["pigPIG_173_GL0089538 [gene] locus=scaffold35130_1:1:1056:+ [Lack 5'-end] codon-table.11"]
["pigPIG_174_GL0160487 [gene] locus=scaffold73905_3:139:921:+ [Lack 3'-end] codon-table.11"]
["pigPIG_177_GL0142182 [gene] locus=scaffold128873_1:199:915:+ [Lack 3'-end] codon-table.11"]
["pigPIG_182_GL0017741 [gene] locus=scaffold15184_3:2:706:+ [Lack both ends] codon-table.11"]
["pigPIG_186_GL0068966 [gene] locus=scaffold265203_1:2:799:+ [Lack 5'-end] codon-table.11"]
["pigPIG_186_GL0089332 [gene] locus=scaffold156153_2:3:1040:+ [Lack 5'-end] codon-table.11"]
["pigPIG_186_GL0277490 [gene] locus=C4249751_1:390:1460:- [Complete] codon-table.11"]
["pigPIG_186_GL0371351 [gene] locus=scaffold124949_7:7309:8262:- [Complete] codon-table.11"]
["pigPIG_189_GL0091475 [gene] locus=scaffold188452_2:1:645:- [Lack 3'-end] codon-table.11"]
["pigPIG_191_GL0209904 [gene] locus=scaffold50212_4:1494:2339:+ [Lack 3'-end] codon-table.11"]
["pigPIG_192_GL0214797 [gene] locus=scaffold58621_1:3:983:+ [Lack 5'-end] codon-table.11"]
["pigPIG_196_GL0082817 [gene] locus=scaffold218260_2:1:846:- [Lack both ends] codon-table.11"]
["pigPIG_196_GL0196824 [gene] locus=scaffold145779_3:2:442:- [Lack 3'-end] codon-table.11"]
["pigPIG_201_GL0074903 [gene] locus=C3028022_1:2:544:- [Lack both ends] codon-table.11"]
["pigPIG_201_GL0107757 [gene] locus=scaffold138844_1:1:915:+ [Lack 5'-end] codon-table.11", "rumen3042_GL2448260_1 [gene] locus=scaffold2096147_1:2:913:-[Lack 3'-end]"]
["pigPIG_204_GL0190733 [gene] locus=scaffold20761_5:3:1112:- [Lack 3'-end] codon-table.11"]

["pigSYZ-388B_GL0068383 [gene] locus=scaffold182951_1:794:1381:+ [Lack 3'-end] codon-table.11"]
["pigSYZ-388B_GL0161697 [gene] locus=scaffold5891_3:95:1126:- [Complete] codon-table.11"]
["pigSYZ-426B_GL0135420 [gene] locus=scaffold142921_1:1:663:+ [Lack both ends] codon-table.11"]
["pigZXZ-10B_GL0067174 [gene] locus=scaffold178907_1:5449:6438:+ [Complete] codon-table.11"]
["pigZXZ-1B_GL0217716 [gene] locus=scaffold90253_2:2:775:- [Lack 3'-end] codon-table.11"]
["pigZXZ-3B_GL0006464 [gene] locus=scaffold871_2:2:889:+ [Lack 5'-end] codon-table.11", "rumen555_GL1691731_1 [gene] locus=scaffold786534_2:2:886:+[Lack both ends]"]
["pigZXZ-4B_GL0176666 [gene] locus=scaffold8454_1:5769:6815:+ [Complete] codon-table.11"]
["pigZXZ-7B_GL0179188 [gene] locus=scaffold31732_1:3529:4506:- [Lack 5'-end] codon-table.11"]
["pigZXZ-8B_GL0117670 [gene] locus=C2182832_1:2:508:- [Lack both ends] codon-table.11"]
["pigZXZ-8B_GL0244838 [gene] locus=scaffold26205_1:1:633:+ [Lack 5'-end] codon-table.11", "rumen554_GL0332524_1 [gene] locus=scaffold1493107_1:1835:2467:-[Lack 5'-end]"]
["pigZXZ-9B_GL0114291 [gene] locus=scaffold179798_1:2:514:+ [Lack 5'-end] codon-table.11"]
["rumen0081_GL0064712_1 [gene] locus=scaffold335362_3:2513:3172:+[Lack 3'-end]", "rumen100058_GL2408121_1 [gene] locus=scaffold3036593_1:3:662:-[Lack 3'-end]"]
["rumen0081_GL0180557_1 [gene] locus=scaffold1726079_2:1457:1981:+[Lack 3'-end]"]
["rumen0081_GL0219362_1 [gene] locus=scaffold1711638_1:427:1014:-[Lack 5'-end]"]
["rumen0081_GL0320729_1 [gene] locus=scaffold22173_5:10552:11130:+[Lack 3'-end]"]
["rumen0081_GL0450092_1 [gene] locus=scaffold948276_1:2:664:-[Lack 3'-end]"]
["rumen0081_GL0466755_1 [gene] locus=scaffold104428_3:1667:2581:-[Lack 5'-end]"]
["rumen0081_GL0496130_1 [gene] locus=scaffold928199_1:1:405:+[Lack 5'-end]"]
["rumen0081_GL0506602_1 [gene] locus=scaffold1885440_2:1:768:-[Lack both ends]"]
["rumen0081_GL0514438_1 [gene] locus=scaffold519995_2:3:518:-[Lack 3'-end]"]
["rumen0081_GL0591288_1 [gene] locus=scaffold695432_2:131:505:-[Lack 5'-end]"]
["rumen0081_GL0622563_1 [gene] locus=scaffold349208_1:1:468:-[Lack 3'-end]", "rumen3042_GL1267162_1 [gene] locus=scaffold1560219_1:206:673:+[Lack 3'-end]"]
["rumen0081_GL0635854_1 [gene] locus=scaffold1129532_1:12771:13778:+[Complete]"]
["rumen0081_GL0647534_1 [gene] locus=C38313395_1:3:437:-[Lack 3'-end]"]
["rumen0081_GL0722202_1 [gene] locus=scaffold1960186_1:3:836:+[Lack both ends]"]
["rumen0081_GL0787985_1 [gene] locus=scaffold411888_2:1:816:-[Lack 3'-end]"]
["rumen0081_GL0837490_1 [gene] locus=scaffold356149_2:2:637:-[Lack 3'-end]", "rumen7049_GL0851061_1 [gene] locus=scaffold2139164_1:3:638:-[Lack 3'-end]"]
["rumen0081_GL1022157_1 [gene] locus=scaffold1342277_3:304:840:+[Lack 3'-end]"]
["rumen0081_GL1036706_1 [gene] locus=scaffold860226_1:1461:2237:+[Lack 3'-end]", "rumen100058_GL0614671_1 [gene] locus=scaffold667058_3:296:1072:+[Lack 3'-end]"]
["rumen0081_GL1060731_1 [gene] locus=scaffold317383_6:262:1125:-[Lack 5'-end]"]
["rumen0081_GL1138368_1 [gene] locus=scaffold888200_2:50:613:-[Lack 5'-end]", "rumen2009040_GL1064927_1 [gene] locus=scaffold1779755_1:1:564:+[Lack 5'-end]", "rumen2009040_GL3211683_1 [gene] locus=scaffold2032426_3:1377:1940:-[Lack 5'-end]"]
["rumen0081_GL1148546_1 [gene] locus=scaffold279507_1:1:618:+[Lack both ends]"]
["rumen0081_GL1259314_1 [gene] locus=scaffold1479207_1:3:683:+[Lack 5'-end]"]
["rumen0081_GL1498862_1 [gene] locus=scaffold1916965_1:3:794:+[Lack both ends]"]
["rumen0081_GL1569460_1 [gene] locus=scaffold1237992_2:1:522:-[Lack both ends]"]

["rumen0081_GL1894171_1 [gene] locus=scaffold1729023_1:336:773:+[Lack 3'-end]"]
["rumen0081_GL2032736_1 [gene] locus=scaffold643617_1:2:658:+[Lack both ends]", "rumen2009040_GL0725324_1 [gene] locus=scaffold921679_7:419:1075:+[Lack 3'-end]"]
["rumen0081_GL2207767_1 [gene] locus=scaffold68961_5:34:780:+[Lack 3'-end]"]
["rumen0081_GL2264799_1 [gene] locus=scaffold570051_3:395:1288:-[Lack 5'-end]"]
["rumen0081_GL2294332_1 [gene] locus=scaffold303130_2:46:1032:-[Complete]", "rumen7049_GL2837273_1 [gene] locus=scaffold23373_2:622:1608:+[Complete]"]
["rumen0081_GL2367573_1 [gene] locus=scaffold1744014_1:2:874:+[Lack both ends]"]
["rumen0081_GL2504313_1 [gene] locus=scaffold1829874_2:463:870:-[Lack 5'-end]"]
["rumen0081_GL2511108_1 [gene] locus=scaffold1835477_4:526:1272:+[Lack 3'-end]"]
["rumen0081_GL2516639_1 [gene] locus=scaffold272372_3:1:546:-[Lack 3'-end]"]
["rumen100058_GL0079654_1 [gene] locus=scaffold2482952_1:287:907:+[Lack 3'-end]", "rumen7049_GL2697687_1 [gene] locus=scaffold1189584_1:530:1150:+[Lack 3'-end]"]
["rumen100058_GL0081051_1 [gene] locus=scaffold669218_1:133:933:-[Lack 5'-end]"]
["rumen100058_GL0261337_1 [gene] locus=C58467978_1:64:600:-[Lack 5'-end]", "rumen100058_GL1879101_1 [gene] locus=scaffold2482952_2:2:538:+[Lack 5'-end]"]
["rumen100058_GL0380841_1 [gene] locus=scaffold287968_2:2:721:+[Lack 5'-end]"]
["rumen100058_GL0421245_1 [gene] locus=C60063984_1:144:1070:-[Lack 5'-end]"]
["rumen100058_GL0465739_1 [gene] locus=C59653742_1:2:859:+[Lack both ends]"]
["rumen100058_GL0478693_1 [gene] locus=scaffold2427909_2:1:501:+[Lack both ends]"]
["rumen100058_GL0506470_1 [gene] locus=scaffold701222_3:2:535:+[Lack 5'-end]"]
["rumen100058_GL0525691_1 [gene] locus=scaffold3220036_1:3:539:-[Lack both ends]"]
["rumen100058_GL0526834_1 [gene] locus=C59209324_1:2:565:-[Lack 3'-end]"]
["rumen100058_GL0557509_1 [gene] locus=scaffold1150310_1:3:674:-[Lack 3'-end]"]
["rumen100058_GL0582312_1 [gene] locus=scaffold1584502_1:3:635:-[Lack 3'-end]"]
["rumen100058_GL0625438_1 [gene] locus=scaffold841425_2:1:522:+[Lack 5'-end]"]
["rumen100058_GL0636960_1 [gene] locus=scaffold2401224_3:3519:4220:-[Lack 5'-end]"]
["rumen100058_GL0682011_1 [gene] locus=scaffold1062049_3:237:917:-[Lack 5'-end]"]
["rumen100058_GL0683357_1 [gene] locus=scaffold304188_6:1:693:+[Lack both ends]"]
["rumen100058_GL0695139_1 [gene] locus=scaffold148552_6:101:634:+[Lack 3'-end]"]
["rumen100058_GL0792543_1 [gene] locus=scaffold2044073_2:1:558:+[Lack 5'-end]"]
["rumen100058_GL0845169_1 [gene] locus=scaffold1747050_1:3:566:-[Lack both ends]"]
["rumen100058_GL0853967_1 [gene] locus=scaffold1326759_8:384:1235:-[Lack 5'-end]"]
["rumen100058_GL0973147_1 [gene] locus=scaffold1383390_2:3:815:+[Lack 5'-end]"]
["rumen100058_GL0992694_1 [gene] locus=scaffold2634064_1:252:779:+[Lack 3'-end]"]
["rumen100058_GL1037585_1 [gene] locus=scaffold2177230_6:2:583:+[Lack 5'-end]"]
["rumen100058_GL1104505_1 [gene] locus=scaffold219305_8:1:885:-[Lack 3'-end]"]
["rumen100058_GL1140300_1 [gene] locus=scaffold1542785_1:1:435:+[Lack 5'-end]"]
["rumen100058_GL1158545_1 [gene] locus=scaffold473697_16:729:1382:-[Lack 5'-end]"]
["rumen100058_GL1191325_1 [gene] locus=scaffold1204567_1:3:1025:+[Lack 5'-end]"]
["rumen100058_GL1202198_1 [gene] locus=scaffold43743_2:1000:1470:-[Lack 5'-end]"]
["rumen100058_GL1235318_1 [gene] locus=scaffold2116946_2:3:659:-[Lack both ends]"]
["rumen100058_GL1456035_1 [gene] locus=scaffold1144469_2:2750:3187:+[Lack 3'-end]"]

["rumen100058_GL1457706_1 [gene] locus=scaffold504761_8:5491:6477:-[Complete]"]
["rumen100058_GL1491609_1 [gene] locus=scaffold2100049_3:551:1108:-[Lack 5'-end]"]
["rumen100058_GL1672632_1 [gene] locus=scaffold1097695_1:1:615:-[Lack both ends]"]
["rumen100058_GL1762175_1 [gene] locus=C59653100_1:2:460:-[Lack 3'-end]"]
["rumen100058_GL1798831_1 [gene] locus=scaffold1034605_2:265:765:-[Lack 5'-end]"]
["rumen100058_GL1852281_1 [gene] locus=C60630239_1:1:744:-[Lack 5'-end]"]
["rumen100058_GL1918829_1 [gene] locus=scaffold460743_1:190:930:-[Lack 5'-end]"]
["rumen100058_GL2180245_1 [gene] locus=scaffold1168088_1:3:443:-[Lack 3'-end]"]
["rumen100058_GL2188441_1 [gene] locus=scaffold1613850_2:2:769:-[Lack 5'-end]"]
["rumen100058_GL2207649_1 [gene] locus=scaffold2065209_3:1:495:-[Lack 3'-end]", "rumen2009040_GL3533319_1 [gene] locus=scaffold1132249_9:85:579:-[Lack 3'-end]"]
["rumen100058_GL2218560_1 [gene] locus=scaffold1231026_2:134:601:-[Lack 3'-end]"]
["rumen100058_GL2343963_1 [gene] locus=scaffold222765_2:3:581:-[Lack both ends]"]
["rumen100058_GL2355416_1 [gene] locus=scaffold601745_1:1:435:-[Lack 3'-end]", "rumen2009040_GL0084699_1 [gene] locus=scaffold2019961_3:1:435:-[Lack 3'-end]", "rumen2009040_GL0764629_1 [gene] locus=scaffold2891642_1:1:435:-[Lack 3'-end]"]
["rumen100058_GL2477506_1 [gene] locus=scaffold2726598_5:3:641:-[Lack both ends]"]
["rumen100058_GL2492340_1 [gene] locus=scaffold2596894_1:3:587:-[Lack both ends]"]
["rumen100058_GL2598903_1 [gene] locus=scaffold2681007_1:3:506:-[Lack both ends]"]
["rumen100058_GL2619329_1 [gene] locus=scaffold2605206_4:3:677:-[Lack 5'-end]"]
["rumen100058_GL2669656_1 [gene] locus=scaffold237071_1:1:615:-[Lack both ends]"]
["rumen100058_GL2673104_1 [gene] locus=scaffold3313772_2:1:612:-[Lack 3'-end]"]
["rumen100058_GL2688429_1 [gene] locus=scaffold2206611_1:1:771:-[Lack both ends]"]
["rumen100058_GL2945045_1 [gene] locus=scaffold893877_2:262:687:-[Lack 3'-end]"]
["rumen100058_GL2988089_1 [gene] locus=scaffold1422792_4:3:554:-[Lack both ends]"]
["rumen100058_GL3012780_1 [gene] locus=scaffold1851187_1:3:974:-[Lack 3'-end]"]
["rumen100058_GL3029535_1 [gene] locus=scaffold2288317_1:1:516:-[Lack 3'-end]"]
["rumen100058_GL3089023_1 [gene] locus=scaffold1751573_2:3:854:-[Lack 3'-end]"]
["rumen100058_GL3158956_1 [gene] locus=scaffold2997315_1:2:502:-[Lack both ends]"]
["rumen100058_GL3180428_1 [gene] locus=scaffold1532957_1:1:750:-[Lack both ends]"]
["rumen100058_GL3312332_1 [gene] locus=scaffold449044_3:1:1479:12450:-[Complete]"]
["rumen100058_GL3672783_1 [gene] locus=scaffold303729_1:3:497:-[Lack 5'-end]"]
["rumen100058_GL3687739_1 [gene] locus=scaffold560984_6:8814:9773:-[Complete]"]
["rumen100058_GL3783820_1 [gene] locus=scaffold3335926_1:3:530:-[Lack 3'-end]"]
["rumen100058_GL3794898_1 [gene] locus=scaffold1511960_1:1:597:-[Lack 3'-end]"]
["rumen100058_GL3849461_1 [gene] locus=scaffold1712369_5:1:717:-[Lack both ends]"]
["rumen100058_GL3850397_1 [gene] locus=scaffold466119_5:2:595:-[Lack 5'-end]"]
["rumen100058_GL3866082_1 [gene] locus=scaffold2163156_1:1698:2636:-[Lack 3'-end]"]
["rumen2009040_GL0013822_1 [gene] locus=scaffold1501276_1:3:572:-[Lack 3'-end]"]
["rumen2009040_GL0033910_1 [gene] locus=scaffold1051144_1:218:634:-[Lack 3'-end]"]
["rumen2009040_GL0044390_1 [gene] locus=scaffold1685100_6:2:484:-[Lack 5'-end]"]
["rumen2009040_GL0053895_1 [gene] locus=scaffold2248574_5:142:702:-[Lack 5'-end]"]
["rumen2009040_GL0120670_1 [gene] locus=scaffold534733_1:2:739:-[Lack 3'-end]"]



["rumen2009040_GL0224376_1 [gene] locus=scaffold1970846_1:1:504:+[Lack both ends]"
["rumen2009040_GL0233242_1 [gene] locus=scaffold1685100_5:1050:1598:+[Lack 3'-end]"
["rumen2009040_GL0398315_1 [gene] locus=scaffold496817_1:3:704:-[Lack 3'-end]"
["rumen2009040_GL0401806_1 [gene] locus=scaffold1884788_1:3:431:-[Lack 3'-end]"
["rumen2009040_GL0471805_1 [gene] locus=scaffold2019961_2:158:688:-[Lack 5'-end]"
["rumen2009040_GL0483013_1 [gene] locus=scaffold2990488_1:5:557:+[Lack 3'-end]"
["rumen2009040_GL0557834_1 [gene] locus=scaffold165733_3:1:759:-[Lack 3'-end]"
["rumen2009040_GL0604477_1 [gene] locus=scaffold2273279_1:918:1922:-[Complete]"
["rumen2009040_GL0633992_1 [gene] locus=scaffold75155_3:364:1440:-[Complete]"
["rumen2009040_GL0718615_1 [gene] locus=scaffold2375838_3:2486:3619:-[Complete]"
["rumen2009040_GL0742998_1 [gene] locus=scaffold1964664_1:1:852:-[Lack 3'-end]"
["rumen2009040_GL0858824_1 [gene] locus=scaffold1072886_1:73:708:-[Lack 5'-end]"
["rumen2009040_GL0864288_1 [gene] locus=scaffold2351439_6:93:1100:-[Complete]"
["rumen2009040_GL0906752_1 [gene] locus=scaffold693703_2:1:513:+[Lack both ends]"
["rumen2009040_GL0946200_1 [gene] locus=scaffold1654167_2_1:5384:6361:+[Complete]"
["rumen2009040_GL1021674_1 [gene] locus=scaffold1083537_5:318:779:+[Lack 3'-end]"
["rumen2009040_GL1031267_1 [gene] locus=scaffold1634141_1:3:611:-[Lack 3'-end]"
["rumen2009040_GL1101606_1 [gene] locus=scaffold1841291_1:3:737:-[Lack both ends]"
["rumen2009040_GL1154903_1 [gene] locus=scaffold1660524_1:3:584:-[Lack both ends]"
["rumen2009040_GL1221597_1 [gene] locus=scaffold1544424_1:1:603:-[Lack both ends]"
["rumen2009040_GL1226175_1 [gene] locus=scaffold1371129_1:48:830:-[Lack 5'-end]"
["rumen2009040_GL1499537_1 [gene] locus=scaffold608886_3:1588:2031:+[Lack 3'-end]"
["rumen2009040_GL1507991_1 [gene] locus=scaffold1631608_1:3:536:-[Lack 3'-end]"
["rumen2009040_GL1641623_1 [gene] locus=scaffold3013358_1:526:1218:-[Lack 5'-end]"
["rumen2009040_GL1752955_1 [gene] locus=scaffold3070662_1:2:529:+[Lack 5'-end]"
["rumen2009040_GL1856502_1 [gene] locus=scaffold2694207_1:691:1164:+[Lack 3'-end]"
["rumen2009040_GL1884793_1 [gene] locus=scaffold486018_9:2:988:+[Lack 5'-end]", "rumen2009040_GL2358267_1 [gene] locus=scaffold568460_3:2867:3853:+[Complete]"
["rumen2009040_GL1934422_1 [gene] locus=scaffold834553_1:3:398:-[Lack 3'-end]"
["rumen2009040_GL1939598_1 [gene] locus=scaffold1973934_1:346:852:-[Lack 5'-end]"
["rumen2009040_GL2038368_1 [gene] locus=scaffold797035_2:3:746:-[Lack both ends]"
["rumen2009040_GL2039335_1 [gene] locus=scaffold1259325_1:1:387:+[Lack 5'-end]"
["rumen2009040_GL2342826_1 [gene] locus=scaffold2038314_4:65:508:-[Lack 5'-end]"
["rumen2009040_GL2358857_1 [gene] locus=scaffold2741049_2:2:517:+[Lack both ends]"
["rumen2009040_GL2450151_1 [gene] locus=scaffold1602463_3:632:1222:-[Lack 5'-end]"
["rumen2009040_GL2457637_1 [gene] locus=scaffold823163_1:3:764:-[Lack both ends]"
["rumen2009040_GL2481382_1 [gene] locus=scaffold1878280_1:290:766:-[Lack 5'-end]"
["rumen2009040_GL2485216_1 [gene] locus=scaffold2673757_1:2:562:-[Lack 3'-end]"
["rumen2009040_GL2540970_1 [gene] locus=scaffold667158_1:231:767:+[Lack 3'-end]"
["rumen2009040_GL2681750_1 [gene] locus=scaffold965356_2:2:541:-[Lack 3'-end]"
["rumen2009040_GL2749566_1 [gene] locus=scaffold1391674_2:2:382:-[Lack 3'-end]"
["rumen2009040_GL2866314_1 [gene] locus=scaffold550879_2:231:725:+[Lack 3'-end]"
["rumen2009040_GL2886490_1 [gene] locus=scaffold399958_1:45:641:-[Lack 5'-end]"

["rumen2009040_GL3002242_1 [gene] locus=scaffold1756732_1:174:602:-[Lack 5'-end]"]
["rumen2009040_GL3003927_1 [gene] locus=scaffold2001010_1:2:565:+[Lack both ends]"]
["rumen2009040_GL3092996_1 [gene] locus=scaffold1065072_5:2:799:-[Lack both ends]"]
["rumen2009040_GL3122018_1 [gene] locus=scaffold2228259_1:1:417:+[Lack 5'-end]"]
["rumen2009040_GL3149034_1 [gene] locus=scaffold1602463_4:3:440:-[Lack 3'-end]"]
["rumen2009040_GL3159796_1 [gene] locus=scaffold1672356_1:2547:2954:+[Lack 3'-end]"]
["rumen2009040_GL3244925_1 [gene] locus=scaffold458366_2:1:618:+[Lack 5'-end]"]
["rumen2009040_GL3252399_1 [gene] locus=scaffold354646_2:248:1126:-[Lack 5'-end]"]
["rumen2009040_GL3500043_1 [gene] locus=scaffold132598_3:555:1229:-[Complete]"]
["rumen2009040_GL3546222_1 [gene] locus=scaffold48956_2:747:1130:+[Lack 3'-end]"]
["rumen2009040_GL3564879_1 [gene] locus=scaffold985728_4:1:468:-[Lack 3'-end]"]
["rumen2009040_GL3572366_1 [gene] locus=scaffold1946553_1:3:716:+[Lack both ends]"]
["rumen2009040_GL3587455_1 [gene] locus=scaffold259684_3:2062:3102:+[Complete]"]
["rumen2009040_GL3604636_1 [gene] locus=scaffold2690405_1:1:495:-[Lack 3'-end]"]
["rumen3042_GL0054416_1 [gene] locus=scaffold2541751_1:3:599:-[Lack both ends]"]
["rumen3042_GL0059726_1 [gene] locus=scaffold2016212_1:2:430:-[Lack 3'-end]"]
["rumen3042_GL0198550_1 [gene] locus=scaffold276854_4:328:1068:+[Lack 3'-end]"]
["rumen3042_GL0254281_1 [gene] locus=scaffold112505_1:3:422:-[Lack 3'-end]"]
["rumen3042_GL0331410_1 [gene] locus=scaffold1938892_1:111:638:-[Lack 5'-end]"]
["rumen3042_GL0398507_1 [gene] locus=scaffold746280_2:3:830:+[Lack 5'-end]"]
["rumen3042_GL0516836_1 [gene] locus=scaffold1536019_1:2:601:-[Lack 3'-end]"]
["rumen3042_GL0807425_1 [gene] locus=scaffold988551_2:1:558:-[Lack both ends]"]
["rumen3042_GL0843767_1 [gene] locus=scaffold1194680_3:1:654:-[Lack both ends]"]
["rumen3042_GL0855634_1 [gene] locus=scaffold1691162_1:2:598:+[Lack both ends]"]
["rumen3042_GL1100163_1 [gene] locus=scaffold2090320_1:1:531:-[Lack both ends]"]
["rumen3042_GL1199332_1 [gene] locus=scaffold464338_1:4103:5077:+[Lack 3'-end]"]
["rumen3042_GL1361504_1 [gene] locus=scaffold2133872_1:2251:3225:-[Complete]"]
["rumen3042_GL1469842_1 [gene] locus=scaffold2246887_1:629:1414:+[Lack 3'-end]"]
["rumen3042_GL1536489_1 [gene] locus=scaffold2366345_2:1:621:-[Lack 3'-end]"]
["rumen3042_GL1778640_1 [gene] locus=scaffold834880_1:125:931:-[Lack 5'-end]"; "rumen7049_GL1145126_1 [gene] locus=scaffold2130139_1:138:944:-[Lack 5'-end]"]
["rumen3042_GL1782499_1 [gene] locus=scaffold1009641_1:1:480:+[Lack 5'-end]"]
["rumen3042_GL1785542_1 [gene] locus=scaffold2071035_1:2:667:+[Lack 5'-end]"]
["rumen3042_GL1828889_1 [gene] locus=scaffold1481722_1:1:675:+[Lack 5'-end]"]
["rumen3042_GL1830411_1 [gene] locus=scaffold1965195_2:1180:2007:+[Lack 3'-end]"]
["rumen3042_GL1974783_1 [gene] locus=scaffold1945171_1:667:1605:+[Lack 3'-end]"]
["rumen3042_GL2019109_1 [gene] locus=C51937322_1:1:822:+[Lack 5'-end]"]
["rumen3042_GL2121460_1 [gene] locus=scaffold405571_1:1:516:-[Lack both ends]"]
["rumen3042_GL2298145_1 [gene] locus=scaffold538723_3:446:1459:-[Complete]"]
["rumen3042_GL2333201_1 [gene] locus=scaffold1999229_1:3:728:-[Lack 3'-end]"]
["rumen3042_GL2429652_1 [gene] locus=scaffold332353_3:1052:1627:+[Lack 3'-end]"]
["rumen3042_GL2547494_1 [gene] locus=scaffold1645370_1:1:825:-[Lack 3'-end]"]
["rumen3042_GL2637606_1 [gene] locus=scaffold2292771_2:12:512:-[Lack 5'-end]"]

"rumen3042_GL2741871_1 [gene] locus=scaffold2292771_3:3:497:-[Lack 3'-end]"
"rumen552_GL0200156_1 [gene] locus=scaffold542591_1:3259:4155:+[Complete]", "rumen583_GL0238724_1 [gene] locus=scaffold53255_1:26447:27343:-[Complete]"
"rumen552_GL0316070_1 [gene] locus=scaffold104431_6:1729:2652:+[Lack 3'-end]"
"rumen552_GL0411876_1 [gene] locus=scaffold283057_11:1162:2178:-[Complete]"
"rumen552_GL0419835_1 [gene] locus=scaffold624963_1:3:593:-[Lack both ends]"
"rumen552_GL0471623_1 [gene] locus=scaffold568062_1:118:540:-[Lack 5'-end]", "rumen2009040_GL3622741_1 [gene] locus=scaffold19258_1:1:423:+[Lack 5'-end]"
"rumen552_GL0498541_1 [gene] locus=scaffold895475_2:2:547:+[Lack both ends]"
"rumen552_GL0611115_1 [gene] locus=scaffold873417_2:3:743:-[Lack both ends]"
"rumen552_GL0729319_1 [gene] locus=scaffold418947_4:3:503:+[Lack 5'-end]"
"rumen552_GL0753092_1 [gene] locus=scaffold688634_2:9436:10461:+[Complete]"
"rumen552_GL0776467_1 [gene] locus=scaffold314335_2:1012:1650:+[Lack 3'-end]"
"rumen552_GL0881705_1 [gene] locus=scaffold209070_8:1:561:+[Lack both ends]"
"rumen552_GL0971070_1 [gene] locus=scaffold819020_2:542:1372:-[Lack 5'-end]"
"rumen552_GL1009831_1 [gene] locus=scaffold929842_1:971:1843:+[Lack 3'-end]"
"rumen552_GL1052702_1 [gene] locus=scaffold415999_7:2:424:+[Lack 5'-end]", "rumen583_GL0332362_1 [gene] locus=scaffold276361_3:129:551:-[Lack 5'-end]"
"rumen552_GL1084015_1 [gene] locus=scaffold415671_1:1:498:+[Lack 5'-end]"
"rumen552_GL1191896_1 [gene] locus=scaffold293306_1:1:759:+[Lack both ends]"
"rumen552_GL1197944_1 [gene] locus=scaffold536502_1:1:693:+[Lack 5'-end]"
"rumen552_GL1201600_1 [gene] locus=scaffold310905_2:98:706:-[Lack 5'-end]"
"rumen552_GL1225439_1 [gene] locus=scaffold907183_2:580:1533:+[Complete]"
"rumen552_GL1380265_1 [gene] locus=scaffold319829_1:35:592:+[Lack 3'-end]"
"rumen552_GL1433053_1 [gene] locus=scaffold689479_1:131:1114:-[Complete]", "rumen3042_GL2654465_1 [gene] locus=C52108410_1:3:986:-[Complete]"
"rumen552_GL1436514_1 [gene] locus=scaffold854013_2:1:792:-[Lack both ends]"
"rumen552_GL1440013_1 [gene] locus=scaffold203264_1:1:525:+[Lack both ends]"
"rumen552_GL1448832_1 [gene] locus=scaffold36046_2:4965:5945:-[Complete]", "rumen555_GL1692780_1 [gene] locus=scaffold1082603_1:3593:4573:-[Complete]", "rumen0081_GL0514064_1 [gene] locus=scaffold5614_1:15852:16832:+[Complete]", "rumen2009040_GL1128095_1 [gene] locus=scaffold1210743_4:2646:3626:+[Complete]"
"rumen552_GL1716125_1 [gene] locus=scaffold604095_1:890:1825:+[Lack 3'-end]", "rumen0081_GL1743851_1 [gene] locus=C39230363_1:1:936:+[Lack both ends]"
"rumen553_GL0025785_1 [gene] locus=scaffold425815_1:5427:6446:+[Complete]"
"rumen553_GL0075427_1 [gene] locus=scaffold206980_7:3:1043:-[Lack 3'-end]"
"rumen553_GL0080409_1 [gene] locus=scaffold389397_1:1515:1895:-[Lack 5'-end]"
"rumen553_GL0136563_1 [gene] locus=scaffold102846_5:6711:7706:-[Complete]"
"rumen553_GL0154606_1 [gene] locus=scaffold44886_1:631:1284:+[Lack 3'-end]"
"rumen553_GL0168381_1 [gene] locus=C7189224_1:3:626:-[Lack both ends]"
"rumen553_GL0205981_1 [gene] locus=scaffold231762_4:1:561:-[Lack both ends]"
"rumen553_GL0237933_1 [gene] locus=C7292662_1:72:728:+[Lack 3'-end]"
"rumen553_GL0248359_1 [gene] locus=scaffold365127_1:57477:58466:+[Complete]"

"rumen554_GL2107679_1 [gene] locus=scaffold8791_1:283:1272:+[Complete]"
"rumen553_GL0298504_1 [gene] locus=scaffold297784_1:3:482:+[Lack 5'-end]"
"rumen553_GL0349357_1 [gene] locus=scaffold352537_1:1:984:+[Lack 5'-end]"
"rumen553_GL0351392_1 [gene] locus=scaffold8660_5:650:1603:-[Lack 5'-end]"
"rumen553_GL0487595_1 [gene] locus=scaffold347884_1:709:1212:-[Lack 5'-end]"
"rumen553_GL0520057_1 [gene] locus=scaffold32864_1:995:1603:-[Lack 5'-end]"
"rumen553_GL0578661_1 [gene] locus=scaffold287449_2:380:1045:+[Lack 3'-end]"
"rumen553_GL0586781_1 [gene] locus=scaffold68115_1:2380:3102:+[Lack 3'-end]"
"rumen553_GL0631439_1 [gene] locus=scaffold32864_2:1:519:-[Lack 3'-end]"
"rumen553_GL0683379_1 [gene] locus=scaffold48905_1:159:785:+[Lack 3'-end]"
"rumen553_GL0695754_1 [gene] locus=scaffold233965_1:19995:21014:-[Complete]", "rumen553_GL0791971_1 [gene] locus=scaffold157426_1:3740:4759:-[Complete]", "rumen553_GL0937811_1 [gene] locus=scaffold196973_1:3721:4740:-[Complete]", "rumen100058_GL2555908_1 [gene] locus=scaffold3356328_2:2223:3242:+[Complete]"
"rumen553_GL0758216_1 [gene] locus=scaffold319491_4:461:1012:+[Lack 3'-end]"
"rumen553_GL0775514_1 [gene] locus=scaffold310536_1:1:828:-[Lack 3'-end]"
"rumen553_GL0818756_1 [gene] locus=scaffold410882_1:3:563:-[Lack 3'-end]"
"rumen553_GL0846785_1 [gene] locus=scaffold2814_1:21934:22956:-[Complete]"
"rumen553_GL0872238_1 [gene] locus=scaffold284531_3:10345:11331:-[Complete]"
"rumen553_GL0881765_1 [gene] locus=scaffold77855_1:2:739:-[Lack 3'-end]"
"rumen553_GL0882230_1 [gene] locus=scaffold280520_4:3626:4585:+[Complete]"
"rumen553_GL0891354_1 [gene] locus=scaffold412990_1:1501:2559:+[Complete]"
"rumen553_GL0917057_1 [gene] locus=scaffold217147_1:710:1123:-[Complete]"
"rumen553_GL0923912_1 [gene] locus=scaffold434298_1:1916:2890:+[Complete]", "rumen555_GL2097775_1 [gene] locus=scaffold587155_4:14857:15831:-[Complete]", "rumen100058_GL0363974_1 [gene] locus=scaffold700814_2:331:1305:-[Complete]"
"rumen553_GL0934327_1 [gene] locus=C7100456_1:1:561:+[Lack both ends]"
"rumen554_GL0138702_1 [gene] locus=scaffold1407868_2:226:1122:+[Lack 3'-end]"
"rumen554_GL0188161_1 [gene] locus=scaffold908510_1:376:1365:+[Lack 3'-end]"
"rumen554_GL0209651_1 [gene] locus=scaffold985276_1:4063:5079:+[Complete]", "rumen2009040_GL3346427_1 [gene] locus=scaffold400904_7:1409:2425:+[Complete]"
"rumen554_GL0216523_1 [gene] locus=scaffold1053227_2:3:941:+[Lack 5'-end]"
"rumen554_GL0271653_1 [gene] locus=C41038322_1:1:1047:+[Lack 5'-end]"
"rumen554_GL0276839_1 [gene] locus=scaffold1257514_2:3:569:-[Lack both ends]"
"rumen554_GL0295893_1 [gene] locus=scaffold2037770_1:3:575:+[Lack both ends]"
"rumen554_GL0346335_1 [gene] locus=scaffold1908839_1:2:598:-[Lack 3'-end]"
"rumen554_GL0413060_1 [gene] locus=scaffold1832768_2:2089:3090:-[Complete]", "rumen555_GL1510587_1 [gene] locus=scaffold593271_5:1738:2739:+[Complete]", "rumen0081_GL0338794_1 [gene] locus=scaffold1190223_1:4567:5568:+[Complete]"
"rumen554_GL0487410_1 [gene] locus=scaffold2065399_1:1:612:-[Lack both ends]"
"rumen554_GL0512500_1 [gene] locus=scaffold1634016_1:3:464:+[Lack 5'-end]", "rumen554_GL2093825_1 [gene] locus=scaffold1423172_2:1:462:+[Lack 5'-end]"
"rumen554_GL0522957_1 [gene] locus=scaffold513938_1:2357:3331:+[Complete]"

"rumen3042_GL0386703_1 [gene] locus=scaffold1839576_1:19:993:-[Complete]"
"rumen554_GL0594724_1 [gene] locus=scaffold182826_1:3:725:-[Lack 3'-end]"
"rumen554_GL0656150_1 [gene] locus=scaffold1051268_4:351:1439:-[Lack 5'-end]"
"rumen554_GL0687567_1 [gene] locus=scaffold1598446_2:3:911:+[Lack 5'-end]", "rumen2009040_GL0482909_1 [gene] locus=scaffold2776935_2:3:911:+[Lack 5'-end]"
"rumen554_GL0786729_1 [gene] locus=scaffold294875_3:62:604:-[Lack 5'-end]"
"rumen554_GL0888247_1 [gene] locus=scaffold2059249_1:973:1815:+[Lack 3'-end]"
"rumen554_GL1045616_1 [gene] locus=scaffold1334142_5:3:782:-[Lack 3'-end]"
"rumen554_GL1053069_1 [gene] locus=scaffold1326175_5:3:545:+[Lack both ends]", "rumen0081_GL1498336_1 [gene] locus=scaffold885327_5:1:543:-[Lack 3'-end]", "rumen2009040_GL2321236_1 [gene] locus=scaffold1136922_1:3:545:+[Lack both ends]"
"rumen554_GL1074659_1 [gene] locus=scaffold1700773_2:3:881:-[Lack 5'-end]"
"rumen554_GL1084182_1 [gene] locus=C40945874_1:3:1001:-[Lack both ends]"
"rumen554_GL1106767_1 [gene] locus=scaffold923869_1:382:1185:-[Lack 5'-end]"
"rumen554_GL1289582_1 [gene] locus=C40465960_1:3:773:+[Lack both ends]"
"rumen554_GL1290684_1 [gene] locus=scaffold2153745_1:3:452:+[Lack 5'-end]"
"rumen554_GL1291809_1 [gene] locus=scaffold997847_2:337:1263:+[Lack 3'-end]"
"rumen554_GL1306149_1 [gene] locus=scaffold2067455_1:3:851:+[Lack 5'-end]"
"rumen554_GL1332124_1 [gene] locus=scaffold1245999_2:3:689:+[Lack both ends]"
"rumen554_GL1389302_1 [gene] locus=scaffold1282684_2:1:462:-[Lack 3'-end]"
"rumen554_GL1486333_1 [gene] locus=scaffold2184403_1:979:1899:-[Complete]"
"rumen554_GL1546605_1 [gene] locus=scaffold1773484_2:151:558:+[Lack 3'-end]", "rumen100058_GL3811027_1 [gene] locus=scaffold3239136_1:122:529:+[Lack 3'-end]"
"rumen554_GL1552216_1 [gene] locus=scaffold977727_1:1552:2214:+[Lack 3'-end]", "rumen554_GL3085806_1 [gene] locus=scaffold1441392_1:739:1401:+[Lack 3'-end]"
"rumen554_GL1564068_1 [gene] locus=scaffold140049_3:3:911:+[Lack 5'-end]"
"rumen554_GL1596247_1 [gene] locus=scaffold623243_2:2:922:+[Lack 5'-end]"
"rumen554_GL1680904_1 [gene] locus=scaffold1049950_2:1:687:+[Lack 5'-end]"
"rumen554_GL1691418_1 [gene] locus=scaffold1964144_2:1:762:-[Lack 3'-end]"
"rumen554_GL1699031_1 [gene] locus=scaffold1761210_1:2:661:-[Lack 3'-end]"
"rumen554_GL1752435_1 [gene] locus=scaffold966121_1:2:592:-[Lack both ends]"
"rumen554_GL1858283_1 [gene] locus=scaffold569612_1:145:609:+[Lack 3'-end]"
"rumen554_GL1886028_1 [gene] locus=scaffold169248_4:3:833:+[Lack 5'-end]"
"rumen554_GL1942394_1 [gene] locus=scaffold48403_2:923:1762:+[Lack 3'-end]"
"rumen554_GL2007459_1 [gene] locus=scaffold514724_2:1:534:-[Lack 3'-end]"
"rumen554_GL2180132_1 [gene] locus=scaffold1350098_1:392:982:+[Lack 3'-end]", "rumen7049_GL0208732_1 [gene] locus=scaffold1779539_1:58:648:+[Lack 3'-end]"
"rumen554_GL2181202_1 [gene] locus=scaffold1993307_1:3:521:-[Lack both ends]"
"rumen554_GL2204014_1 [gene] locus=scaffold168929_2:243:698:-[Lack 5'-end]"
"rumen554_GL2320728_1 [gene] locus=scaffold1657544_1:165:1064:+[Lack 3'-end]"
"rumen554_GL2333867_1 [gene] locus=scaffold172759_4:1:528:+[Lack both ends]"
"rumen554_GL2381327_1 [gene] locus=scaffold896143_1:2:841:-[Lack both ends]", "rumen100058_GL1849897_1 [gene] locus=scaffold1014378_2:138:980:-[Lack 5'-end]"

["rumen554_GL2419500_1 [gene] locus=scaffold629415_3:2:1027:+[Lack 5'-end]"]
["rumen554_GL2430171_1 [gene] locus=scaffold37293_4:2434:3495:+[Complete]"]
["rumen554_GL2538378_1 [gene] locus=scaffold618786_1:1345:2427:-[Complete]"]
["rumen554_GL2569972_1 [gene] locus=scaffold519696_2:3:515:+[Lack both ends]"]
["rumen554_GL2594229_1 [gene] locus=scaffold148046_3:3:677:-[Lack both ends]"]
["rumen554_GL2685462_1 [gene] locus=scaffold1675218_5:1419:2237:-[Lack 5'-end]"]
["rumen554_GL2858882_1 [gene] locus=scaffold536857_2:2022:2966:+[Complete]"]
["rumen554_GL3011202_1 [gene] locus=scaffold281160_1:3:602:+[Lack both ends]"]
["rumen554_GL3041864_1 [gene] locus=scaffold1113550_1:3:515:+[Lack both ends]"]
["rumen555_GL0049897_1 [gene] locus=scaffold950560_1:2163:3146:-[Complete]", "rumen555_GL1918340_1 [gene] locus=scaffold43756_2:362:1345:-[Complete]", "rumen0081_GL1273748_1 [gene] locus=scaffold1500703_2:1198:2181:+[Complete]", "rumen0081_GL2044562_1 [gene] locus=scaffold379348_2:1775:2758:-[Complete]", "rumen3042_GL2436629_1 [gene] locus=scaffold1565584_1:299:1282:-[Complete]", "rumen7049_GL0845113_1 [gene] locus=scaffold1942404_1:765:1748:-[Complete]", "rumen7049_GL1603343_1 [gene] locus=scaffold950038_1:16:999:+[Complete]"]
["rumen555_GL0083119_1 [gene] locus=scaffold1326084_2:3:509:+[Lack both ends]"]
["rumen555_GL0153393_1 [gene] locus=scaffold648523_2:138:707:-[Lack 5'-end]"]
["rumen555_GL0344450_1 [gene] locus=scaffold681804_1:2:898:-[Lack 3'-end]"]
["rumen555_GL0421868_1 [gene] locus=C27783126_1:2:583:-[Lack 3'-end]"]
["rumen555_GL0429628_1 [gene] locus=scaffold315835_2:1:534:-[Lack both ends]"]
["rumen555_GL0484815_1 [gene] locus=scaffold220815_1:2:883:+[Lack 5'-end]"]
["rumen555_GL0512705_1 [gene] locus=scaffold81084_1:4206:5255:+[Complete]"]
["rumen555_GL0604705_1 [gene] locus=scaffold1587368_1:4744:5214:-[Lack 5'-end]", "rumen555_GL2027931_1 [gene] locus=scaffold864373_3:432:902:-[Lack 5'-end]"]
["rumen555_GL0648913_1 [gene] locus=scaffold483787_2:430:1455:-[Complete]", "rumen0081_GL0214676_1 [gene] locus=scaffold568171_2:13847:14872:+[Complete]"]
["rumen555_GL0707718_1 [gene] locus=scaffold1539616_1:1:366:-[Lack 3'-end]"]
["rumen555_GL0797869_1 [gene] locus=scaffold173345_1:317:1045:-[Lack 5'-end]"]
["rumen555_GL0818579_1 [gene] locus=scaffold566320_1:3:725:+[Lack both ends]"]
["rumen555_GL0845101_1 [gene] locus=scaffold1401950_2:615:1463:-[Lack 5'-end]"]
["rumen555_GL0896488_1 [gene] locus=scaffold1067912_1:65:673:+[Lack 3'-end]"]
["rumen555_GL0897443_1 [gene] locus=scaffold1307507_1:676:1293:-[Lack 5'-end]"]
["rumen555_GL0934013_1 [gene] locus=scaffold1273003_2:541:1140:-[Lack 5'-end]"]
["rumen555_GL1214084_1 [gene] locus=scaffold82015_1:110:571:+[Lack 3'-end]"]
["rumen555_GL1264915_1 [gene] locus=scaffold546110_2:2:730:+[Lack 5'-end]"]
["rumen555_GL1276327_1 [gene] locus=scaffold663978_2:3:662:+[Lack both ends]"]
["rumen555_GL1343406_1 [gene] locus=scaffold384420_1:3:512:+[Lack both ends]"]
["rumen555_GL1433997_1 [gene] locus=scaffold239327_1:2:490:+[Lack 5'-end]", "rumen2009040_GL1177891_1 [gene] locus=scaffold2940965_1:1:489:+[Lack 5'-end]"]
["rumen555_GL1456295_1 [gene] locus=scaffold1111929_1:2:508:-[Lack both ends]"]
["rumen555_GL149522_1 [gene] locus=scaffold745838_1:2:646:-[Lack 3'-end]"]
["rumen555_GL1541124_1 [gene] locus=scaffold1013143_2:656:1306:+[Lack 3'-end]",

"rumen2009040_GL0831948_1 [gene] locus=scaffold1501331_1:3:653:-[Lack 3'-end]"
"rumen555_GL1566027_1 [gene] locus=scaffold161735_3:1:546:+[Lack both ends]"
"rumen555_GL1819046_1 [gene] locus=scaffold108362_1:13152:14216:+[Complete]"
"rumen555_GL1947555_1 [gene] locus=scaffold838986_3:2:505:+[Lack both ends]"
"rumen555_GL2015365_1 [gene] locus=scaffold1579934_1:4008:4703:-[Lack 5'-end]"
"rumen555_GL2018653_1 [gene] locus=scaffold451620_1:2:592:-[Lack 3'-end]"
"rumen555_GL2153281_1 [gene] locus=scaffold668923_4:600:1079:-[Lack 5'-end]"
"rumen555_GL2160909_1 [gene] locus=scaffold357577_1:3:992:-[Lack 3'-end]"
"rumen555_GL2231739_1 [gene] locus=scaffold672646_3:3:551:-[Lack both ends]"
"rumen555_GL2305192_1 [gene] locus=scaffold52641_2:160:1065:+[Lack 3'-end]"
"rumen555_GL2310630_1 [gene] locus=scaffold689420_1:1808:2665:+[Lack 3'-end]"
"rumen555_GL2318656_1 [gene] locus=scaffold1577776_1:1675:2454:+[Lack 3'-end]"
"rumen555_GL2345539_1 [gene] locus=scaffold21142_2:6235:7278:+[Complete]"
"rumen555_GL2418108_1 [gene] locus=scaffold1515378_1:2:544:+[Lack both ends]"
"rumen555_GL2427390_1 [gene] locus=scaffold1315192_2:3:893:+[Lack 5'-end]"
"rumen555_GL2510502_1 [gene] locus=scaffold74091_1:365:1093:+[Lack 3'-end]"
"rumen583_GL0016108_1 [gene] locus=scaffold10500_5:431:1423:-[Complete]"
"rumen583_GL0019139_1 [gene] locus=scaffold69391_16:3:725:+[Lack both ends]"
"rumen583_GL0083314_1 [gene] locus=C5090830_1:3:488:-[Lack 3'-end]"
"rumen583_GL0092370_1 [gene] locus=scaffold224822_3:17635:18684:+[Complete]"
"rumen583_GL0151880_1 [gene] locus=scaffold275785_2:2:583:+[Lack both ends]"
"rumen583_GL0182159_1 [gene] locus=scaffold1284_3:3:821:+[Lack 5'-end]"
"rumen583_GL0183524_1 [gene] locus=scaffold81430_1:1:522:+[Lack both ends]"
"rumen583_GL0271792_1 [gene] locus=C5234690_1:2:586:+[Lack 5'-end]",
"rumen554_GL2065060_1 [gene] locus=C39950904_1:1:585:+[Lack 5'-end]"
"rumen583_GL0291504_1 [gene] locus=scaffold25451_4:2:595:+[Lack 5'-end]"
"rumen583_GL0316776_1 [gene] locus=scaffold18285_2:7328:8341:+[Complete]"
"rumen583_GL0319058_1 [gene] locus=scaffold263136_1:1:654:+[Lack both ends]"
"rumen583_GL0396177_1 [gene] locus=scaffold102_1:13768:14760:-[Complete]"
"rumen583_GL0435588_1 [gene] locus=scaffold100224_4:2:499:+[Lack both ends]"
"rumen583_GL0437819_1 [gene] locus=scaffold20151_6:1:690:+[Lack 5'-end]"
"rumen583_GL0496825_1 [gene] locus=scaffold335338_1:674:1801:-[Complete]"
"rumen583_GL0500606_1 [gene] locus=scaffold275354_2:3:878:+[Lack 5'-end]"
"rumen583_GL0598887_1 [gene] locus=scaffold42773_3:1730:2170:-[Lack 5'-end]"
"rumen583_GL0629430_1 [gene] locus=scaffold26514_10:2:841:-[Lack 3'-end]"
"rumen583_GL0639840_1 [gene] locus=scaffold111711_3:23:613:-[Lack 5'-end]"
"rumen583_GL0668222_1 [gene] locus=scaffold326943_1:3:590:-[Lack both ends]"
"rumen583_GL0701828_1 [gene] locus=scaffold131765_1:747:1193:-[Lack 5'-end]"
"rumen583_GL0748094_1 [gene] locus=scaffold310884_1:27:1097:-[Complete]"
"rumen583_GL0771066_1 [gene] locus=scaffold187279_1:3:611:-[Lack both ends]"
"rumen583_GL0778639_1 [gene] locus=scaffold244346_1:67:939:+[Lack 3'-end]"
"rumen583_GL0787681_1 [gene] locus=scaffold115326_1:3775:4722:+[Complete]"
"rumen7049_GL0117431_1 [gene] locus=scaffold1138349_1:2:721:+[Lack 5'-end]"

["rumen7049_GL0158322_1 [gene] locus=scaffold1437026_1:3:401:-[Lack 3'-end]"]
["rumen7049_GL0296794_1 [gene] locus=C51326938_1:50:529:+[Lack 3'-end]"]
["rumen7049_GL0374971_1 [gene] locus=scaffold2218975_1:3:821:-[Lack 3'-end]"]
["rumen7049_GL0453631_1 [gene] locus=scaffold1773472_3:421:849:-[Lack 5'-end]"]
["rumen7049_GL0608548_1 [gene] locus=C52414850_1:53:760:+[Lack 3'-end]"]
["rumen7049_GL0704107_1 [gene] locus=scaffold1603165_2:3:48:1025:-[Lack 5'-end]"]
["rumen7049_GL0751922_1 [gene] locus=scaffold706614_2:2:649:+[Lack both ends]"]
["rumen7049_GL0757384_1 [gene] locus=scaffold430277_1:150:1262:+[Lack 3'-end]"]
["rumen7049_GL1171663_1 [gene] locus=scaffold2128948_1:239:868:+[Lack 3'-end]"]
["rumen7049_GL1375179_1 [gene] locus=scaffold324796_1:713:1741:+[Complete]"]
["rumen7049_GL1461620_1 [gene] locus=scaffold1399925_1:3:884:-[Lack 3'-end]"]
["rumen7049_GL1487928_1 [gene] locus=C53276822_1:751:1569:+[Lack 3'-end]"]
["rumen7049_GL1590079_1 [gene] locus=scaffold908729_3:515:994:-[Lack 5'-end]"]
["rumen7049_GL1610216_1 [gene] locus=scaffold1755913_1:3:506:+[Lack 5'-end]"]
["rumen7049_GL1883047_1 [gene] locus=scaffold511205_1:273:728:-[Lack 5'-end]"]
["rumen7049_GL1901348_1 [gene] locus=scaffold1594254_1:2:820:-[Lack both ends]"]
["rumen7049_GL2118237_1 [gene] locus=scaffold1642567_1:426:896:+[Lack 3'-end]"]
["rumen7049_GL2152036_1 [gene] locus=scaffold207751_3:52:540:-[Lack 5'-end]"]
["rumen7049_GL2158537_1 [gene] locus=scaffold472765_4:1:612:+[Lack 5'-end]"]
["rumen7049_GL2456196_1 [gene] locus=scaffold407158_2:150:983:+[Lack 3'-end]"]
["rumen7049_GL2603710_1 [gene] locus=C52626822_1:31:849:-[Lack 5'-end]"]
["rumen7049_GL2651904_1 [gene] locus=scaffold17328_2:2:916:+[Lack 5'-end]"]
["rumen7049_GL2706827_1 [gene] locus=scaffold1205539_1:3:530:-[Lack both ends]"]
["rumen7049_GL2804593_1 [gene] locus=scaffold569104_1:3:779:+[Lack 5'-end]"]

### C3

["cazyCCgij156109243 gb EDO10988.1 β-1", "2-mannosidase_hypothetical protein BACOVA_03624 [Bacteroides ovatus ATCC 8483]"; "cazy SCV07919.1 secreted hypothetical protein [Bacteroides ovatus V975]"; "cazygij938484278 gb ALJ48509.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides ovatus]"; "cazygij295088161 emb CBK69684.1  Predicted glycosylase [Bacteroides xylanisolvens XB1A]"]
["cazyCCgij254949689 gb ACT94389.1 β-1", "2-mannosidase_glycosidase PH1107-related [Dyadobacter fermentans DSM 18053]"]
["cazyCCgij29341096 gb AAO78885.1 β-1", "2-mannosidase_putative glycosidase", " PH117-related [Bacteroides thetaiotaomicron VPI-5482]"; "humangutMH0041_GL0075740 [gene] locus=scaffold7438_6:102:1253:+ [Complete] codon-table.11"; "humangutMH0266_GL0124116 [gene] locus=scaffold1405_1:4558:5709:+ [Complete] codon-table.11"; "humangutT2D-135A_GL0063918 [gene] locus=scaffold53973_1:3589:4740:+ [Complete] codon-table.11"; "mouseS-Fe10_GL0001513 [gene] locus=scaffold1118_3:596:1747:+ [Complete] codon-table.11"; "mouse1A-dyr3-06_GL0015591 [gene] locus=scaffold1150_2:2092:3243:- [Complete] codon-table.11"; "cazygij1045271614 gb ANU56305.1  hypothetical protein A4V03_00905 [Bacteroides sp. I48]"; "cazygij938479793 gb ALJ44025.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides thetaiotaomicron]"]
["cazygij1006704447 gb AMQ56248.1  pesticidal protein Cry15Aa [Algoriphagus sp. M8-2]"]
["cazygij1008902929 gb AMR34594.1  hypothetical protein A0256_16760 [Mucilaginibacter sp. PAMC 26640]"]
["cazygij1028469421 gb ANE52341.1  glycosidase [Flavisolibacter sp. LCS9]"]
["cazygij1033842095 gb ANH82948.1  hypothetical protein A8C56_19890 [Niabella sp. BS26]"]



["cazygi 1035430157 gb ANI89637.1  hypothetical protein A9P82_10265 [Arachidococcus sp. BS20]"]
["cazygi 1045274436 gb ANU59127.1  hypothetical protein A4V03_17495 [Bacteroides sp. I48]"]
["cazygi 116226858 gb ABJ85567.1  glycosidase", " PH1107-related [Candidatus Solibacter usitatus Ellin6076]"]
["cazygi 167351664 gb ABZ74394.1  glycosidase PH1107-related (plasmid) [Caulobacter sp. K31]"]
["cazygi 18893919 gb AAL81871.1  hypothetical protein PF1747 [Pyrococcus furiosus DSM 3638], "cazygi 12018068 gb AAG45396.1 AF307053_11 unknown [Thermococcus litoralis], "cazygi 242264750 gb ACS89432.1  Glycosidase [Thermococcus sibiricus MM 739]"]
["cazygi 225791433 gb ACO31523.1  conserved hypothetical protein [Acidobacterium capsulatum ATCC 51196]"]
["cazygi 239505942 gb ACR79429.1  glycosidase PH1107-related [Kosmotoga olearia TBF 19.5.1]"]
["cazygi 239911180 gb ACS3407.1  Glycosylase [Thermococcus gammatolerans EJ3]"]
["cazygi 256040022 gb ACU63566.1  glycosidase PH1107-related [Chitinophaga pinensis DSM 2588]"]
["cazygi 260062546 ref EAR15283.1  hypothetical protein RB2501_13184 [Robiginitalea biformata HTCC2501]"]
["cazygi 294980338 gb ADF50803.1  glycosidase", " PH1107-related protein [Zunongwangia profunda SM-A87]"]
["cazygi 296849618 gb ADH62633.1  glycosidase PH1107-related protein [Meiothermus silvanus DSM 9946]"]
["cazygi 305667514 ref YP_003863801.1  hypothetical protein FB2170_14743 [Maribacter sp. HTCC2170]"]
["cazygi 315592348 gb ADU51644.1  glycosidase related protein [Thermaerobacter marianensis DSM 12885]"]
["cazygi 319927679 gb ADV84754.1  glycosidase related protein [Terriglobus saanensis SP1PR4]"]
["cazygi 321164890 gb ADW70595.1  glycosidase related protein [Granulicella tundricola MP5ACTX9]"]
["cazygi 3257523 dbj BAA30206.1  299aa long hypothetical protein [Pyrococcus horikoshii OT3]"]
["cazygi 326552918 gb ADZ81303.1  glycosidase related protein [Sphingobacterium sp. 21]"]
["cazygi 332333126 gb AEE50227.1  glycosidase related protein [Haliscomenobacter hydrossis DSM 1100]"]
["cazygi 343954774 gb AEM70573.1  glycosidase related protein [Muricauda ruestringensis DSM 13258]"]
["cazygi 361059038 gb AEV98029.1  glycosidase related protein [Niastellella koreensis GR20-10]"]
["cazygi 378567994 gb AFC28304.1  glycosidase PH1107-like protein [Paenibacillus mucilaginosus 3016], "cazygi 384089041 gb AFH60477.1  glycosidase [Paenibacillus mucilaginosus K02], "cazygi 336298945 gb AEI42048.1  glycosidase PH1107-related protein [Paenibacillus mucilaginosus KNP414]"]
["cazygi 381386860 gb BAM03676.1  hypothetical protein PSMK_15170 [Phycisphaera mikurensis NBRC 102666]"]
["cazygi 387855701 gb AFK03798.1  glycosidase related protein [Emticicia oligotrophica DSM 17448]"]
["cazygi 388249740 gb AFK22593.1  putative Glycosidase [Pyrococcus sp. ST04]"]
["cazygi 390411660 gb AFL87164.1  putative glycosylase [Terriglobus roseus DSM 18391]"]
["cazygi 393190195 gb AFN04893.1  hypothetical protein PFC_09860 [Pyrococcus furiosus COM1], "cazygi 374742097 gb EHR78506.1  glycosidase [Thermococcus litoralis DSM 5473], "cazygi 971361817 gb ALV61989.1  Glycoside hydrolase 130 family enzyme", " beta-1", "4 mannoooligosaccharide phosphorilase [Thermococcus sp. 2319x1]"]
["cazygi 5458549 emb CAB50037.1  Hypothetical protein PAB1622 [Pyrococcus abyssii GE5]"]
["cazygi 570745856 gb AHF16368.1  glycosidase [Niabella soli DSM 19437]"]
["cazygi 573024216 gb AHF79750.1  putative glycoside hydrolase [Thermococcus parvalvinellae]"]
["cazygi 663075784 gb AIE87939.1  glycosidase related protein [Fimbrimonas ginsengisoli Gsoil 348]"]
["cazygi 664801792 gb AIF70025.1  hypothetical protein PAP_08185 [Palaeococcus pacificus DY20341]"]
["cazygi 672715017 emb CDS94299.1  Glycosidase related protein [Sphingobacterium sp. PM2-P1-29]"]
["cazygi 744793298 gb AJC70877.1  glycosidase [Thermococcus guaymasensis DSM 11113]"]
["cazygi 787938705 gb AKA35180.1  Glycosidase related protein [Muricauda lutaonensis]"]
["cazygi 808696030 gb AKD56869.1  glycosidase [Spirosoma radiotolerans]"]
["cazygi 827413726 gb AKI98278.1  glycosidase [Kosmotoga pacifica]"]

["cazy 873497534 gb AKP53038.1  Putative glycoside hydrolase [Cyclobacterium amurskyense]"]
["cazy 926468532 gb ALD22883.1  glycosidase [Hymenobacter sp. DG25A]"]
["cazy 94549995 gb ABF39919.1  glycosidase", " PH1107-related protein [Candidatus Koribacter versatilis Ellin345]"]
["cazy 946529133 gb ALM09124.1  hypothetical protein SB49_02230 [Sediminicola sp. YIK13]"]
["cazy 996010572 gb AMJ67963.1  hypothetical protein AXW84_01505 [Hymenobacter sp. PAMC 26628]"]
["cazy 998619775 db BAU55708.1  Beta-1", "4-mannooligosaccharide phosphorylase [Mucilagibacter gotjawali]"]
["cazy APG61045.1 pesticidal protein Cry15Aa [Gramella salexigens]"]
["cazy APQ16221.1 hypothetical protein BTR34_02150 [Maribacter sp. T28]"]
["cazy APU67835.1 putative glycoside hydrolase [Gramella flava JLT2011]"]
["cazy APU97438.1 hypothetical protein BV902_14695 [Sphingobacterium sp. B29]"]
["cazy ARK09600.1 glycosidase [Fibrella sp. ES10-3-2-2]"]
["cazy ASA78004.1 glycosidase [Thermococcus sp. 5-4]", "cazy ASJ14742.1 glycosidase [Thermococcus radiotolerans]", "cazy 340810641 gb AEK73798.1  Glycosylase [Thermococcus sp. 4557]"]
["cazy ASJ05082.1 glycosidase [Thermococcus barossii]"]
["cazy ASJ07914.1 glycosidase [Thermococcus siculi]"]
["cazy ASJ13038.1 glycosidase [Thermococcus thioreducers]"]
["cazy ASJ17080.1 glycosidase [Thermococcus chitonophagus]", "cazy 1001992192 gb AMM53793.1  glycosidase [Pyrococcus sp. NCB100]", "cazy 1019365031 emb CUX77680.1  COG2152 predicted glycoside hydrolase [Thermococcus chitonophagus]"]
["cazy AST55815.1 hypothetical protein C1960_21960 [Parabacteroides sp. CT06]", "humangutMH0012_GL0065470 [gene] locus=scaffold7537_4:1953:3101:- [Complete] codon-table.11", "mouseS-Fe1_GL0174490 [gene] locus=scaffold80917_1:43528:44676:- [Complete] codon-table.11"]
["cazy ASU31942.1 hypothetical protein MuYL_0039 [Mucilagibacter sp. BJC16-A31]"]
["cazy ASV31696.1 hypothetical protein CJ263_16555 [Maribacter cobaltidurans]"]
["cazy ASZ10702.1 glycosidase [Chitinophaga sp. MD30]"]
["cazy ATL49712.1 hypothetical protein COR50_03215 [Chitinophaga caeni]"]
["cazy ATP57941.1 hypothetical protein CPT03_16470 [Pedobacter ginsengisoli]"]
["cazy AUD04348.1 glycosidase [Spirosoma pollinicola]", "cazy 283818071 gb ADB39909.1  glycosidase PH1107-related protein [Spirosoma linguale DSM 74]"]
["cazy AVI52417.1 glycosidase [Aureitalea sp. RR4-38]"]
["cazy AVR44446.1 pesticidal protein Cry15Aa [Gramella sp. SH35]"]
["cazy AWL09983.1 Beta-1", "4-mannooligosaccharide phosphorylase [Pseudarcicella sp. HME7025]"]
["cazy AWM35477.1 glycosidase [Hymenobacter nivis]"]
["cazy AXC09738.1 putative glycoside hydrolase [Acidobacteriaceae bacterium SBC82]"]
["cazy AXE19877.1 glycosidase [Runella sp. HYN0085]", "cazy 336305538 gb AEI48640.1  glycosidase related protein [Runella slithyformis DSM 19594]"]
["cazy AYB30495.1 glycosidase [Chryseolinea sp. KIS68-18]"]
["cazy AYD47492.1 hypothetical protein D6B99_07660 [Arachidicoccus sp. KIS59-12]"]
["cazy AYL95667.1 hypothetical protein HYN43_010370 [Mucilagibacter sp. HYN0043]"]
["cazy AYQ36400.1 glycosidase [Runella sp. SP2]"]
["cazy SCD19903.1 Glycosyl hydrolase families 32 and 68 [Proteiniphilum saccharofermentans]"]
["cazy SCV07002.1 glycosyl hydrolase [Bacteroides ovatus V975]"]

"humangutMH0020_GL0014507 [gene] locus=scaffold21608_9:7559:8704:+ [Complete] codon-table.11",
"humangutMH0021_GL0015154 [gene] locus=scaffold39537_5:574:1719:+ [Complete] codon-table.11",
"humangutMH0054_GL0022277 [gene] locus=scaffold55358_3:7139:8284:+ [Complete] codon-table.11",
"humangutNLF015_GL0019781 [gene] locus=scaffold3041_1:10604:11749:- [Complete] codon-table.11",
"cazygi 938483372 gb ALJ47603.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides ovatus]",
"cazygi 156110526 gb EDO12271.1  hypothetical protein BACOVA_02161 [Bacteroides ovatus ATCC 8483]"
["cazy SCV08357.1 glycosyl hydrolase", " family 32 protein [Bacteroides ovatus V975]",
"humangutMH0010_GL0029842 [gene] locus=scaffold7356_38:62:1195:+ [Complete] codon-table.11",
"humangutMH0041_GL0070376 [gene] locus=scaffold1298_16:5317:6450:- [Complete] codon-table.11",
"humangutMH0106_GL0099321 [gene] locus=scaffold44499_2:850:1983:- [Complete] codon-table.11",
"humangutMH0199_GL0030986 [gene] locus=scaffold5142_1:1117:2250:- [Complete] codon-table.11",
"humangutV1.CD7-0_GL0082857 [gene] locus=C639715_1:137:1270:+ [Complete] codon-table.11",
"humangutT2D-118A_GL0058838 [gene] locus=scaffold2929_3:845:1978:- [Complete] codon-table.11",
"humangut159146620-stool1_revised_scaffold7674_1_gene7987 strand:- start:610 stop:1743 length:1134 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",
"humangut159227541-stool1_revised_scaffold11082_1_gene13325 strand:- start:125 stop:1258 length:1134 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",
"mouse A-dyr3-06_GL0043666 [gene] locus=scaffold8255_5:62656:63789:+ [Complete] codon-table.11",
"cazygi 938484706 gb ALJ48937.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides ovatus]",
"cazygi 938479426 gb ALJ43658.1  4-O-beta-D-mannosyl-D-glucose phosphorylase [Bacteroides thetaiotaomicron]",
"cazygi 29341411 gb AAO79199.1  glycosidase [Bacteroides thetaiotaomicron VPI-5482]",
"cazygi 295086662 emb CBK68185.1  Predicted glycosylase [Bacteroides xylanisolvens XB1A]"
["cazy SDB32688.1 Predicted glycosyl hydrolase", " GH43/DUF377 family [Flavobacteriaceae bacterium MAR_2010_188]"
["cazy SDS05868.1 Predicted glycosyl hydrolase", " GH43/DUF377 family [Gramella sp. MAR_2010_147]"
["cazy SMD42156.1 Predicted glycosyl hydrolase", " GH43/DUF377 family [Aquiflexum balticum DSM 16537]"
["cazy SNV50569.1 Beta-xylosidase [Sphingobacterium mizutaii]"
["cazy SOE20032.1 Predicted glycosyl hydrolase", " GH43/DUF377 family [Cytophagales bacterium TFI 002]"
["cazy SSC12643.1 putative glycosylase [Mesotoga infera]",
"cazygi 387859460 gb AFK07551.1  putative glycosylase [Mesotoga prima MesG1.Ag.4.2]"
["humangut158337416-stool2_revised_C1016974_1_gene120380 strand:- start:87 stop:1787 length:1701 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut158337416-stool2_revised_C1029828_1_gene88239 strand:- start:1328 stop:2680 length:1353 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut158337416-stool2_revised_scaffold5531_1_gene84699 strand:- start:508 stop:1701 length:1194 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut159551223-stool1_revised_scaffold2984_2_gene68717 strand:+ start:3065 stop:5104 length:2040 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut702443.CUY_2888 [Complete]:- codon-table.11"]
["humangut763536994-stool1_revised_scaffold30524_3_gene66393 strand:- start:1 stop:1176 length:1176 start_codon:no stop_codon:no gene_type:incomplete [Lack both ends] codon-table.11"]
["humangut764588959-stool1_revised_scaffold10732_1_gene99975 strand:+ start:23500 stop:25908 length:2409 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut764588959-stool1_revised_scaffold28890_1_gene49945 strand:- start:3 stop:818 length:816 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]

["humangut764588959-stool1_revised_scaffold3488_2_gene128211 strand:+ start:9758 stop:10948 length:1191 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut765013792-stool1_revised_scaffold4953_1_gene23639 strand:- start:137 stop:1255 length:1119 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangutDLF007_GL0034958 [gene] locus=scaffold6278_2:2:1150:+ [Lack 5'-end] codon-table.11"]
["humangutDOM019_GL0055493 [gene] locus=scaffold8800_7:3:482:+ [Lack 5'-end] codon-table.11"]
["humangutED9A_GL0116165 [gene] locus=C732188_1:2:1120:+ [Lack 5'-end] codon-table.11", "pigPIG-093_GL0174800 [gene] locus=scaffold17146_18:602:1720:- [Complete] codon-table.11"]
["humangutMH0012_GL0081352 [gene] locus=scaffold48048_1:10079:11314:- [Complete] codon-table.11", "pigPIG-001_GL0046149 [gene] locus=scaffold31148_1:10628:11863:- [Complete] codon-table.11"]
["humangutMH0020_GL0038350 [gene] locus=scaffold646_7:5468:6628:+ [Complete] codon-table.11", "cazygij149938150[gb]ABR44847.1 conserved hypothetical protein [Parabacteroides distasonis ATCC 8503"]
["humangutMH0020_GL0038773 [gene] locus=scaffold33764_1:8209:9348:+ [Complete] codon-table.11", "humangutMH0309_GL0091870 [gene] locus=scaffold97527_2:10171:11310:- [Complete] codon-table.11", "humangutT2D-51A_GL0015257 [gene] locus=scaffold90715_2:3784:4923:+ [Complete] codon-table.11"]
["humangutMH0026_GL0034282 [gene] locus=scaffold724_9:1540:2736:+ [Complete] codon-table.11", "mouseS-Fe11_GL0011000 [gene] locus=scaffold2607_1:980:2176:+ [Complete] codon-table.11"]
["humangutMH0041_GL0041441 [gene] locus=scaffold16152_2:309:1457:- [Complete] codon-table.11", "humangutMH0094_GL0100167 [gene] locus=scaffold70088_2:1210:2358:+ [Complete] codon-table.11", "humangutMH0101_GL0016856 [gene] locus=scaffold61835_1:25127:26275:+ [Complete] codon-table.11", "humangutMH0333_GL0042919 [gene] locus=scaffold52124_1:37755:38903:- [Complete] codon-table.11", "mouse1A-dyr3-06_GL0009044 [gene] locus=scaffold13200_1:35730:36878:+ [Complete] codon-table.11", "cazygij938475581[gb]ALJ39813.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides thetaiotaomicron"]
["humangutMH0051_GL0007813 [gene] locus=scaffold46064_2:179:1348:- [Lack 5'-end] codon-table.11", "humangutMH0085_GL0010429 [gene] locus=scaffold7997_4:3200:4369:+ [Complete] codon-table.11", "cazygij939201713[gb]ALJ59886.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides cellulosilyticus"]
["humangutMH0055_GL0072634 [gene] locus=scaffold22578_5:4211:5374:+ [Complete] codon-table.11", "humangutV1_CD38-0_GL0055924 [gene] locus=scaffold36707_2:1441:2604:+ [Complete] codon-table.11", "mouse1A-dyr2-07_GL0065353 [gene] locus=scaffold6960_10:14888:16051:+ [Complete] codon-table.11"]
["humangutMH0057_GL0037539 [gene] locus=scaffold4165_5:7455:8618:- [Complete] codon-table.11"]
["humangutMH0066_GL0031540 [gene] locus=scaffold2763_4:6077:7243:- [Complete] codon-table.11"]
["humangutMH0085_GL0023163 [gene] locus=scaffold15198_1:3547:4698:- [Complete] codon-table.11", "humangutMH0133_GL0079918 [gene] locus=scaffold48549_1:1259:2410:+ [Complete] codon-table.11", "humangutO2_UC53-2_GL0046015 [gene] locus=scaffold62013_3:7862:9013:- [Complete] codon-table.11", "humangutNOM004_GL0051874 [gene] locus=scaffold21992_1:23808:24959:- [Complete] codon-table.11"]
["humangutMH0089_GL0109551 [gene] locus=scaffold8881_27:3839:4942:+ [Complete] codon-table.11"]
["humangutMH0100_GL0065892 [gene] locus=scaffold22486_16:18542:19729:- [Complete] codon-table.11"]
["humangutMH0108_GL0094577 [gene] locus=scaffold5563_7:1181:1786:+ [Lack 3'-end] codon-table.11"]
["humangutMH0116_GL0066798 [gene] locus=scaffold71313_3:2:940:+ [Lack 5'-end] codon-table.11"]
["humangutMH0122_GL0034515 [gene] locus=scaffold25847_3:899:2041:- [Lack 5'-end] codon-table.11"]
["humangutMH0124_GL0021158 [gene] locus=scaffold22583_4:163:1356:- [Complete] codon-table.11"]
["humangutMH0129_GL0061913 [gene] locus=scaffold101300_2:4336:5454:+ [Complete] codon-table.11"]
["humangutMH0137_GL0025089 [gene] locus=scaffold63161_1:9120:10346:- [Complete] codon-table.11"]

["humangutMH0138_GL0020687 [gene] locus=scaffold22140_2:154:1365:- [Complete] codon-table.11"]
["humangutMH0141_GL0130465 [gene] locus=scaffold18875_3:6192:7382:- [Complete] codon-table.11"]
["humangutMH0181_GL0022584 [gene] locus=scaffold28989_5:64:1260:- [Complete] codon-table.11", "humangutMH0187_GL0080429 [gene] locus=scaffold51749_1:37297:38493:+ [Complete] codon-table.11"]
["humangutMH0183_GL0083894 [gene] locus=scaffold87893_8:3:641:+ [Lack 5'-end] codon-table.11"]
["humangutMH0189_GL0113658 [gene] locus=scaffold35684_13:1031:3979:- [Complete] codon-table.11"]
["humangutMH0192_GL0171168 [gene] locus=scaffold42030_18:369:1508:- [Complete] codon-table.11"]
["humangutMH0193_GL0078195 [gene] locus=scaffold62144_9:944:2182:+ [Complete] codon-table.11"]
["humangutMH0195_GL0159559 [gene] locus=scaffold45515_2:3475:4584:+ [Complete] codon-table.11"]
["humangutMH0199_GL0008694 [gene] locus=scaffold57343_1:3851:5047:- [Lack 5'-end] codon-table.11"]
["humangutMH0200_GL0056196 [gene] locus=scaffold130159_1:44904:46067:- [Complete] codon-table.11"]
["humangutMH0212_GL0048360 [gene] locus=scaffold50771_2:909:2063:+ [Complete] codon-table.11", "pigPIG-001_GL0156765 [gene] locus=scaffold92880_2:1027:2181:- [Complete] codon-table.11"]
["humangutMH0222_GL0038110 [gene] locus=scaffold77473_4:6064:8496:- [Complete] codon-table.11"]
["humangutMH0230_GL0077374 [gene] locus=scaffold71928_1:115768:116970:+ [Complete] codon-table.11"]
["humangutMH0244_GL0155053 [gene] locus=scaffold213_13:658:1947:- [Complete] codon-table.11"]
["humangutMH0274_GL0010583 [gene] locus=scaffold93764_3:14026:15246:+ [Complete] codon-table.11"]
["humangutMH0274_GL0122424 [gene] locus=scaffold93988_1:21895:23082:- [Complete] codon-table.11"]
["humangutMH0286_GL0091580 [gene] locus=scaffold121555_1:2:1639:+ [Lack both ends] codon-table.11"]
["humangutMH0289_GL0164495 [gene] locus=scaffold77783_10:7690:8826:+ [Complete] codon-table.11"]
["humangutMH0335_GL0084956 [gene] locus=scaffold33310_4:52257:53381:- [Complete] codon-table.11", "mouse1A-dyr2-07_GL0030947 [gene] locus=scaffold11171_4:5417:6541:- [Complete] codon-table.11"]
["humangutMH0350_GL0202447 [gene] locus=scaffold6299_14:546:1442:+ [Lack 3'-end] codon-table.11"]
["humangutMH0357_GL0171132 [gene] locus=scaffold108150_2:49:921:+ [Lack 3'-end] codon-table.11"]
["humangutMH0361_GL0098667 [gene] locus=scaffold49262_1:2500:4911:- [Complete] codon-table.11"]
["humangutMH0369_GL0008313 [gene] locus=scaffold38633_1:62820:63929:- [Complete] codon-table.11"]
["humangutMH0378_GL0024253 [gene] locus=scaffold18755_3:2:1192:+ [Lack 5'-end] codon-table.11"]
["humangutMH0378_GL0079806 [gene] locus=scaffold23929_19:1:1302:+ [Lack both ends] codon-table.11"]
["humangutMH0383_GL0069535 [gene] locus=scaffold82472_2:329:1519:- [Complete] codon-table.11"]
["humangutMH0388_GL0138141 [gene] locus=scaffold79628_1:5851:6978:- [Complete] codon-table.11"]
["humangutMH0413_GL0067508 [gene] locus=scaffold44909_1:10839:11966:- [Complete] codon-table.11"]
["humangutMH0415_GL0094360 [gene] locus=scaffold341_3:67886:68998:+ [Complete] codon-table.11"]
["humangutMH0429_GL0034540 [gene] locus=scaffold85161_1:3046:5451:- [Complete] codon-table.11", "humangut158499257-stool2_revised_C1325755_1_gene187214 strand:- start:96 stop:2501 length:2406 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangutMH0439_GL0123154 [gene] locus=scaffold4255_11:2:430:- [Lack 3'-end] codon-table.11"]
["humangutMH0453_GL0139557 [gene] locus=scaffold50617_1:1:1836:+ [Lack 5'-end] codon-table.11"]
["humangutN024A_GL0026144 [gene] locus=scaffold20549_2:2:1033:+ [Lack 5'-end] codon-table.11"]
["humangutN035A_GL0060277 [gene] locus=scaffold1299_6:51752:52900:+ [Complete] codon-table.11"]
["humangutN038A_GL0085108 [gene] locus=scaffold17346_5:203:1378:- [Lack 5'-end] codon-table.11"]
["humangutNOM023_GL0008696 [gene] locus=scaffold6280_11:14774:15997:+ [Complete] codon-table.11"]
["humangutO2_CD2-0_GL0013688 [gene] locus=scaffold15209_1:3407:4612:+ [Complete] codon-table.11", "pigPIG-008_GL0060387 [gene] locus=scaffold142563_2:2247:3452:- [Complete] codon-table.11"]

["humangutO2.UC11-2_GL0042558 [gene] locus=scaffold39495_3:1637:2773:- [Complete] codon-table.11"]
["humangutO2.UC2-2_GL0005274 [gene] locus=scaffold20781_1:7374:8471:+ [Complete] codon-table.11"]
["humangutO2.UC21-2_GL0054119 [gene] locus=scaffold50675_22:3:1172:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC44-0_GL0005851 [gene] locus=scaffold50768_10:3:995:+ [Lack both ends] codon-table.11"]
["humangutO2.UC48-0_GL0055178 [gene] locus=scaffold132969_1:1085:2236:- [Complete] codon-table.11"]
["humangutT2D-11A_GL0139780 [gene] locus=scaffold31288_2:2:850:+ [Lack both ends] codon-table.11"]
["humangutT2D-135A_GL0017292 [gene] locus=scaffold7557_5:5284:6399:- [Complete] codon-table.11"]
["humangutT2D-48A_GL0072608 [gene] locus=scaffold33749_3:10367:11497:+ [Complete] codon-table.11", "humangut764487809-stool1_revised_scaffold44332_1_gene14323 strand:- start:1 stop:1128 length:1128 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangutT2D-70A_GL0056825 [gene] locus=scaffold1160_4:29:862:+ [Lack 3'-end] codon-table.11"]
["humangutT2D-8A_GL0016983 [gene] locus=scaffold1359_13:1:669:+ [Lack 5'-end] codon-table.11"]
["humangutV1.CD3-3-PN_GL0023210 [gene] locus=scaffold39892_3:6392:7543:- [Complete] codon-table.11", "humangut160765029-stool1_revised_scaffold21574_1_gene29821 strand:+ start:4252 stop:5403 length:1152 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangutV1.FI28_GL0230259 [gene] locus=scaffold100310_8:2:622:- [Lack both ends] codon-table.11"]
["humangutV1.FI34_GL0128785 [gene] locus=scaffold59159_3:821:1816:+ [Lack 3'-end] codon-table.11"]
["humangutV1.UC17-0_GL0023683 [gene] locus=scaffold14974_3:776:1324:- [Lack 5'-end] codon-table.11"]
["humangutV1.UC4-5_GL0061566 [gene] locus=scaffold1889_5:1:804:- [Lack 3'-end] codon-table.11"]
["mouse16_GL0106917 [gene] locus=scaffold69501_2:23081:24208:+ [Complete] codon-table.11"]
["mouse4-1_GL0056131 [gene] locus=scaffold43684_1:221390:224281:- [Complete] codon-table.11"]
["mouseG1-1A_GL0001040 [gene] locus=scaffold120_1:57678:58793:+ [Complete] codon-table.11"]
["mouseG1-4A_GL0012400 [gene] locus=scaffold7238_4:2:511:- [Lack 3'-end] codon-table.11"]
["mouseG1-4A_GL0065519 [gene] locus=scaffold51446_1:353:1492:+ [Lack 3'-end] codon-table.11"]
["mouseG1-5A_GL0031042 [gene] locus=scaffold16192_1:2:661:- [Lack both ends] codon-table.11"]
["mouseG1-6A_GL0011841 [gene] locus=scaffold3133_3:478:1080:- [Lack 5'-end] codon-table.11"]
["mouseG1-6A_GL0079350 [gene] locus=scaffold45043_4:3:986:+ [Lack 5'-end] codon-table.11"]
["mouseMC-6-2_GL0142574 [gene] locus=scaffold115293_1:165:749:- [Lack 5'-end] codon-table.11"]
["mouseMC-6-2_GL0142575 [gene] locus=scaffold115293_2:3:710:- [Lack both ends] codon-table.11"]
["mouseMC-6-3_GL0103379 [gene] locus=scaffold77658_4:2:715:+ [Lack both ends] codon-table.11"]
["mouseMC-6-4_GL0037048 [gene] locus=scaffold21497_5:1:603:+ [Lack both ends] codon-table.11"]
["mouseS-Fe10_GL0025736 [gene] locus=scaffold51837_1:4789:7089:- [Complete] codon-table.11"]
["mouseS-Fe10_GL0041139 [gene] locus=scaffold2483_2:5386:6516:- [Complete] codon-table.11", "mouse2B-dyr19-06_GL0008379 [gene] locus=scaffold740_10:695:1825:- [Complete] codon-table.11"]
["mouseS-Fe10_GL0055926 [gene] locus=scaffold57598_1:20125:22446:+ [Complete] codon-table.11"]
["mouseS-Fe10_GL0084620 [gene] locus=scaffold64647_1:40469:41668:- [Complete] codon-table.11"]
["mouseS-Fe10_GL0130324 [gene] locus=scaffold327_6:31001:32179:+ [Complete] codon-table.11"]
["pigBHZ-6B_GL0151827 [gene] locus=scaffold990_3:6800:7978:+ [Complete] codon-table.11"]
["pigBMZ-17B_GL0054550 [gene] locus=scaffold62536_5:686:1801:- [Complete] codon-table.11"]
["pigDB-537B_GL0095012 [gene] locus=scaffold88829_8:51:1169:+ [Complete] codon-table.11"]
["pigDB-537B_GL0107503 [gene] locus=scaffold3109_3:2351:4654:- [Complete] codon-table.11"]
["pigEYZ-353B_GL0228570 [gene] locus=scaffold148936_1:86:1069:+ [Complete] codon-table.11"]
["pigPIG-009_GL0034422 [gene] locus=scaffold22982_2:2803:3897:- [Lack 5'-end] codon-table.11"]

["pigPIG-011_GL0063271 [gene] locus=C2002064_1:3:1784:+ [Lack 5'-end] codon-table.11"]
["pigPIG-011_GL0206789 [gene] locus=scaffold153707_5:1:819:+ [Lack both ends] codon-table.11"]
["pigPIG-015_GL0018584 [gene] locus=scaffold77075_1:922:2070:- [Complete] codon-table.11"]
["pigPIG-018_GL0009170 [gene] locus=scaffold115433_2:3:839:- [Lack 3'-end] codon-table.11"]
["pigPIG-023_GL0161560 [gene] locus=scaffold132720_2:2:505:+ [Lack both ends] codon-table.11"]
["pigPIG-027_GL0043017 [gene] locus=scaffold20702_3:7880:9016:- [Complete] codon-table.11"]
["pigPIG-027_GL0090201 [gene] locus=scaffold104690_6:488:2791:- [Complete] codon-table.11"]
["pigPIG-028_GL0025267 [gene] locus=scaffold8938_2:2394:3551:+ [Complete] codon-table.11"]
["pigPIG-029_GL0094936 [gene] locus=scaffold11947_2:2:1144:+ [Lack both ends] codon-table.11"]
["pigPIG-036_GL0031679 [gene] locus=scaffold21832_2:2:523:+ [Lack both ends] codon-table.11"]
["pigPIG-052_GL0008222 [gene] locus=scaffold121254_1:4272:6683:- [Complete] codon-table.11", "rumen553_GL0779074_1 [gene] locus=C7766909_1:34895:37306:+[Complete]"]
["pigPIG-052_GL0134708 [gene] locus=scaffold187325_3:7603:8691:- [Complete] codon-table.11"]
["pigPIG-052_GL0231560 [gene] locus=scaffold161331_1:11503:12633:+ [Complete] codon-table.11", "rumen553_GL0186123_1 [gene] locus=scaffold29911_3:29968:31098:-[Complete]"]
["pigPIG-093_GL0025039 [gene] locus=C1915055_1:2:955:- [Lack 3'-end] codon-table.11"]
["pigPIG-095_GL0118967 [gene] locus=scaffold95652_2:964:1785:+ [Complete] codon-table.11"]
["pigPIG_114_GL0056339 [gene] locus=scaffold36302_2:2:1201:+ [Lack 5'-end] codon-table.11"]
["pigPIG_124_GL0137253 [gene] locus=scaffold112837_1:4633:7080:- [Complete] codon-table.11", "pigPIG-026_GL0232589 [gene] locus=scaffold177914_1:7954:10401:- [Complete] codon-table.11"]
["pigPIG_130_GL0244308 [gene] locus=scaffold154735_2:2:991:+ [Lack both ends] codon-table.11"]
["pigPIG_151_GL0226406 [gene] locus=scaffold190994_1:3:575:- [Lack both ends] codon-table.11"]
["pigPIG_151_GL0245739 [gene] locus=scaffold213322_1:3:1328:+ [Lack 5'-end] codon-table.11"]
["pigPIG_171_GL0207592 [gene] locus=scaffold230377_1:1075:2079:+ [Lack 3'-end] codon-table.11"]
["pigPIG_175_GL0210073 [gene] locus=scaffold153980_1:3:914:- [Lack both ends] codon-table.11"]
["pigPIG_189_GL0023829 [gene] locus=scaffold145928_3:2:2152:+ [Lack 5'-end] codon-table.11"]
["pigPIG_190_GL0064267 [gene] locus=scaffold19076_2:2:937:- [Lack both ends] codon-table.11"]
["pigPIG_200_GL0045959 [gene] locus=scaffold157948_2:317:946:+ [Lack 3'-end] codon-table.11"]
["pigPIG_200_GL0174839 [gene] locus=scaffold50705_2:686:3208:+ [Complete] codon-table.11"]
["pigSYZ-635B_GL0188356 [gene] locus=scaffold774_1:2:2317:- [Lack both ends] codon-table.11"]
["pigSYZ-639B_GL0079434 [gene] locus=scaffold83973_1:3:1706:+ [Lack both ends] codon-table.11"]
["rumen0081_GL0018308_1 [gene] locus=scaffold1707031_1:53:595:-[Lack 5'-end]"]
["rumen0081_GL0217456_1 [gene] locus=scaffold936411_1:1:4941:+[Lack 5'-end]"]
["rumen0081_GL0564217_1 [gene] locus=C37935053_1:1:525:+[Lack both ends]"]
["rumen0081_GL0861149_1 [gene] locus=scaffold569877_2:2:952:+[Lack 5'-end]"]
["rumen0081_GL1500808_1 [gene] locus=scaffold1219931_6:2:511:-[Lack both ends]"]
["rumen0081_GL1521727_1 [gene] locus=scaffold3083_1:2949:8456:-[Complete]"]
["rumen0081_GL1843532_1 [gene] locus=scaffold1472887_1:1:519:+[Lack both ends]"]
["rumen0081_GL1934982_1 [gene] locus=scaffold1748454_1:2048:3247:-[Complete]"]
["rumen0081_GL2263554_1 [gene] locus=scaffold1701902_1:230:685:+[Lack 3'-end]"]
["rumen100058_GL0113072_1 [gene] locus=scaffold598027_1:280:2838:+[Complete]"]
["rumen100058_GL0403439_1 [gene] locus=scaffold1138840_4:2:1195:+[Lack 5'-end]"]
["rumen100058_GL1917898_1 [gene] locus=scaffold3212573_1:1:975:-[Lack 3'-end]"]

["rumen100058_GL2225638_1 [gene] locus=scaffold56557_5:3:1163:-[Lack 3'-end]"]
["rumen100058_GL3095310_1 [gene] locus=scaffold746023_6:763:1911:-[Complete]"]
["rumen100058_GL3404804_1 [gene] locus=C59223072_1:174:731:+[Lack 3'-end]"]
["rumen100058_GL3648478_1 [gene] locus=scaffold2081806_1:2023:3039:-[Lack 5'-end]"]
["rumen2009040_GL0335525_1 [gene] locus=scaffold597333_2:2:670:+[Lack 5'-end]"]
["rumen2009040_GL0849204_1 [gene] locus=scaffold658670_2:11796:12725:-[Complete]"]
["rumen2009040_GL1278742_1 [gene] locus=scaffold908923_1:299636:302218:-[Complete]"]
["rumen2009040_GL1638798_1 [gene] locus=scaffold982511_1:1:951:+[Lack 5'-end]"]
["rumen2009040_GL2024614_1 [gene] locus=scaffold725108_1:3:1022:-[Lack both ends]"]
["rumen2009040_GL2470304_1 [gene] locus=scaffold747333_1:148:1287:+[Complete]"]
["rumen2009040_GL2513307_1 [gene] locus=scaffold411342_2:1:516:+[Lack both ends]"]
["rumen2009040_GL2838540_1 [gene] locus=scaffold516193_3:10389:11534:-[Complete]"]
["rumen2009040_GL3390821_1 [gene] locus=scaffold1683667_3:53:2179:+[Complete]"]
["rumen3042_GL0122552_1 [gene] locus=scaffold860228_2:3:536:-[Lack 3'-end]"]
["rumen3042_GL0231557_1 [gene] locus=scaffold1469926_2:2:2455:+[Lack both ends]"]
["rumen3042_GL0286054_1 [gene] locus=scaffold1634175_1:212:895:+[Lack 3'-end]"]
["rumen3042_GL0456759_1 [gene] locus=scaffold928852_1:3:767:-[Lack 3'-end]"]
["rumen3042_GL1567465_1 [gene] locus=scaffold1448515_1:3:749:-[Lack 3'-end]"]
["rumen3042_GL1900522_1 [gene] locus=scaffold1539956_2:693:1928:-[Complete]"]
["rumen3042_GL2068048_1 [gene] locus=scaffold533713_2:3:761:+[Lack 5'-end]"]
["rumen3042_GL2223721_1 [gene] locus=C51529607_1:23:829:-[Lack 5'-end]"]
["rumen3042_GL2588302_1 [gene] locus=C50500639_1:1:429:+[Lack 5'-end]"]
["rumen3042_GL2659811_1 [gene] locus=scaffold2554224_1:856:1551:+[Lack 3'-end]"]
["rumen552_GL0166750_1 [gene] locus=scaffold736128_1:3:530:+[Lack both ends]"]
["rumen552_GL0214002_1 [gene] locus=scaffold964823_2:54851:57121:-[Complete]"]
["rumen552_GL0801114_1 [gene] locus=scaffold467322_1:41055:42179:-[Complete]", "rumen0081_GL0126292_1 [gene] locus=scaffold332114_3:660:1784:+[Complete]"]
["rumen552_GL1023644_1 [gene] locus=scaffold7740_3:86586:87689:-[Complete]", "rumen583_GL0741327_1 [gene] locus=scaffold342004_1:40774:41877:+[Complete]", "rumen0081_GL1181816_1 [gene] locus=scaffold234247_3:228:1331:-[Complete]"]
["rumen552_GL1536499_1 [gene] locus=scaffold658342_1:39774:40904:-[Complete]"]
["rumen553_GL0294380_1 [gene] locus=C7764951_1:19517:20605:+[Complete]"]
["rumen553_GL0415727_1 [gene] locus=scaffold311384_2:6050:8380:-[Complete]"]
["rumen553_GL0481082_1 [gene] locus=scaffold3744_2:4315:5445:-[Complete]"]
["rumen553_GL0653290_1 [gene] locus=scaffold30284_4:16535:18841:-[Complete]", "rumen555_GL1877630_1 [gene] locus=scaffold268090_4:694:3000:-[Complete]", "rumen555_GL1881090_1 [gene] locus=scaffold946831_5:1062:3368:-[Complete]"]
["rumen554_GL0424050_1 [gene] locus=C41249349_1:1:498:+[Lack 5'-end]"]
["rumen554_GL0722787_1 [gene] locus=C41478849_1:6:1172:-[Complete]"]
["rumen554_GL0798826_1 [gene] locus=scaffold1703033_1:2:571:-[Lack 3'-end]"]
["rumen554_GL2279888_1 [gene] locus=scaffold2137980_1:3:1889:+[Lack both ends]"]
["rumen554_GL2576864_1 [gene] locus=scaffold1347888_4:3:1568:-[Lack 3'-end]"]
["rumen555_GL0476822_1 [gene] locus=scaffold437598_2:1:4062:+[Lack 5'-end]"]



["rumen555_GL0484805_1 [gene] locus=scaffold1581487_1:3:1310:+[Lack 5'-end]"]
["rumen555_GL0645598_1 [gene] locus=scaffold1265563_1:387:788:-[Lack 5'-end]"]
["rumen555_GL1084251_1 [gene] locus=scaffold1543929_1:2:517:-[Lack 3'-end]"]
["rumen555_GL1314332_1 [gene] locus=C27734054_1:3:629:+[Lack both ends]"]
["rumen555_GL1846163_1 [gene] locus=scaffold344520_4:1542:2699:+[Complete]"]
["rumen555_GL2441297_1 [gene] locus=scaffold1119893_1:2:553:-[Lack both ends]"]
["rumen555_GL2469032_1 [gene] locus=scaffold402776_1:2770:3411:+[Lack 3'-end]"]
["rumen555_GL2500413_1 [gene] locus=scaffold590573_1:2:1252:-[Lack both ends]"]
["rumen555_GL2504734_1 [gene] locus=scaffold293509_1:3:791:+[Lack both ends]"]
["rumen583_GL0534788_1 [gene] locus=scaffold12672_1:764:2794:-[Complete]"]
["rumen7049_GL0859720_1 [gene] locus=scaffold1646031_3:57:1661:-[Complete]"]
["rumen7049_GL0939381_1 [gene] locus=scaffold1728221_2:2:1777:+[Lack both ends]"]
["rumen7049_GL1012174_1 [gene] locus=scaffold1938312_2:407:2641:-[Complete]"]
["rumen7049_GL1068002_1 [gene] locus=scaffold1369585_1:1:2196:+[Lack both ends]"]
["rumen7049_GL1176168_1 [gene] locus=scaffold897496_1:2768:5314:-[Complete]"]
["rumen7049_GL1225084_1 [gene] locus=scaffold2075975_1:218:1384:+[Complete]"]
["rumen7049_GL1834282_1 [gene] locus=scaffold2118351_1:1:552:-[Lack both ends]"]
["rumen7049_GL2133015_1 [gene] locus=scaffold1426321_1:102:1232:-[Complete]"]
["rumen7049_GL2224832_1 [gene] locus=C52640272_1:1:852:+[Lack 5'-end]"]
["rumen7049_GL2592886_1 [gene] locus=scaffold389306_1:1:1149:+[Lack 5'-end]"]
["rumen7049_GL2741019_1 [gene] locus=scaffold1423006_3:2245:3204:-[Complete]"]

## C4

["Ncazy AOC93207.1 Beta-1", "4-mannooligosaccharide phosphorylase [Flavobacterium anhuiense]", "Ncazy AOE51475.1 glycosidase [Flavobacterium psychrophilum]", "cazy AWK05320.1 glycosidase [Flavobacterium sp. HYN0056]", "cazy 947264313 gb ALM47851.1 glycosidase [Flavobacterium psychrophilum]", "cazy 255346869 gb ACU06195.1 glycosidase PH1107-related [Pedobacter heparinus DSM 2366]"]
["Ncazy AOE51603.1 glycosidase [Flavobacterium psychrophilum]", "cazy AWH86432.1 glycosidase [Flavobacterium sp. HYN0059]", "cazy 947264444 gb ALM47982.1 glycosidase [Flavobacterium psychrophilum]"]
["cazy CCgi 16413308 emb CAC96089.1 β-1", "2-mannobiose phosphorylase_lin0857 [Listeria innocua Clp11262]", "cazy APH75866.1 Putative glycosylase [Listeria monocytogenes]", "cazy APH78842.1 Putative glycosylase [Listeria monocytogenes]", "cazy APO61046.1 glycosidase [Listeria monocytogenes]", "cazy APQ09030.1 glycosidase [Listeria monocytogenes]", "cazy APV02038.1 glycosidase [Listeria monocytogenes]", "cazy APV05006.1 glycosidase [Listeria monocytogenes]", "cazy APV08055.1 glycosidase [Listeria monocytogenes]", "cazy APV11155.1 glycosidase [Listeria monocytogenes]", "cazy AQY50881.1 glycosidase [Listeria welhenstephanensis]", "cazy AUB53497.1 glycosidase [Enterococcus mundtii]", "cazy SNV21540.1 Domain of uncharacterised function (DUF377) [Listeria welshimeri]"]

"cazy|SNV39278.1 Domain of uncharacterised function (DUF377) [Listeria ivanovii subsp. ivanovii]",

"cazy|SNV87103.1 Domain of uncharacterised function (DUF377) [Listeria ivanovii subsp. ivanovii]",

"cazygi|346981339|emb|CBW85288.1| Hypothetical protein of unknown function [Listeria ivanovii subsp. ivanovii PAM 55]",

"cazygi|694158253|gb|AIS64822.1| glycosidase [Listeria ivanovii subsp. ivanovii]",

"cazygi|694155550|gb|AIS62120.1| glycosidase [Listeria ivanovii subsp. londoniensis]",

"cazygi|694152715|gb|AIS59286.1| glycosidase [Listeria ivanovii subsp. londoniensis]",

"cazygi|583837501|gb|AHI55363.1| glycosidase [Listeria ivanovii WSLC3009]",

"cazygi|384390376|gb|AFH79446.1| hypothetical protein MUO\_04580 [Listeria monocytogenes 07PF0776]",

"cazygi|284056755|gb|ADB67696.1| hypothetical protein LM5578\_0943 [Listeria monocytogenes 08-5578]",

"cazygi|284059802|gb|ADB70741.1| hypothetical protein LM5923\_0897 [Listeria monocytogenes 08-5923]",

"cazygi|345536422|gb|AEO05862.1| hypothetical protein LMRG\_02287 [Listeria monocytogenes 10403S]",

"cazygi|987005979|gb|AMD51570.1| glycosidase [Listeria monocytogenes]",

"cazygi|1009069741|gb|AMR53417.1| glycosidase [Listeria monocytogenes]",

"cazygi|584270596|emb|CDM19439.1| conserved protein of unknown function [Listeria monocytogenes 6179]",

"cazygi|957750430|gb|ALQ20171.1| glycosidase [Listeria monocytogenes]",

"cazygi|957746227|gb|ALQ15969.1| glycosidase [Listeria monocytogenes]",

"cazygi|404218417|emb|CBY69781.1| glycosylase", " putative [Listeria monocytogenes ATCC 19117]",

"cazygi|957744515|gb|ALQ14258.1| glycosidase [Listeria monocytogenes]",

"cazygi|523836882|gb|AGR00748.1| glycosidase [Listeria monocytogenes]",

"cazygi|630374582|gb|AHY98922.1| glycosidase [Listeria monocytogenes]",

"cazygi|820768138|gb|AKG85006.1| glycosidase [Listeria monocytogenes]",

"cazygi|820771048|gb|AKG87829.1| glycosidase [Listeria monocytogenes]",

"cazygi|985617591|gb|AMD23908.1| glycosidase [Listeria monocytogenes]",

"cazygi|985620610|gb|AMD26829.1| glycosidase [Listeria monocytogenes]",

"cazygi|873259059|gb|AKP38021.1| glycosidase [Listeria monocytogenes]",

"cazygi|543860150|emb|CDG44729.1| COG2152 predicted glycoside hydrolase [Listeria monocytogenes EGD]",

"cazygi|16410267|emb|CAC98942.1| lmo0864 [Listeria monocytogenes EGD-e]",

"cazygi|346645782|gb|AEO38407.1| conserved hypothetical protein [Listeria monocytogenes Finland 1998]",

"cazygi|346423637|gb|AEO25162.1| conserved hypothetical protein [Listeria monocytogenes FSL R2-561]",

"cazygi|1028455793|gb|ANE38727.1| glycosidase [Listeria monocytogenes]",

"cazygi|217334311|gb|ACK40105.1| conserved hypothetical protein [Listeria monocytogenes HCC23]",

"cazygi|973722941|gb|ALX68318.1| glycosidase [Listeria monocytogenes]",

"cazygi|741044297|gb|AJA82576.1| hypothetical protein LO81\_895 [Listeria monocytogenes]",

"cazygi|345533517|gb|AEO02958.1| hypothetical protein LMOG\_00867 [Listeria monocytogenes J0161]",

"cazygi|523918212|gb|AGR32608.1| glycosidase [Listeria monocytogenes J1816]",

"cazygi|523852774|gb|AGR16549.1| glycosidase [Listeria monocytogenes]",

"cazygi|328467137|gb|EGF38227.1| glycosidase [Listeria monocytogenes J1-220]",

"cazygi|523858659|gb|AGR20893.1| glycosidase [Listeria monocytogenes]",

"cazygi|523861765|gb|AGR22441.1| glycosidase [Listeria monocytogenes]",

"cazygi|523844661|gb|AGR09328.1| glycosidase [Listeria monocytogenes]",

"cazygi|523840688|gb|AGR05429.1| glycosidase [Listeria monocytogenes]",

"cazygi|523846520|gb|AGR11186.1| glycosidase [Listeria monocytogenes]",

"cazygi|827392101|gb|AKI51637.1| glycosylase", " putative [Listeria monocytogenes]",

"cazygi|827395179|gb|AKI54714.1| glycosylase",

"cazygi|827386497|gb|AKI46035.1| glycosylase",

"cazygi|827389275|gb|AKI48812.1| glycosylase",

"cazygi|827381008|gb|AKI40548.1| glycosylase",

"cazygi|827383592|gb|AKI43131.1| glycosylase",

"cazygi|406360669|emb|CBY66942.1| glycosylase", " putative [Listeria monocytogenes L312]",

"cazygi|307570398|emb|CAR83577.1| glycosylase", " putative [Listeria monocytogenes L99]",

"cazygi|441470505|emb|CCQ20260.1| 4-O-beta-D-mannosyl-D-glucose phosphorylase [Listeria monocytogenes]",

"cazygi|970873353|gb|ALU79259.1| glycosidase [Listeria monocytogenes]",

"cazygi|970870907|gb|ALU76814.1| glycosidase [Listeria monocytogenes]",

"cazygi|970878247|gb|ALU84066.1| glycosidase [Listeria monocytogenes]",

"cazygi|675332820|gb|AIL67335.1| glycosidase [Listeria monocytogenes]",

"cazygi|908215484|gb|AKS53473.1| glycosidase [Listeria monocytogenes]",

"cazygi|336022763|gb|AEH91900.1| hypothetical protein LMM7\_0895 [Listeria monocytogenes M7]",

"cazygi|523850609|gb|AGR15274.1| glycosidase [Listeria monocytogenes]",

"cazygi|767261784|gb|AJT44649.1| glycosidase [Listeria monocytogenes]",

"cazygi|597804344|gb|AHN32126.1| glycosidase [Listeria monocytogenes]",

"cazygi|730594505|gb|AIZ38159.1| hypothetical protein LMntsn\_0870 [Listeria monocytogenes]",

"cazygi|523866984|gb|AGR26266.1| glycosidase [Listeria monocytogenes]",

"cazygi|597566513|emb|CDM16105.1| conserved protein of unknown function [Listeria monocytogenes R479a]",

"cazygi|584097980|gb|AHI69537.1| hypothetical protein N881\_0896 [Listeria monocytogenes serotype 1/2a str. 01-1280]",

"cazygi|571336176|gb|AHF31620.1| hypothetical protein A430\_0935 [Listeria monocytogenes serotype 1/2a str. 08-6569]",

"cazygi|571339168|gb|AHF34611.1| hypothetical protein A431\_0935 [Listeria monocytogenes serotype 1/2a str. 08-6997]",

"cazygi|571342523|gb|AHF37602.1| hypothetical protein A435\_0935 [Listeria monocytogenes serotype 1/2a str. 10-0815]",

"cazygi|571345473|gb|AHF40551.1| hypothetical protein A437\_0893 [Listeria monocytogenes serotype 1/2a str. 10-1047]",

"cazygi|571348415|gb|AHF43492.1| hypothetical protein A422\_0893 [Listeria monocytogenes serotype 1/2a str. 88-0478]",

"cazygi|571333267|gb|AHF28713.1| hypothetical protein A407\_0933 [Listeria monocytogenes serotype 4b str. 81-0861]",

"cazygi|225875944|emb|CAS04648.1| Hypothetical protein of unknown function [Listeria monocytogenes serotype 4b str. CLIP 80459]",

"cazygi|46880362|gb|AAT03661.1| conserved hypothetical protein [Listeria monocytogenes serotype 4b str. F2365]",

"cazygi|424012926|emb|CCO63466.1| Putative uncharacterized protein [Listeria monocytogenes serotype 4b str. LL195]",

"cazygi|404245201|emb|CBY03426.1| glycosylase", " putative [Listeria monocytogenes serotype 7 str. SLCC2482]",

"cazygi|957754843|gb|ALQ24582.1| glycosidase [Listeria monocytogenes]",

"cazygi|404232807|emb|CBY54210.1| putative glycosylase [Listeria monocytogenes SLCC2372]",

"cazygi|404241464|emb|CBY62864.1| putative glycosylase [Listeria monocytogenes SLCC2376]",

"cazygi|404221282|emb|CBY72645.1| putative glycosylase [Listeria monocytogenes SLCC2378]",

"cazygi|404235742|emb|CBY57144.1| putative glycosylase [Listeria monocytogenes SLCC2479]",

"cazygi|404224140|emb|CBY75502.1| putative glycosylase [Listeria monocytogenes SLCC2540]",

"cazygi|404227049|emb|CBY48454.1| putative glycosylase [Listeria monocytogenes SLCC2755]",

"cazygi|404229928|emb|CBY51332.1| putative glycosylase [Listeria monocytogenes SLCC5850]",

"cazygi|404238646|emb|CBY60047.1| putative glycosylase [Listeria monocytogenes SLCC7179]",

"cazygi|584468276|gb|AHJ05359.1| glycosidase [Listeria monocytogenes WSLC1001]",

"cazygi|585113906|gb|AHJ34943.1| glycosidase [Listeria monocytogenes WSLC1042]",

"cazygi|289170376|emb|CBH26916.1| glycosidase family protein [Listeria seeligeri serovar 1/2b str. SLCC3954]",

"cazygi|116741155|emb|CAK20275.1| conserved hypothetical protein [Listeria welshimeri serovar 6b str. SLCC5334]"

["cazygi|100537271|gb|AMP98486.1| Glycosidase [Pedobacter cryoconitis]"]

<p>["cazygi 1024276011 gb ANB58156.1  hypothetical protein GFC28_2854 [Anoxybacillus sp. B2M1]",  "cazygi 1024284646 gb ANB66085.1  hypothetical protein GFC29_2580 [Anoxybacillus sp. B7M1]",  "cazygi 239807208 gb ACS24273.1  glycosidase PH1107-related [Geobacillus sp. WCH70]"]</p>
<p>["cazygi 1027453386 gb AND84186.1  glycosidase [Clostridium tyrobutyricum]",  "cazygi 1042047022 gb ANP68912.1  glycosidase [Clostridium tyrobutyricum]"]</p>
<p>["cazygi 1032540981 gb ANG92560.1  glycosidase [Lelliottia amnigena]"]</p>
<p>["cazygi 1043656552 gb ANS75672.1  glycosidase [Paenibacillus yonginensis]"]</p>
<p>["cazygi 255344607 gb ACU03933.1  glycosidase PH1107-related [Pedobacter heparinus DSM 2366]"]</p>
<p>["cazygi 257477059 gb ACV57378.1  glycosidase PH1107-related [Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446]"]</p>
<p>["cazygi 257477852 gb ACV58171.1  glycosidase PH1107-related [Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446]"]</p>
<p>["cazygi 302197954 gb ADL05525.1  glycosidase related protein [[Clostridium] saccharolyticum WM1]"]</p>
<p>["cazygi 306533137 gb ADN02671.1  putative glycosidase [Spirochaeta thermophila DSM 6192]",  "cazygi 339412501 gb AEJ62066.1  glycosidase related protein [Spirochaeta thermophila DSM 6578]"]</p>
<p>["cazygi 32443505 emb CAD72947.1  conserved hypothetical protein [Rhodopirellula baltica SH 1]"]</p>
<p>["cazygi 339288290 gb AEJ42400.1  glycosidase [Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1]"]</p>
<p>["cazygi 371590351 gb AEX54081.1  putative glycosylase [Rahnella aquatilis CIP 78.65 = ATCC 33071]",  "cazygi 321170106 gb ADW75805.1  glycosidase related protein [Rahnella sp. Y9602]"]</p>
<p>["cazygi 374849826 dbj BAL52831.1  hypothetical conserved protein [uncultured prokaryote]"]</p>
<p>["cazygi 383801351 gb AFH48431.1  Putative glycosylase [Ignavibacterium album JCM 16511]"]</p>
<p>["cazygi 384067260 emb CCH00470.1  glycosidase PH1107-related protein [Fibrella aestuarina BUZ 2]"]</p>
<p>["cazygi 430016147 gb AGA27861.1  putative glycosylase [Singulisphaera acidiphila DSM 18658]"]</p>
<p>["cazygi 430735424 gb AGA59369.1  putative glycosylase [Thermobacillus composti KWC4]"]</p>
<p>["cazygi 553906840 gb AGY76890.1  glycosidase related protein [Clostridium autoethanogenum DSM 10061]",  "cazygi 300433903 gb ADK13670.1  putative glycosylase [Clostridium ljungdahlii DSM 13528]"]</p>
<p>["cazygi 575462749 gb AHG93800.1  glycosidase related protein (plasmid) [Gemmatirosa kalamazoonesis]"]</p>
<p>["cazygi 686549430 gb AIQ60126.1  glycosidase [Paenibacillus borealis]"]</p>
<p>["cazygi 686555438 gb AIQ66133.1  glycosidase [Paenibacillus stellifer]"]</p>
<p>["cazygi 68655705 gb AIQ66399.1  glycosidase [Paenibacillus graminis]",  "cazygi 806910096 emb CQR51519.1  glycosidase related protein [Paenibacillus riograndensis SBR5]",  "cazygi 686516280 gb AIQ26981.1  glycosidase [Paenibacillus sp. FSL P4-0081]",  "cazygi 686528088 gb AIQ38787.1  glycosidase [Paenibacillus sp. FSL R5-0912]"]</p>
<p>["cazygi 690615442 gb AIQ16655.1  glycosidase [Paenibacillus sp. FSL H7-0357]"]</p>
<p>["cazygi 695168010 gb AIT09333.1  glycosidase [Francisella sp. FSC1006]"]</p>
<p>["cazygi 728870108 gb AIY80771.1  glycosyl hydrolases 43 family protein [Clostridium botulinum 202F]",  "cazygi 187722970 gb ACD24191.1  conserved hypothetical protein [Clostridium botulinum B str. Eklund 17B (NRP)],  "cazygi 545681614 emb CDH90966.1  COG2152 predicted glycoside hydrolase [Clostridium botulinum B str. Eklund 17B (NRP)],  "cazygi 188498409 gb ACD51545.1  unknwon conserved protein [Clostridium botulinum E3 str. Alaska E43]",  "cazygi 749705022 gb AJF29534.1  glycosidase [Clostridium botulinum]",  "cazygi 749710554 gb AJF32595.1  glycosidase [Clostridium botulinum]"]</p>
<p>["cazygi 755430297 gb AJJ86868.1  hypothetical protein AK38_125 [Yersinia pestis CO92]",  "Ncazy ANW14472.1  glycosidase [Yersinia pestis]",  "cazy AXY33556.1  glycosidase [Yersinia pseudotuberculosis]",  "cazy AYM90937.1  glycosidase [Serratia sp. 3ACOL1]"]</p>

"cazygi 820755130 gb AKG72003.1  glycosidase [Serratia fonticola]",
"cazygi 908264718 gb AKT02677.1  hypothetical protein M486_3813 [Yersinia pestis 1045]",
"cazygi 908217808 gb AKS55794.1  hypothetical protein M479_819 [Yersinia pestis 1412]",
"cazygi 908238790 gb AKS76764.1  hypothetical protein M480_305 [Yersinia pestis 1413]",
"cazygi 908244811 gb AKS82782.1  hypothetical protein M481_2141 [Yersinia pestis 1522]",
"cazygi 908223667 gb AKS61650.1  hypothetical protein M478_551 [Yersinia pestis 2944]",
"cazygi 908259389 gb AKS97348.1  hypothetical protein M482_3682 [Yersinia pestis 3067]",
"cazygi 908255234 gb AKS93196.1  hypothetical protein M483_3786 [Yersinia pestis 3770]",
"cazygi 908246559 gb AKS84529.1  hypothetical protein M477_1652 [Yersinia pestis 790]",
"cazygi 908250010 gb AKS87975.1  hypothetical protein M484_436 [Yersinia pestis 8787]",
"cazygi 342854830 gb AEL73383.1  hypothetical protein A1122_13770 [Yersinia pestis A1122]",
"cazygi 162353816 gb ABX87764.1  conserved hypothetical protein [Yersinia pestis Angola]",
"cazygi 108779878 gb ABG13936.1  hypothetical protein YPA_1970 [Yersinia pestis Antiqua]",
"cazygi 320014697 gb ADV98268.1  hypothetical protein YPC_1654 [Yersinia pestis biovar Medievalis str. Harbin 35]",
"cazygi 45436946 gb AAS62499.1  putative glycosylase [Yersinia pestis biovar Microtus str. 91001]",
"cazygi 15980468 emb CAC91279.1  conserved hypothetical protein [Yersinia pestis CO92]",
"cazygi 262362349 gb ACY59070.1  hypothetical protein YPD4_2163 [Yersinia pestis D106004]",
"cazygi 262366341 gb ACY62898.1  hypothetical protein YPD8_2223 [Yersinia pestis D182038]",
"cazygi 755418713 gb AJJ31721.1  hypothetical protein CH61_1690 [Yersinia pestis]",
"cazygi 755396092 gb AJJ13298.1  hypothetical protein CH46_2636 [Yersinia pestis]",
"cazygi 755341047 gb AJK06559.1  hypothetical protein CH55_135 [Yersinia pestis]",
"cazygi 755438037 gb AJJ38157.1  hypothetical protein CH62_1978 [Yersinia pestis]",
"cazygi 21958517 gb AAM85283.1 AE013775_3 hypothetical [Yersinia pestis KIM10+]",
"cazygi 805414091 gb AKB88847.1  hypothetical protein CH44_3749 [Yersinia pestis]",
"cazygi 108775878 gb ABG18397.1  hypothetical protein YPN_2068 [Yersinia pestis Nepal516]",
"cazygi 755444841 gb AJJ44957.1  hypothetical protein CH63_545 [Yersinia pestis]",
"cazygi 755292360 gb AJI89544.1  hypothetical protein CH59_14 [Yersinia pestis]",
"cazygi 145210865 gb ABP40272.1  hypothetical protein YPDSF_1887 [Yersinia pestis Pestoides F]",
"cazygi 755461690 gb AJK26402.1  hypothetical protein CH43_3273 [Yersinia pestis Pestoides G]",
"cazygi 755357531 gb AJJ51421.1  hypothetical protein BZ15_1056 [Yersinia pestis]",
"cazygi 755447598 gb AJK11582.1  hypothetical protein CH60_2211 [Yersinia pestis str. Pestoides B]",
"cazygi 294354691 gb ADE65032.1  hypothetical protein YPZ3_2122 [Yersinia pestis Z176003]",
"cazygi 755390043 gb AJJ71613.1  hypothetical protein BZ23_2096 [Yersinia pseudotuberculosis]",
"cazygi 682104129 gb AIN16006.1  hypothetical protein DJ40_4027 [Yersinia pseudotuberculosis]",
"cazygi 755374609 gb AJJ07981.1  hypothetical protein BZ20_3694 [Yersinia pseudotuberculosis]",
"cazygi 152959496 gb ABS46957.1  conserved hypothetical protein [Yersinia pseudotuberculosis IP 31758]",
"cazygi 51590118 emb CAH21753.1  conserved hypothetical protein [Yersinia pseudotuberculosis IP 32953]",
"cazygi 755361980 gb AJJ55864.1  hypothetical protein BZ17_4122 [Yersinia pseudotuberculosis IP 32953]",
"cazygi 755370962 gb AJJ04336.1  hypothetical protein BZ21_1812 [Yersinia pseudotuberculosis]",
"cazygi 186698940 gb ACC89569.1  glycosidase PH1107-related [Yersinia pseudotuberculosis PB1/+]",
"cazygi 755451715 gb AJK14889.1  hypothetical protein BZ19_1877 [Yersinia pseudotuberculosis str. PA3606]",
"cazygi 169750412 gb ACA67930.1  glycosidase PH1107-related [Yersinia pseudotuberculosis YPIII]",
"cazygi 588288895 gb AHK21631.1  glycosidase [Yersinia similis]"
["cazygi 764069457 gb AJR09471.1  hypothetical protein H744_2c2818 [Photobacterium gaetbulicola Gung47]"]

["cazy 808695811 gb AKD56650.1  glycosidase [Spirosoma radiotolerans]"]
["cazy 921143555 dbj BAS26641.1  glycosidase [Limnochorda pilosa]"]
["cazy 961446961 gb ALS25162.1  glycosidase [Paenibacillus naphthalenovorans]"]
["cazy AOL35885.1 glycosidase [Geobacillus thermoleovorans]", "cazy ARA99753.1 glycosidase [Geobacillus thermodenitrificans]", "cazy ASS87210.1 glycosidase [Geobacillus lituanicus]", "cazy ASS98017.1 glycosidase [Geobacillus thermocatenulatus]", "cazy ATA61571.1 glycosidase [Geobacillus stearothermophilus]", "cazy ATO39034.1 glycosidase [Geobacillus thermodenitrificans]", "cazy AUJ37061.1 glycosidase [[Bacillus] caldolyticus]", "cazy AWO74588.1 glycosidase [Geobacillus thermoleovorans]", "cazy 1049091670 gb ANX13869.1  glycosidase [Fictibacillus arsenicus]", "cazy 56381647 dbj BAD77555.1  unknwon conserved protein [Geobacillus kaustophilus HTA426]", "cazy 831465583 gb AKM20513.1  Beta-1", "4-mannooligosaccharide phosphorylase [Geobacillus sp. 12AMOR1]", "cazy 297254748 gb ADI28194.1  glycosidase related protein [Geobacillus sp. C56-T3]", "cazy 445208365 gb AGE23830.1  glycosidase-like protein [Geobacillus sp. GH01]", "cazy 530459040 gb AGT33616.1  glycosidase [Geobacillus sp. JF8]", "cazy 1005661602 gb AMQ21821.1  glycosidase [Geobacillus sp. JS12]", "cazy 909997033 gb AKU26540.1  glycosidase [Geobacillus sp. LC300]", "cazy 317113247 gb ADU95739.1  glycosidase related protein [Geobacillus sp. Y412MC52]", "cazy 261377168 gb ACX79911.1  glycosidase PH1107-related protein [Geobacillus sp. Y412MC61]", "cazy 922673678 gb ALA70195.1  glycosidase [Geobacillus stearothermophilus 10]", "cazy 1016892674 gb AMX85135.1  glycosidase [Geobacillus subterraneus]", "cazy 359286548 gb AEV18232.1  hypothetical protein GTCCBUS3UF5_9090 [Geobacillus thermoleovorans CCB_US3_UF5]", "cazy 359289298 gb AEV20982.1  hypothetical protein GTCCBUS3UF5_36820 [Geobacillus thermoleovorans CCB_US3_UF5]", "cazy 1015430632 gb AMV12421.1  glycosidase [Geobacillus thermoleovorans]"]
["cazy AOM76197.1 glycosidase [Pedobacter steynii]", "cazy 1008900574 gb AMR32239.1  glycosidase [Mucilaginibacter sp. PAMC 26640]"]
["cazy AOM80960.1 glycosidase [Pedobacter steynii]"]
["cazy AOP88942.1 glycosidase [Enterobacter kobei]", "cazy ASE43069.1 glycosidase [Citrobacter braakii]", "cazy AST78187.1 glycosidase [Citrobacter farmeri]", "cazy AUJ83518.1 glycosidase [Enterobacter cancerogenus]", "cazy AUV28075.1 glycosidase [Citrobacter freundii complex sp. CFNIH3]", "cazy AYL04052.1 glycosidase [Enterobacter kobei]", "cazy AYN28795.1 glycosidase [Buttiauxella sp. 3AFRM03]", "humangut888063.HMPREF9086_4365 [Complete]:- codon-table.11", "cazy 742984607 gb AJB69241.1  glycosidase [Enterobacter hormaechei subsp. hormaechei]", "cazy 723224067 gb AIX56719.1  glycosidase [Enterobacter cloacae]", "cazy 400177221 gb AFP72070.1  putative glycosylase [Enterobacter cloacae subsp. cloacae ENHKU01]", "cazy 1020389709 gb AMZ76608.1  glycosidase [Enterobacter sp. ODB01]", "cazy 440047269 gb AGB78327.1  putative glycosylase [Enterobacteriaceae bacterium strain FGI 57]"]
["cazy APB30668.1 glycosidase [Vagococcus teuberi]"]
["cazy APM80098.1 glycosidase [Parageobacillus thermoglucosidasius]",

"cazygi 311217674 gb ADP76278.1  glycosidase related protein [Geobacillus sp. Y4.1MC1]",
"cazygi 335363887 gb AEH49567.1  glycosidase related protein [Geobacillus thermoglucosidasius C56-YS93]",
"cazygi 929559699 gb ALF09277.1  glycosidase [Geobacillus thermoglucosidasius]",
"cazygi 1050291544 gb ANZ29359.1  glycosidase [Geobacillus thermoglucosidasius]"
["cazy APW63726.1 beta-mannosaccharide phosphorylase or inverting beta-mannosidase [Paludisphaera borealis]",
"cazygi 1015455907 gb AMV37689.1  Beta-1", "4-mannooligosaccharide phosphorylase [Planctomyces sp. SH-PL62]"
["cazy AQG78684.1 glycosidase [Spirosoma montaniterrae]"
["cazy AQQ71142.1 Beta-1", "4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium SM-Chi-D1]"
["cazy AQT69235.1 Beta-1", "4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium ST-NAGAB-D1]"
["cazy ARI76287.1 glycosidase [Halobacillus mangrovi]"
["cazy ARK13695.1 glycosidase [Fibrella sp. ES10-3-2-2]"
["cazy ARN56426.1 Beta-1", "4-mannooligosaccharide phosphorylase [Sedimentisphaera salicampi]"
["cazy ARP44250.1 4-O-beta-D-mannosyl-D-glucose phosphorylase [Geobacillus thermodenitrificans]",
"cazygi 134268352 gb ABO68547.1  Conserved hypothetical protein [Geobacillus thermodenitrificans NG80-2]",
"cazygi 961451687 gb ALS29887.1  glycosidase [Paenibacillus sp. 32O-W]"
["cazy ARS41135.1 glycosidase [Sphingobacteriaceae bacterium GW460-11-11-14-LB5]",
"cazy AXB57297.1 glycosidase [Flavobacterium sp. HYN0086]"
["cazy ARV07385.1 glycosidase [Polaribacter sp. SA4-10]",
"cazy ASO04138.1 1", "4-beta-mannosyl-N-acetylglucosamine phosphorylase [Arenibacter algicola]"
["cazy ASA26088.1 glycosidase [Paenibacillus donghaensis]"
["cazy ASS66915.1 glycosidase [Paenibacillus sp. RUD330]",
"cazy AVV55254.1 glycosidase [Paenibacillus glucanolyticus]",
"cazy AYB46670.1 glycosidase [Paenibacillus lautus]",
"cazy AYQ71337.1 glycosidase [Cohnella sp. 18JY8-7]",
"cazy AYQ74948.1 glycosidase [Cohnella sp. 18JY8-7]",
"cazy SMF87879.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Paenibacillus uliginis N3/975]",
"cazygi 1022706313 gb ANA80675.1  glycosidase [Paenibacillus glucanolyticus]",
"cazygi 690624393 gb AIQ25407.1  glycosidase [Paenibacillus sp. FSL H7-0737]",
"cazygi 686526420 gb AIQ37120.1  glycosidase [Paenibacillus sp. FSL R5-0345]",
"cazygi 766904484 gb AJS61216.1  glycosidase [Paenibacillus sp. IHBB 10380]",
"cazygi 1049759967 gb ANY73220.1  glycosidase [Paenibacillus sp. IHBB 9852]",
"cazygi 247547003 gb ACT04022.1  glycosidase PH1107-related [Paenibacillus sp. JDR-2]",
"cazygi 261280906 gb ACX62877.1  glycosidase PH1107-related protein [Paenibacillus sp. Y412MC10]",
"cazygi 1028465960 gb ANE48883.1  glycosidase [Paenibacillus swuensis]"
["cazy ASS88943.1 glycosidase [Aeribacillus pallidus]"
["cazy AUD00665.1 glycosidase [Spirosoma pollinicola]",
"cazygi 283814993 gb ADB36831.1  glycosidase PH1107-related protein [Spirosoma linguale DSM 74]"
["cazy AUP79214.1 glycosidase [Flavivirga eckloniae]"
["cazy AWA31523.1 glycosidase [Flavobacterium sp. HYN0048]"
["cazy AWI10611.1 glycosidase [Ereboglobus luteus]"
["cazy AXP79353.1 Beta-1-2C4-mannooligosaccharide phosphorylase [Mariniflexile sp. TRM1-10]"
["cazy AXY72757.1 glycosidase [Pseudoflavitalea sp. 5GH32-13]"
["cazy AYA09469.1 glycosidase [Rahnella aquatilis]"

"cazygi 380756103 gb AFE60494.1  glycosidase-like protein [Rahnella aquatilis HX2]"
["cazy AYB35551.1 glycosidase [Chryseolinea sp. KIS68-18]"]
["cazy AYF99945.1 glycosidase [Lactococcus sp. 1JSPR-7]"]
["cazy BAX79962.1 glycosidase [Marinifilaceae bacterium SPP2]", "humangutMH0014_GL0051264 [gene] locus=scaffold54938_2:3608:4654:+ [Complete] codon-table.11", "humangutMH0037_GL0005385 [gene] locus=scaffold47410_3:5545:6591:+ [Complete] codon-table.11", "humangutMH0035_GL0084958 [gene] locus=scaffold33310_4:54850:55896:- [Complete] codon-table.11", "humangutT2D-109A_GL0063585 [gene] locus=scaffold60146_4:129:1175:+ [Complete] codon-table.11", "humangut764588959-stool1_revised_scaffold38709_2_gene87075 strand:+ start:15730 stop:16776 length:1047 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "mouseS-Fe12_GL0087179 [gene] locus=scaffold23004_1:5238:6284:+ [Complete] codon-table.11", "mouseMC-0-1_GL0004796 [gene] locus=scaffold2636_8:8463:9509:- [Complete] codon-table.11", "mouse1A-dyr2-07_GL0030949 [gene] locus=scaffold11171_4:8010:9056:- [Complete] codon-table.11"]
["cazy SCV07281.1 hypothetical protein BACOV975_01042 [Bacteroides ovatus V975]", "mouseG1-6A_GL0040776 [gene] locus=scaffold19912_9:1208:2266:- [Complete] codon-table.11", "cazygi 938483646 gb ALJ47877.1  Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides ovatus]", "cazygi 1045274582 gb ANU59273.1  glycosidase [Bacteroides sp. I48]", "cazygi 295085869 emb CBK67392.1  Predicted glycosylase [Bacteroides xylanisolvens XB1A]"]
["humangut158337416-stool1_revised_scaffold30369_1_gene206870 strand:- start:11597 stop:12682 length:1086 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "humangut457396.CSBG_00342 [Complete]:- codon-table.11", "pigEYZ-542B_GL0066681 [gene] locus=scaffold86043_2:1290:2375:- [Complete] codon-table.11"]
["humangut159611913-stool1_revised_scaffold5797_1_gene123151 strand:- start:2 stop:679 length:678 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut340101.Vvad_PD1448 [Complete]:- codon-table.11"]
["humangutDLM006_GL0005590 [gene] locus=scaffold29343_2:3:1100:+ [Lack 5'-end] codon-table.11"]
["humangutMH0012_GL0142045 [gene] locus=scaffold26779_1:67335:68417:+ [Complete] codon-table.11", "mouseGroup2-3A_GL0213569 [gene] locus=scaffold128315_2:21860:22942:- [Complete] codon-table.11"]
["humangutMH0014_GL0069724 [gene] locus=scaffold49710_2:3757:4800:- [Complete] codon-table.11", "humangutMH0159_GL0085170 [gene] locus=scaffold12930_17:350:1393:- [Complete] codon-table.11", "humangutV1.CD3-3-PN_GL0029462 [gene] locus=scaffold25745_2:4954:5997:+ [Complete] codon-table.11", "humangutT2D-63A_GL0036826 [gene] locus=scaffold39161_1:12178:13221:+ [Complete] codon-table.11", "pigPIG-007_GL0142532 [gene] locus=scaffold73421_3:2214:3257:+ [Complete] codon-table.11", "pigPIG-041_GL0038390 [gene] locus=scaffold57657_1:12268:13311:+ [Complete] codon-table.11", "rumen553_GL0119562_1 [gene] locus=scaffold98429_1:36766:37809:+ [Complete]"]
["humangutMH0014_GL0073411 [gene] locus=scaffold14920_1:6186:7241:- [Complete] codon-table.11", "humangutNLF006_GL0047622 [gene] locus=scaffold12808_1:37:1092:- [Lack 5'-end] codon-table.11", "pigPIG-020_GL0032968 [gene] locus=scaffold71803_1:61:1116:+ [Complete] codon-table.11"]
["humangutMH0016_GL0015997 [gene] locus=scaffold43604_2:1158:2207:+ [Complete] codon-table.11"]
["humangutMH0055_GL0053168 [gene] locus=C955156_1:2878:3924:- [Complete] codon-table.11", "humangutMH0196_GL0196356 [gene] locus=scaffold48076_5:453:1499:+ [Complete] codon-table.11"]
["humangutMH0062_GL0010083 [gene] locus=scaffold4489_4:5033:6097:+ [Complete] codon-table.11"]
["humangutMH0097_GL0032324 [gene] locus=scaffold855_9:15133:16173:- [Complete] codon-table.11"]
["humangutMH0105_GL0062872 [gene] locus=scaffold61381_1:8141:9193:- [Complete] codon-table.11",



"humangutMH0413_GL0067116 [gene] locus=C1802962_1:5426:6478:+ [Complete] codon-table.11",
"humangutO2.UC18-1_GL0036015 [gene] locus=scaffold66669_1:29141:30193:- [Complete] codon-table.11"]
["humangutMH0115_GL0027027 [gene] locus=scaffold58318_2:449:1198:- [Complete] codon-table.11"]
["humangutMH0189_GL0168818 [gene] locus=scaffold70100_4:3:560:- [Lack both ends] codon-table.11"]
["humangutMH0196_GL0120768 [gene] locus=scaffold59375_8:3537:4595:+ [Complete] codon-table.11"]
["humangutMH0211_GL0167548 [gene] locus=scaffold39813_1:6555:7661:+ [Complete] codon-table.11"]
["humangutMH0220_GL0201857 [gene] locus=scaffold42842_1:133:1167:+ [Complete] codon-table.11"]
["humangutMH0239_GL0137758 [gene] locus=scaffold11517_17:1161:2219:+ [Complete] codon-table.11"]
["humangutMH0243_GL0119314 [gene] locus=scaffold15770_15:295:1017:- [Lack 5'-end] codon-table.11"]
["humangutMH0280_GL0025120 [gene] locus=scaffold65354_3:436:1467:+ [Complete] codon-table.11"]
["humangutMH0290_GL0113903 [gene] locus=scaffold97851_3:12401:13456:+ [Complete] codon-table.11", "cazygi 324318222 gb ADY36113.1  glycosidase related protein [Bacteroides salanitronis DSM 18170]"]
["humangutMH0303_GL0040232 [gene] locus=scaffold4470_4:133:1119:+ [Complete] codon-table.11"]
["humangutMH0303_GL0115766 [gene] locus=scaffold35690_12:457:1518:- [Complete] codon-table.11"]
["humangutMH0358_GL0145329 [gene] locus=scaffold15796_1:4275:5348:- [Complete] codon-table.11"]
["humangutMH0372_GL0113203 [gene] locus=scaffold6873_1:18256:19350:+ [Complete] codon-table.11"]
["humangutMH0378_GL0064238 [gene] locus=scaffold58681_7:760:1689:- [Lack 5'-end] codon-table.11"]
["humangutMH0441_GL0146058 [gene] locus=scaffold27271_4:148:1233:- [Complete] codon-table.11", "humangut763496533-stool2_revised_C1197182_1_gene53282 strand:+ start:1541 stop:2626 length:1086 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangutN051A_GL0058783 [gene] locus=scaffold22037_2:3361:4422:+ [Complete] codon-table.11"]
["humangutO2.UC24-1_GL0037345 [gene] locus=scaffold29098_7:2:2731:+ [Lack both ends] codon-table.11"]
["humangutO2.UC24-2_GL0099256 [gene] locus=scaffold7692_4:3069:4112:- [Complete] codon-table.11"]
["humangutO2.UC8-0_GL0115872 [gene] locus=scaffold69940_1:6116:7165:- [Complete] codon-table.11", "pigPIG-094_GL0135180 [gene] locus=scaffold164212_1:11777:12826:- [Complete] codon-table.11", "pigBHZ-9B_GL0130273 [gene] locus=scaffold24258_1:10658:11707:- [Complete] codon-table.11", "rumen553_GL0522716_1 [gene] locus=scaffold280765_3:6549:7598:-[Complete]", "rumen552_GL1343129_1 [gene] locus=scaffold21669_1:24548:25597:+[Complete]", "rumen583_GL0213147_1 [gene] locus=scaffold275383_4:3456:4505:+[Complete]", "rumen554_GL2251975_1 [gene] locus=scaffold628736_2:7267:8316:+[Complete]", "rumen554_GL2623584_1 [gene] locus=scaffold409446_1:4020:5069:+[Complete]"]
["humangutT2D-132A_GL0027678 [gene] locus=scaffold9899_2:238:984:- [Complete] codon-table.11"]
["humangutT2D-176A_GL0103346 [gene] locus=scaffold5807_1:1:537:- [Lack both ends] codon-table.11"]
["humangutT2D-22A_GL0041535 [gene] locus=scaffold22674_3:10035:11006:- [Complete] codon-table.11"]
["humangutT2D-62A_GL0056684 [gene] locus=scaffold171_35:4359:5444:- [Complete] codon-table.11"]
["humangutV1.FI14_GL0248150 [gene] locus=scaffold36117_2:569:1639:+ [Complete] codon-table.11"]
["humangutV1.FI17_GL0002751 [gene] locus=scaffold101446_1:8612:9712:- [Complete] codon-table.11"]
["humangutV1.UC11-5_GL0177487 [gene] locus=scaffold7500_5:514:1278:+ [Lack 3'-end] codon-table.11"]
["mouse1-1_GL0019987 [gene] locus=scaffold73066_8:602:1675:+ [Complete] codon-table.11"]
["mouse2-5_GL0007716 [gene] locus=scaffold26666_5:148:1215:- [Complete] codon-table.11"]
["mouse2-7_GL0062403 [gene] locus=scaffold11147_18:1649:2725:- [Complete] codon-table.11", "mouse4-8_GL0081522 [gene] locus=scaffold81590_1_2:4674:5750:- [Complete] codon-table.11"]
["mouse5-3_GL0042311 [gene] locus=scaffold26612_23:1:1095:+ [Lack 5'-end] codon-table.11"]

["mouse7-1_GL0049658 [gene] locus=scaffold3842_2:438:1538:+ [Complete] codon-table.11"]
["mouse7_GL0026892 [gene] locus=scaffold8143_5:3:569:- [Lack both ends] codon-table.11"]
["mouse8-1_GL0050491 [gene] locus=scaffold80992_5:3:860:- [Lack both ends] codon-table.11"]
["mouse8-7_GL0075670 [gene] locus=scaffold6819_16:1014:2105:+ [Complete] codon-table.11"]
["mouse8-8_GL0049431 [gene] locus=scaffold47381_1:127:810:+ [Lack 3'-end] codon-table.11"]
["mouseG1-3A_GL0088964 [gene] locus=scaffold56982_1:21876:22949:+ [Complete] codon-table.11"]
["mouseGroup2-3A_GL0117339 [gene] locus=scaffold66609_8:1:864:- [Lack 3'-end] codon-table.11"]
["mouseMC-6-2_GL0009829 [gene] locus=scaffold3586_4:4248:5288:- [Complete] codon-table.11"]
["pigBMZ-14B_GL0021115 [gene] locus=C754686_1:132:875:+ [Lack 3'-end] codon-table.11"]
["pigPIG-001_GL0136080 [gene] locus=scaffold35781_2:90:1133:+ [Complete] codon-table.11", "pigPIG-049_GL0022449 [gene] locus=scaffold31742_4:1518:2561:+ [Complete] codon-table.11"]
["pigPIG-006_GL0221372 [gene] locus=scaffold53550_3:1406:2050:+ [Complete] codon-table.11"]
["pigPIG-011_GL0203320 [gene] locus=scaffold157161_3:3:815:+ [Lack both ends] codon-table.11"]
["pigPIG-033_GL0111560 [gene] locus=scaffold146717_1:3179:3592:+ [Lack 3'-end] codon-table.11"]
["pigZXZ-8B_GL0225664 [gene] locus=scaffold83522_1:476:1519:- [Complete] codon-table.11"]
["rumen0081_GL0710021_1 [gene] locus=scaffold467528_3:224:1282:- [Complete]"]
["rumen0081_GL1007727_1 [gene] locus=scaffold390530_7:1:501:+ [Lack 5'-end]"]
["rumen0081_GL1287973_1 [gene] locus=C39534641_1:2:1033:+ [Lack 5'-end]"]
["rumen0081_GL1837401_1 [gene] locus=scaffold390530_6:5921:6400:+ [Lack 3'-end]"]
["rumen100058_GL1198898_1 [gene] locus=scaffold3188968_4:547:1566:+ [Complete]"]
["rumen100058_GL1216971_1 [gene] locus=scaffold1156004_3:2:583:- [Lack both ends]"]
["rumen2009040_GL2109527_1 [gene] locus=scaffold1839399_3:1:567:+ [Lack both ends]"]
["rumen2009040_GL2738549_1 [gene] locus=scaffold1323786_1:1:573:- [Lack both ends]"]
["rumen553_GL0463185_1 [gene] locus=scaffold362985_1:2:595:+ [Lack both ends]"]
["rumen554_GL2751937_1 [gene] locus=scaffold1270830_2:111:614:+ [Lack 3'-end]"]
["rumen7049_GL0273481_1 [gene] locus=scaffold171004_5:2075:3049:- [Complete]"]
["rumen7049_GL0840078_1 [gene] locus=scaffold771181_2:2:823:- [Lack 3'-end]"]

## C5

["cazyCCgij339731040 emb CAZ94304.1 β-1", "3-mannooligosaccharide phosphorylase_Putative glycoside hydrolase [Zobellia galactanivorans]"]
["cazygi 1043655617 gb ANS74737.1  glycosidase [Paenibacillus yonginensis]"]
["cazygi 145411098 gb ABP68102.1  glycosidase", " PH1107-related protein [Caldicellulosiruptor saccharolyticus DSM 8903]"]
["cazygi 247546669 gb ACT03688.1  glycosidase PH1107-related [Paenibacillus sp. JDR-2]"]
["cazygi 333741104 gb AEF86594.1  glycosylase [Treponema primitia ZAS-2]"]
["cazygi 548726044 gb AGX07472.1  glycosidase [Bacteroides sp. CF50]"]
["cazygi 573472633 gb AHF89644.1  glycosidase [Opitutaceae bacterium TAV5]"]
["cazygi 937514713 gb ALI35200.1  Beta-1", "4-mannooligosaccharide phosphorylase [Thaumarchaeota archaeon MY3]"]
["cazygi 937516583 gb ALI37070.1  Beta-1", "4-mannooligosaccharide phosphorylase [Thaumarchaeota archaeon MY3]"]
["cazygi 961449486 gb ALS27686.1  glycosidase [Paenibacillus sp. 32O-W], "cazygi 1049754616 gb ANY67870.1  glycosidase [Paenibacillus sp. BIHB4019], "cazygi 1049761654 gb ANY74907.1  glycosidase [Paenibacillus sp. IHBB 9852]"]
["cazy AOS44340.1  Beta-1", "4-mannooligosaccharide phosphorylase [Lacunisphaera limnophila]"]
["cazy APU09962.1  glycosidase [Cellulophaga lytica]"]

<p>"cazylg 319422203 gb ADV49312.1  glycosidase related protein [Cellulophaga algicola DSM 14237]",</p> <p>"cazylg 730598614 gb AIZ41409.1  glycosidase [Cellulophaga baltica 18]",</p> <p>"cazylg 723619670 gb AIY13042.1  glycosidase [Cellulophaga baltica NN016038]",</p> <p>"cazylg 324321587 gb ADY29052.1  glycosidase related protein [Cellulophaga lytica DSM 7489]",</p> <p>"cazylg 682032970 gb AIM60094.1  glycosidase [Cellulophaga lytica]"</p>
<p>["cazy APU67656.1 glycosidase [Gramella flava JLT2011]"]</p>
<p>["cazy APZ44771.1 glycosidase [Polaribacter reichenbachii]",</p> <p>"cazy AUC18635.1 glycosidase [Polaribacter reichenbachii]",</p> <p>"cazy SDR76681.1 Predicted glycosyl hydrolase", GH43/DUF377 family [Polaribacter sp. KT25b]",</p> <p>"cazy SDS17865.1 Predicted glycosyl hydrolase", GH43/DUF377 family [Winogradskyella sp. RHA_55]"</p>
<p>["cazy AQQ69861.1 Beta-1", "4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium SM-Chi-D1]"]</p>
<p>["cazy ARV07990.1 glycosidase [Polaribacter sp. SA4-10]",</p> <p>"humangutMH0302_GL0042500 [gene] locus=scaffold44658_4:10707:11720:+ [Complete] codon-table.11",</p> <p>"humangutNLM023_GL10107797 [gene] locus=scaffold7778_4:8646:9659:+ [Complete] codon-table.11",</p> <p>"mouseGroup2-5A_GL0019481 [gene] locus=scaffold8542_25:2043:3056:- [Complete] codon-table.11"]</p>
<p>["cazy ASA24208.1 glycosidase [Paenibacillus donghaensis]",</p> <p>"cazy AYB43185.1 glycosidase [Paenibacillus lautus]",</p> <p>"cazy AYB44639.1 glycosidase [Paenibacillus lautus]",</p> <p>"cazylg 806915729 emb CQR58337.1  hypothetical protein PRIO_5968 [Paenibacillus riograndensis SBR5]",</p> <p>"cazylg 806911822 emb CQR54430.1  hypothetical protein PRIO_2021 [Paenibacillus riograndensis SBR5]",</p> <p>"cazylg 690619362 gb AIQ20575.1  glycosidase [Paenibacillus sp. FSL H7-0357]",</p> <p>"cazylg 686521741 gb AIQ32442.1  glycosidase [Paenibacillus sp. FSL P4-0081]",</p> <p>"cazylg 686533062 gb AIQ43761.1  glycosidase [Paenibacillus sp. FSL R5-0912]",</p> <p>"cazylg 686529476 gb AIQ40175.1  glycosidase [Paenibacillus sp. FSL R5-0912]",</p> <p>"cazylg 261283103 gb ACX65074.1  glycosidase PH1107-related protein [Paenibacillus sp. Y412MC10]",</p> <p>"cazylg 261284734 gb ACX66705.1  glycosidase PH1107-related protein [Paenibacillus sp. Y412MC10]"</p>
<p>["cazy AUS97932.1 glycosidase [Pseudoclostridium thermosuccinogenes]"</p>
<p>["humangut158499257-stool1_revised_scaffold31131_1_gene27031 strand:+ start:12494 stop:13561 length:1068 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",</p> <p>"mouseS-Fe10_GL0049071 [gene] locus=scaffold538_1:73033:74100:- [Complete] codon-table.11"]</p>
<p>["humangut158499257-stool1_revised_scaffold31543_1_gene156346 strand:+ start:3549 stop:4652 length:1104 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut158802708-stool2_revised_C1031219_1_gene117434 strand:- start:3 stop:800 length:798 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut763678604-stool1_revised_scaffold30604_1_gene41349 strand:- start:315 stop:1211 length:897 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut764588959-stool1_revised_scaffold16928_8_gene33966 strand:+ start:24161 stop:25240 length:1080 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangutMH0012_GL0093348 [gene] locus=scaffold132858_1:24919:25950:+ [Complete] codon-table.11"]</p>
<p>["humangutMH0014_GL0066051 [gene] locus=scaffold8330_2:4931:5965:+ [Complete] codon-table.11",</p> <p>"humangutMH0167_GL0006781 [gene] locus=scaffold31306_2:6878:7912:- [Complete] codon-table.11",</p> <p>"humangutMH0186_GL0027767 [gene] locus=scaffold38775_2:7237:8271:+ [Complete] codon-table.11",</p> <p>"rumen555_GL0572326_1 [gene] locus=scaffold127633_2:1897:2931:-[Lack 5'-end]"</p>
<p>["humangutMH0016_GL0053524 [gene] locus=scaffold46174_3:6312:7340:+ [Complete] codon-table.11",</p>

"humangutN074A_GL0059945 [gene] locus=scaffold56516_1:2:1030:+ [Lack 5'-end] codon-table.11", "rumen2009040_GL2178254_1 [gene] locus=scaffold211162_3:3:1031:-[Complete]"
["humangutMH0023_GL0016923 [gene] locus=scaffold20961_1:12521:13549:- [Complete] codon-table.11", "humangutMH0196_GL0001501 [gene] locus=scaffold26105_2:22792:23820:+ [Complete] codon-table.11", "cazygii291513983[emb]CBK63193.1 Predicted glycosylase [Alistipes shahii WAL 8301]"
["humangutMH0026_GL0052936 [gene] locus=scaffold3225_10:4730:5767:+ [Complete] codon-table.11", "humangutT2D-97A_GL0086248 [gene] locus=scaffold47425_1:2:1039:+ [Lack 5'-end] codon-table.11", "cazygii938475940[gb]ALJ40172.1 Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides thetaiotaomicron]"
["humangutMH0045_GL0027487 [gene] locus=scaffold14473_8:8138:9163:- [Complete] codon-table.11", "cazygii295085749[emb]CBK67272.1 Predicted glycosylase [Bacteroides xylanisolvens XB1A]"
["humangutMH0062_GL0029872 [gene] locus=scaffold49596_2:9880:10911:- [Complete] codon-table.11", "rumen553_GL0577581_1 [gene] locus=C7760091_1:2929:3960:+[Complete]", "cazygii939202099[gb]ALJ60272.1 Beta-1", "4-mannooligosaccharide phosphorylase [Bacteroides cellulosilyticus]"
["humangutMH0068_GL0060254 [gene] locus=scaffold43571_3:8486:9505:+ [Complete] codon-table.11", "humangutMH0234_GL0052623 [gene] locus=scaffold5329_5:191:1210:- [Complete] codon-table.11", "mouse1A-dyr3-06_GL0042287 [gene] locus=scaffold26745_1:53299:54318:+ [Complete] codon-table.11]"
["humangutMH0069_GL0064711 [gene] locus=scaffold28096_1:118:1149:- [Lack 5'-end] codon-table.11"]
["humangutMH0128_GL0088065 [gene] locus=scaffold20450_1:1792:2811:- [Complete] codon-table.11", "humangutDOF006_GL0061826 [gene] locus=scaffold7860_1:16727:17746:- [Complete] codon-table.11"]
["humangutMH0189_GL0032527 [gene] locus=scaffold51471_7:14022:15062:+ [Complete] codon-table.11"]
["humangutMH0191_GL0020808 [gene] locus=scaffold58268_10:10061:11167:- [Complete] codon-table.11"]
["humangutMH0206_GL0244042 [gene] locus=scaffold153070_2:2915:3943:- [Complete] codon-table.11"]
["humangutMH0262_GL0038935 [gene] locus=scaffold67926_1:273:1313:- [Complete] codon-table.11"]
["humangutMH0276_GL0064691 [gene] locus=scaffold2519_6:2502:3539:- [Complete] codon-table.11", "humangutMH0286_GL0145651 [gene] locus=scaffold99187_1:38:1075:- [Complete] codon-table.11", "pigPIG-046_GL0212765 [gene] locus=scaffold58095_1:17:1054:- [Complete] codon-table.11"]
["humangutMH0281_GL0039814 [gene] locus=scaffold2190_4:46074:47090:- [Complete] codon-table.11"]
["humangutMH0286_GL0002200 [gene] locus=scaffold119380_1:11409:12434:- [Complete] codon-table.11"]
["humangutMH0318_GL0224344 [gene] locus=scaffold47629_5:244:1185:+ [Lack 3'-end] codon-table.11"]
["humangutMH0322_GL0010496 [gene] locus=scaffold79063_1:1:531:- [Lack 3'-end] codon-table.11"]
["humangutMH0366_GL0029491 [gene] locus=scaffold88536_2:269:724:- [Lack 5'-end] codon-table.11", "pigPIG-046_GL0043927 [gene] locus=scaffold56558_5:1:456:+ [Lack 5'-end] codon-table.11"]
["humangutMH0390_GL0070600 [gene] locus=scaffold139512_3:2139:3215:+ [Complete] codon-table.11"]
["humangutMH0398_GL0157238 [gene] locus=scaffold47606_9:16412:17446:+ [Complete] codon-table.11"]
["humangutMH0409_GL0198050 [gene] locus=scaffold8931_5:581:1291:+ [Lack 3'-end] codon-table.11"]
["humangutMH0411_GL0047193 [gene] locus=scaffold1090_11:2:604:+ [Lack 5'-end] codon-table.11"]
["humangutMH0411_GL0085735 [gene] locus=scaffold1090_10:8334:8768:+ [Lack 3'-end] codon-table.11"]
["humangutMH0425_GL0001594 [gene] locus=scaffold95950_1:862:1893:+ [Complete] codon-table.11"]
["humangutMH0426_GL0157669 [gene] locus=scaffold51080_3:210:1226:- [Complete] codon-table.11"]
["humangutMH0447_GL0292365 [gene] locus=scaffold167208_1:1:678:- [Lack 3'-end] codon-table.11"]
["humangutO2_UC13-1_GL0033296 [gene] locus=scaffold126607_3:2:688:- [Lack both ends] codon-table.11"]
["humangutT2D-112A_GL0012182 [gene] locus=scaffold16786_1:35354:36463:+ [Complete] codon-table.11"]
["humangutT2D-6A_GL0067893 [gene] locus=scaffold43829_1:1:984:+ [Lack 5'-end] codon-table.11"]

["humangutV1_CD6-0-PT_GL0047798 [gene] locus=scaffold26829_4:3:599:+ [Lack 5'-end] codon-table.11"]
["humangutV1_CD6-0-PT_GL0078280 [gene] locus=scaffold26829_1:430:1455:+ [Complete] codon-table.11"]
["humangutV1_FI05_GL0003190 [gene] locus=scaffold11689_19:3:956:- [Lack 3'-end] codon-table.11"]
["humangutV1_UC4-5_GL0079869 [gene] locus=scaffold54277_5:2:556:+ [Lack 5'-end] codon-table.11"]
["humangutV1_UC62-0_GL0063006 [gene] locus=scaffold33739_2:690:1724:+ [Complete] codon-table.11"]
["mouseMC-6-4_GL0055591 [gene] locus=scaffold34577_1:209:820:+ [Lack 3'-end] codon-table.11"]
["mouseMH-6-2_GL0037285 [gene] locus=scaffold25512_12:568:1497:- [Lack 5'-end] codon-table.11"]
["pigPIG-012_GL0150297 [gene] locus=scaffold43096_1:9612:10637:- [Complete] codon-table.11", "pigPIG-014_GL0174399 [gene] locus=scaffold158793_1:12263:13288:- [Complete] codon-table.11", "rumen552_GL0927921_1 [gene] locus=scaffold1072884_1:3040:4065:+[Complete]", "rumen554_GL0022084_1 [gene] locus=scaffold622384_2:2638:3663:+[Complete]", "rumen555_GL1659128_1 [gene] locus=scaffold664035_1:394:1419:+[Complete]", "rumen0081_GL1003999_1 [gene] locus=scaffold263265_2:1736:2761:-[Complete]", "rumen0081_GL1905194_1 [gene] locus=scaffold790637_1:4621:5646:-[Complete]", "rumen3042_GL0055097_1 [gene] locus=scaffold2449642_1:493:1518:-[Complete]"]
["pigPIG-017_GL0116062 [gene] locus=C2023154_1:2:526:- [Lack both ends] codon-table.11", "pigPIG-025_GL0042532 [gene] locus=scaffold3569_2:2:526:+ [Lack both ends] codon-table.11"]
["pigPIG-046_GL0008088 [gene] locus=scaffold56558_3:1:435:+ [Lack 5'-end] codon-table.11"]
["pigPIG-046_GL0021973 [gene] locus=scaffold56558_2:327:881:+ [Lack 3'-end] codon-table.11"]
["pigPIG-046_GL0129164 [gene] locus=scaffold149693_1:2:772:- [Lack 5'-end] codon-table.11"]
["pigPIG-046_GL0163660 [gene] locus=C1667800_1:3:611:- [Lack both ends] codon-table.11"]
["pigPIG-046_GL0237761 [gene] locus=scaffold20873_7:3:713:+ [Lack 5'-end] codon-table.11"]
["pigPIG_111_GL0029163 [gene] locus=scaffold123134_5:1:834:- [Lack 3'-end] codon-table.11"]
["pigPIG_137_GL0081919 [gene] locus=scaffold5229_1:2:712:- [Lack 3'-end] codon-table.11"]
["rumen0081_GL0640070_1 [gene] locus=scaffold1031570_3:693:1742:-[Complete]"]
["rumen0081_GL1300067_1 [gene] locus=scaffold1981037_2:1:627:+[Lack both ends]"]
["rumen0081_GL1389475_1 [gene] locus=scaffold831809_1:66:554:+[Lack 3'-end]"]
["rumen0081_GL2024644_1 [gene] locus=scaffold558964_1:309:1061:-[Lack 5'-end]"]
["rumen0081_GL2142218_1 [gene] locus=scaffold29161_4:27306:28388:-[Complete]"]
["rumen100058_GL1011093_1 [gene] locus=scaffold2937549_1:3:809:-[Lack 3'-end]"]
["rumen100058_GL1148192_1 [gene] locus=scaffold1522361_1:1:534:+[Lack 5'-end]"]
["rumen2009040_GL0477798_1 [gene] locus=scaffold142321_4:1:597:-[Lack 3'-end]"]
["rumen2009040_GL1500910_1 [gene] locus=scaffold3043092_1:279:1289:+[Complete]"]
["rumen2009040_GL3126245_1 [gene] locus=C53776001_1:77:634:-[Lack 5'-end]"]
["rumen3042_GL0871115_1 [gene] locus=scaffold406494_2:1:516:-[Lack 3'-end]"]
["rumen3042_GL1840057_1 [gene] locus=scaffold1758679_3:2:655:-[Lack both ends]"]
["rumen3042_GL2361409_1 [gene] locus=scaffold2116171_1:3:611:-[Lack 3'-end]"]
["rumen552_GL0162218_1 [gene] locus=scaffold432661_1:3:788:-[Lack 3'-end]"]
["rumen552_GL0476189_1 [gene] locus=scaffold213780_1:1:897:+[Lack 5'-end]"]
["rumen552_GL0753098_1 [gene] locus=scaffold688634_2:18320:19339:+[Complete]"]
["rumen552_GL0997047_1 [gene] locus=scaffold330587_1:1:879:-[Lack 3'-end]"]
["rumen552_GL1413436_1 [gene] locus=scaffold293764_2:1333:2271:+[Lack 3'-end]"]
["rumen553_GL0808474_1 [gene] locus=scaffold355381_4:1012:2028:-[Complete]"]

"rumen3042_GL2824996_1 [gene] locus=scaffold1806622_7:857:1873:-[Complete]", "rumen7049_GL2316902_1 [gene] locus=scaffold605401_1:140:1156:+[Complete]"
"rumen554_GL0341862_1 [gene] locus=scaffold1672451_1:12614:13660:-[Complete]"
"rumen554_GL0890173_1 [gene] locus=scaffold267620_1:1509:2537:+[Complete]", "rumen555_GL0416390_1 [gene] locus=scaffold471885_2:26470:27498:+[Complete]"
"rumen554_GL0946684_1 [gene] locus=scaffold2008995_1:103:585:+[Lack 3'-end]"
"rumen554_GL1055110_1 [gene] locus=scaffold973006_3:451:1467:-[Complete]", "rumen555_GL2016462_1 [gene] locus=scaffold1270480_2:4117:5133:+[Complete]", "rumen7049_GL1493557_1 [gene] locus=scaffold105706_1:667:1683:-[Complete]"
"rumen554_GL1136972_1 [gene] locus=C40775586_1:283:903:-[Lack 5'-end]"
"rumen554_GL1319092_1 [gene] locus=scaffold382194_1:4652:5656:-[Complete]", "rumen555_GL1209450_1 [gene] locus=scaffold278130_1:190:1194:-[Complete]", "rumen3042_GL0887001_1 [gene] locus=scaffold982322_2:3140:4144:+[Complete]", "rumen7049_GL0425070_1 [gene] locus=scaffold112622_1:1082:2086:-[Complete]"
"rumen554_GL1378425_1 [gene] locus=scaffold2137257_1:1055:1921:-[Lack 5'-end]"
"rumen554_GL1682678_1 [gene] locus=scaffold2034588_1:179:931:+[Lack 3'-end]"
"rumen554_GL2224399_1 [gene] locus=scaffold1392349_7:1614:2693:+[Complete]"
"rumen554_GL2266656_1 [gene] locus=scaffold1961010_1:788:1279:+[Lack 3'-end]"
"rumen554_GL2994839_1 [gene] locus=scaffold1195703_1:3:767:+[Lack 5'-end]"
"rumen554_GL3008154_1 [gene] locus=scaffold1001714_5:1076:2137:+[Complete]"
"rumen555_GL0339542_1 [gene] locus=scaffold437008_2:5979:7010:-[Complete]"
"rumen555_GL0441372_1 [gene] locus=scaffold157828_1:2:742:-[Lack both ends]"
"rumen555_GL1411799_1 [gene] locus=C27467200_1:3:569:-[Lack both ends]"
"rumen555_GL1554843_1 [gene] locus=scaffold136922_1:639:1346:-[Lack 5'-end]"
"rumen555_GL2096312_1 [gene] locus=scaffold1400378_1:1:834:-[Lack both ends]"
"rumen555_GL2224517_1 [gene] locus=C28442876_1:157:915:+[Lack 3'-end]"
"rumen583_GL0495572_1 [gene] locus=scaffold192603_1:15447:16469:-[Complete]", "rumen554_GL2400409_1 [gene] locus=scaffold452350_2:1290:2312:-[Complete]"
"rumen7049_GL0211861_1 [gene] locus=scaffold851395_2:626:1399:-[Lack 5'-end]"
"rumen7049_GL0530323_1 [gene] locus=scaffold895891_1:3:548:-[Lack 3'-end]"
"rumen7049_GL1535513_1 [gene] locus=scaffold1811297_1:3:566:-[Lack 3'-end]"
"rumen7049_GL2132576_1 [gene] locus=scaffold1972480_1:3:542:+[Lack both ends]"
"rumen7049_GL2619815_1 [gene] locus=scaffold893286_1:1:639:-[Lack both ends]"

## C6

"Ncazy ANQ53725.1 glycosidase [Thermosiphon sp. 1070]", "cazy APT72171.1 glycosidase [Thermosiphon sp. 1063]", "cazy APT73767.1 glycosidase [Thermosiphon melanesiensis]", "cazy APT76830.1 glycosidase [Marinitoga sp. 1137]", "cazygi 372102538 gb AEX86442.1  putative glycosylase [Marinitoga piezophila KA3]", "cazygi 217037868 gb ACJ76390.1  glycosylase [Thermosiphon africanus TCF52B]"
"cazy CCgi 166854664 gb ABY93073.1 β-1", "2-oligomannan phosphorylase_glycosidase", "PH1107-related [Thermoanaerobacter sp. X514]", "cazygi 319930046 gb ADV80731.1  glycosidase related protein [Thermoanaerobacter brockii subsp. finni Ako-1]"

<p>"cazygi 694165108 gb AIS51279.1  beta-1", "4-manno oligosaccharide phosphorylase [Thermoanaerobacter kivui]",</p> <p>"cazygi 166857394 gb ABY95802.1  glycosidase", " PH1107-related [Thermoanaerobacter pseudethanolicus ATCC 33223]",</p> <p>"cazygi 307580336 gb ADN53735.1  glycosidase related protein [Thermoanaerobacter sp. X513]",</p> <p>"cazygi 344031860 gb AEM77586.1  glycosidase related protein [Thermoanaerobacter wiegellii Rf8.B1]"</p>
<p>["cazyCCgij 166854665 gb ABY93074.1 β-1", "2-mannobiose phosphorylase_glycosidase", " PH1107-related [Thermoanaerobacter sp. X514]",</p> <p>"cazy AST56542.1  glycosidase [Thermoanaerobacterium thermosaccharolyticum]",</p> <p>"cazygi 20515037 gb AAM23369.1  predicted glycosylase [Caldanaerobacter subterraneus subsp. tengcongensis MB4]",</p> <p>"cazygi 319930047 gb ADV80732.1  glycosidase related protein [Thermoanaerobacter brockii subsp. finni Ako-1]",</p> <p>"cazygi 289527030 gb ADD01382.1  glycosidase PH1107-related protein [Thermoanaerobacter italicus Ab9]",</p> <p>"cazygi 694165107 gb AIS51278.1  beta-1", "4-manno oligosaccharide phosphorylase [Thermoanaerobacter kivui]",</p> <p>"cazygi 296841381 gb ADH59897.1  glycosidase related protein [Thermoanaerobacter mathranii subsp. mathranii str. A3]",</p> <p>"cazygi 166857395 gb ABY95803.1  glycosidase", " PH1107-related [Thermoanaerobacter pseudethanolicus ATCC 33223]",</p> <p>"cazygi 307580335 gb ADN53734.1  glycosidase related protein [Thermoanaerobacter sp. X513]",</p> <p>"cazygi 344031859 gb AEM77585.1  glycosidase related protein [Thermoanaerobacter wiegellii Rf8.B1]",</p> <p>"cazygi 389570918 gb AFK87323.1  glycosidase related protein [Thermoanaerobacterium saccharolyticum JW/SL-YS485]",</p> <p>"cazygi 302778855 gb ADL69414.1  glycosidase-related [Thermoanaerobacterium thermosaccharolyticum DSM 571]",</p> <p>"cazygi 43293724 gb AGB19546.1  putative glycosylase [Thermoanaerobacterium thermosaccharolyticum M0795]",</p> <p>"cazygi 333112032 gb AEF16969.1  glycosidase related protein [Thermoanaerobacterium xylanolyticum LX-11]"</p>
<p>["cazygi 1015666959 gb AMW33320.1  glycosidase [Fervidobacterium islandicum]",</p> <p>"cazygi 383110225 gb AFG35828.1  putative glycosylase [Fervidobacterium pennivorans DSM 9078]",</p> <p>"cazygi 1028458645 gb ANE41578.1  glycosidase [Fervidobacterium pennivorans]",</p> <p>"cazygi 4982436 gb AAD36914.1 AE001822_7 conserved hypothetical protein [Thermotoga maritima MSB8]",</p> <p>"cazygi 811643070 gb AKE31479.1  glycosidase [Thermotoga maritima]",</p> <p>"cazygi 811631134 gb AKE27733.1  glycosidase [Thermotoga maritima]",</p> <p>"cazygi 281373141 gb ADA66703.1  glycosidase PH1107-related protein [Thermotoga naphthophila RKU-10]",</p> <p>"cazygi 147735625 gb ABQ46965.1  glycosidase", " PH1107-related [Thermotoga petrophila RKU-1]",</p> <p>"cazygi 728865343 gb AIY86523.1  glycosidase PH1107-related protein [Thermotoga sp. 2812B]",</p> <p>"cazygi 728867102 gb AIY88281.1  glycosidase PH1107-related protein [Thermotoga sp. Cell2]",</p> <p>"cazygi 170176262 gb ACB09314.1  glycosidase PH1107-related [Thermotoga sp. RQ2]",</p> <p>"cazygi 752580369 gb AJG40882.1  glycosidase [Thermotoga sp. RQ7]"</p>
<p>["cazygi 1028461733 gb ANE44663.1  glycosidase [Deinococcus puniceus]"</p>
<p>["cazygi 166854675 gb ABY93084.1  glycosidase", " PH1107-related [Thermoanaerobacter sp. X514]"</p>
<p>["cazygi 20515038 gb AAM23370.1  predicted glycosylase [Caldanaerobacter subterraneus subsp. tengcongensis MB4]"</p>
<p>["cazygi 221572151 gb ACM22963.1  Glycosidase [Thermotoga neapolitana DSM 4359]"</p>
<p>["cazygi 222455400 gb ACM59662.1  glycosidase PH1107-related [Caldicellulosiruptor besicii DSM 6725]",</p> <p>"cazygi 311778340 gb ADQ07826.1  glycosidase related protein [Caldicellulosiruptor hydrothermalis 108]",</p> <p>"cazygi 311778489 gb ADQ07975.1  glycosidase related protein [Caldicellulosiruptor hydrothermalis 108]",</p> <p>"cazygi 312179921 gb ADQ40091.1  glycosidase related protein [Caldicellulosiruptor kristjanssonii I77R1B]",</p> <p>"cazygi 312203613 gb ADQ46940.1  glycosidase related protein [Caldicellulosiruptor kronotskyensis 2002]",</p> <p>"cazygi 302574013 gb ADL41804.1  glycosidase related protein [Caldicellulosiruptor obsidiensis OB47]",</p> <p>"cazygi 311774490 gb ADQ03977.1  glycosidase related protein [Caldicellulosiruptor owensensis OL]",</p> <p>"cazygi 145408902 gb ABP65906.1  glycosidase", " PH1107-related protein [Caldicellulosiruptor saccharolyticus DSM 8903]",</p> <p>"cazygi 145409377 gb ABP66381.1  glycosidase",</p> <p>"cazygi 332698671 gb AEE95612.1  glycosidase related protein [Mahella australiensis 50-1 BON]"</p>

<p>["cazygi 239505941 gb ACR79428.1  glycosidase PH1107-related [Kosmotoga olearia TBF 19.5.1]",</p> <p>"cazygi 827412316 gb AKI96868.1  glycosidase [Kosmotoga pacifica]",</p> <p>"cazygi 744796242 gb AJC73818.1  glycosidase [Pseudothermotoga hypogea DSM 11164 = NBRC 106472]",</p> <p>"cazygi 157314496 gb ABV33595.1  glycosidase PH1107-related [Pseudothermotoga lettingae TMO]",</p> <p>"cazygi 149793179 gb ABR30627.1  glycosidase", " PH1107-related [Thermosipho melanesiensis BI429]"</p>
<p>["cazygi 268323645 emb CBH37233.1  conserved hypothetical protein",</p> <p>" DUF377 family [uncultured archaeon]",</p> <p>"cazygi 268324206 emb CBH37794.1  conserved hypothetical protein",</p> <p>"cazygi 268323527 emb CBH37115.1  conserved hypothetical protein"]</p>
<p>["cazygi 289527031 gb ADD01383.1  glycosidase PH1107-related protein [Thermoanaerobacter italicus Ab9]",</p> <p>"cazygi 296841382 gb ADH59898.1  glycosidase related protein [Thermoanaerobacter mathranii subsp. mathranii str. A3]"</p>
<p>["cazygi 297165231 gb AD14942.1  glycosidase-related protein [Truepera radiovictrix DSM 17093]"</p>
<p>["cazygi 311778490 gb ADQ07976.1  glycosidase related protein [Caldicellulosiruptor hydrothermalis 108]",</p> <p>"cazygi 145408901 gb ABP65905.1  glycosidase", " PH1107-related protein [Caldicellulosiruptor saccharolyticus DSM 8903]"</p>
<p>["cazygi 319995140 dbj BAJ6391.1.1  hypothetical protein ANT_18850 [Anaerolinea thermophila UNI-1]"</p>
<p>["cazygi 328450346 gb AEB11247.1  glycosidase related protein [Marinithermus hydrothermalis DSM 14884]"</p>
<p>["cazygi 343965244 gb AEM74391.1  glycosidase related protein [Caldicellulosiruptor lactoaceticus 6A]"</p>
<p>["cazygi 381383208 dbj BAM00025.1  hypothetical protein CLDAP_19850 [Caldilinea aerophila DSM 14535 = NBRC 104270]"</p>
<p>["cazygi 383110168 gb AFG35771.1  putative glycosylase [Fervidobacterium pennivorans DSM 9078]",</p> <p>"cazygi 827412798 gb AKI97350.1  glycosidase [Kosmotoga pacifica]",</p> <p>"cazygi 335365667 gb AEH51612.1  glycosidase related protein [Pseudothermotoga thermanum DSM 5069]"</p>
<p>["cazygi 51856141 dbj BAD40299.1  glycosylase [Symbiobacterium thermophilum IAM 14863]"</p>
<p>["cazygi 51856142 dbj BAD40300.1  glycosylase [Symbiobacterium thermophilum IAM 14863]"</p>
<p>["cazygi 762220183 emb CEP78012.1  putative glycosylase [Defluviitoga tunisiensis]"</p>
<p>["cazy AST56541.1  glycosidase [Thermoanaerobacterium thermosaccharolyticum]",</p> <p>"cazy SNX53831.1  Predicted glycosyl hydrolase",</p> <p>" GH43/DUF377 family [Thermoanaerobacterium sp. RBITD]",</p> <p>"cazygi 389570917 gb AFK87322.1  glycosidase related protein [Thermoanaerobacterium saccharolyticum JW/SL-YS485]",</p> <p>"cazygi 302778854 gb ADL69413.1  glycosidase-related [Thermoanaerobacterium thermosaccharolyticum DSM 571]",</p> <p>"cazygi 433293723 gb AGB19545.1  putative glycosylase [Thermoanaerobacterium thermosaccharolyticum M0795]",</p> <p>"cazygi 333112033 gb AEF16970.1  glycosidase related protein [Thermoanaerobacterium xylanolyticum LX-11]"</p>
<p>["cazy ATY84875.1  glycosidase [Kyrpidia spormannii]",</p> <p>"cazygi 295411899 gb ADG06391.1  glycosidase PH1107-related protein [Kyrpidia tusciae DSM 2912]"</p>
<p>["cazy SSC12642.1  Glycosidase related protein [Mesotoga infera]",</p> <p>"cazygi 387859461 gb AFK07552.1  putative glycosylase [Mesotoga prima MesG1.Ag.4.2]"</p>
<p>["humangutMH0143_GL0072439 [gene] locus=scaffold109036_3:3:515:+ [Lack both ends] codon-table.11"]</p>
<p>["humangutO2_UC58-0_GL0085426 [gene] locus=scaffold117881_8:2:955:+ [Lack 5'-end] codon-table.11"]</p>

## UC1

<p>["cazygi 1049185275 gb ANY05114.1  glycosidase [Pseudonocardia sp. HH130630-07]"</p>
<p>["cazygi 378568459 gb AFC28769.1  glycosidase PH1107-like protein [Paenibacillus mucilaginosus 3016]"</p>
<p>["cazygi 384089509 gb AFH60945.1  glycosidase [Paenibacillus mucilaginosus K02]",</p> <p>"cazygi 336297017 gb AEI40120.1  glycosidase PH1107-related protein [Paenibacillus mucilaginosus KNP414]"</p>



["cazygi 573473777 gb AHF90788.1  glycosidase [Opitutaceae bacterium TAV5]"]
["cazygi 686546439 gb AIQ57135.1  glycosidase [Paenibacillus borealis]"]
["cazygi 686546447 gb AIQ57143.1  glycosidase [Paenibacillus borealis]"]
["cazygi 686557089 gb AIQ67783.1  glycosidase [Paenibacillus graminis]", "cazygi 806911715 emb CQR54323.1  glycosidase PH1107-like protein [Paenibacillus riograndensis SBR5]", "cazygi 690615589 gb AIQ16802.1  glycosidase [Paenibacillus sp. FSL H7-0357]", "cazygi 686529396 gb AIQ40095.1  glycosidase [Paenibacillus sp. FSL R5-0912]", "cazygi 686535254 gb AIQ45952.1  glycosidase [Paenibacillus sp. FSL R7-0273]"]
["cazygi 744796135 gb AJC73711.1  glycosidase [Pseudothromotoga hypogea DSM 11164 = NBRC 106472]"]
["cazygi 806913148 emb CQR55756.1  glycosidase PH1107-like protein [Paenibacillus riograndensis SBR5]"]
["cazygi 921143607 dbj BAS26693.1  glycosidase [Limnochorda pilosa]"]
["cazy AVM43645.1 glycosidase [Victivallales bacterium CCUG 44730]"]
["cazy AVM43672.1 glycosidase [Victivallales bacterium CCUG 44730]"]
["cazy AWV34616.1 glycosidase [Paenibacillus odorifer]", "cazygi 686558155 gb AIQ68849.1  glycosidase [Paenibacillus graminis]", "cazygi 686564617 gb AIQ75310.1  glycosidase [Paenibacillus odorifer]", "cazygi 686517487 gb AIQ28188.1  glycosidase [Paenibacillus sp. FSL P4-0081]", "cazygi 686519867 gb AIQ30568.1  glycosidase [Paenibacillus sp. FSL P4-0081]", "cazygi 686517655 gb AIQ28356.1  glycosidase [Paenibacillus sp. FSL P4-0081]", "cazygi 686529388 gb AIQ40087.1  glycosidase [Paenibacillus sp. FSL R5-0912]", "cazygi 686537901 gb AIQ48599.1  glycosidase [Paenibacillus sp. FSL R7-0273]", "cazygi 686543388 gb AIQ54085.1  glycosidase [Paenibacillus sp. FSL R7-0331]"]
["cazy AYB44207.1 glycosidase [Paenibacillus lautus]", "cazygi 806911723 emb CQR54331.1  glycosidase PH1107-like protein [Paenibacillus riograndensis SBR5]", "cazygi 261283676 gb ACX65647.1  glycosidase PH1107-related protein [Paenibacillus sp. Y412MC10]"]
["cazy SDR97174.1 beta-1", "4-mannooligosaccharide/beta-1", "4-mannosyl-N-acetylglucosamine phosphorylase [Microlunatus soli]"]
["cazy SDU29472.1 beta-1", "4-mannooligosaccharide/beta-1", "4-mannosyl-N-acetylglucosamine phosphorylase [Verrucomicrobium sp. GAS474]"]
["humangut158499257-stool2_revised_C1311791_1_gene93858 strand:+ start:3 stop:749 length:747 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut159551223-stool1_revised_scaffold42234_1_gene163963 strand:- start:1 stop:783 length:783 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut159551223-stool1_revised_scaffold43769_1_gene35004 strand:- start:2 stop:508 length:507 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut159571453-stool2_revised_C1054305_1_gene27241 strand:+ start:3 stop:392 length:390 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut160582958-stool1_revised_C631198_1_gene91844 strand:+ start:508 stop:1035 length:528 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut340101.Vvad_PD3034 [Complete]:- codon-table.11", "pigPIG-011_GL0202905 [gene] locus=C1978068_1:308:1303:+ [Complete] codon-table.11"]
["humangut763860675-stool1_revised_scaffold25687_1_gene80256 strand:- start:3158 stop:4159 length:1002 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangutMH0063_GL0054584 [gene] locus=scaffold27192_5:1012:2076:+ [Complete] codon-table.11"]
["humangutMH0096_GL0011911 [gene] locus=scaffold104643_2:2039:3028:+ [Complete] codon-table.11",

"pigPIG-017_GL0234446 [gene] locus=scaffold149736_5:550:1539:+ [Complete] codon-table.11"
["humangutMH0189_GL0133064 [gene] locus=scaffold92118_1:2232:3311:+ [Complete] codon-table.11", "pigPIG-076_GL0239818 [gene] locus=scaffold157416_2:386:1465:+ [Complete] codon-table.11"]
["humangutMH0262_GL0124216 [gene] locus=scaffold29483_4:518:1501:+ [Complete] codon-table.11", "pigBHZ-10B_GL0265814 [gene] locus=scaffold53263_4:624:1607:- [Complete] codon-table.11", "rumen100058_GL1687178_1 [gene] locus=scaffold1731614_5:2129:3112:+[Complete]", "rumen100058_GL2709543_1 [gene] locus=scaffold1462025_2:340:1323:-[Complete]", "rumen100058_GL2832159_1 [gene] locus=scaffold1857139_1:412:1395:+[Complete]", "rumen7049_GL2266359_1 [gene] locus=scaffold1768654_1:359:1342:+[Complete]"]
["humangutMH0280_GL0194891 [gene] locus=scaffold22230_3:105:1103:+ [Complete] codon-table.11", "humangut158802708-stool2_revised_C1062115_1_gene170068 strand:+ start:241 stop:1239 length:999 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "pigPIG-011_GL0096946 [gene] locus=scaffold34023_2:73773:74771:+ [Complete] codon-table.11"]
["humangutMH0303_GL0047987 [gene] locus=scaffold24795_3:211:909:+ [Lack 3'-end] codon-table.11"]
["humangutMH0389_GL0081058 [gene] locus=scaffold47280_7:3:599:+ [Lack 5'-end] codon-table.11"]
["humangutMH0409_GL0033903 [gene] locus=scaffold90767_2:1:387:- [Lack 3'-end] codon-table.11"]
["humangutMH0415_GL0280858 [gene] locus=scaffold113323_4:1038:1616:+ [Lack 3'-end] codon-table.11"]
["humangutMH0426_GL0152356 [gene] locus=scaffold70372_3:1641:2387:- [Lack 5'-end] codon-table.11"]
["humangutMH0431_GL0150624 [gene] locus=scaffold48508_1:162:1193:- [Complete] codon-table.11"]
["humangutMH0454_GL0218883 [gene] locus=scaffold32134_2:3:905:- [Lack 3'-end] codon-table.11"]
["humangutO2_UC18-0_GL0002941 [gene] locus=scaffold24479_5:1130:2125:- [Complete] codon-table.11"]
["humangutO2_UC40-1_GL0043667 [gene] locus=scaffold113353_5:526:1038:- [Lack 5'-end] codon-table.11"]
["humangutO2_UC40-1_GL0211370 [gene] locus=scaffold74444_2:21712:22695:+ [Complete] codon-table.11"]
["humangutO2_UC58-0_GL0099960 [gene] locus=scaffold95984_2:683:1207:+ [Lack 3'-end] codon-table.11"]
["humangutO2_UC58-0_GL0154017 [gene] locus=scaffold92913_2:3:416:- [Lack 3'-end] codon-table.11"]
["humangutT2D-51A_GL0099954 [gene] locus=scaffold9328_6:1:771:+ [Lack 5'-end] codon-table.11"]
["humangutV1_F114_GL0166326 [gene] locus=scaffold97924_1:2254:3243:+ [Complete] codon-table.11"]
["humangutV1_F114_GL0201044 [gene] locus=scaffold65910_3:536:1390:+ [Lack 3'-end] codon-table.11"]
["humangutV1_F117_GL0038393 [gene] locus=scaffold56763_3:349:1350:- [Complete] codon-table.11"]
["humangutV1_UC14-1_GL0099520 [gene] locus=scaffold18051_3:9664:10695:+ [Complete] codon-table.11"]
["humangutV1_UC52-0_GL0119016 [gene] locus=scaffold45779_2:3:503:- [Lack both ends] codon-table.11"]
["mouse29_GL0012345 [gene] locus=scaffold12062_11:1021:2025:- [Complete] codon-table.11"]
["pigBHZ-7B_GL0080054 [gene] locus=scaffold142141_1:1:720:+ [Lack 5'-end] codon-table.11"]
["pigBMZ-17B_GL0166977 [gene] locus=scaffold88433_2:1:525:+ [Lack 5'-end] codon-table.11"]
["pigDB-512B_GL0166967 [gene] locus=scaffold65887_2:3:632:+ [Lack both ends] codon-table.11"]
["pigEYZ-120B_GL0131454 [gene] locus=scaffold14870_3:1:462:+ [Lack 5'-end] codon-table.11"]
["pigPIG-004_GL0134140 [gene] locus=scaffold53576_2:1903:2481:+ [Lack 3'-end] codon-table.11"]
["pigPIG-008_GL0185116 [gene] locus=scaffold9783_10:4216:5184:+ [Complete] codon-table.11"]
["pigPIG-012_GL0060903 [gene] locus=scaffold150081_3:1065:1895:+ [Lack 3'-end] codon-table.11"]
["pigPIG-014_GL0106503 [gene] locus=scaffold105721_2:220:1296:+ [Complete] codon-table.11"]
["pigPIG-026_GL0093671 [gene] locus=scaffold175883_1:10384:11400:+ [Complete] codon-table.11"]
["pigPIG-027_GL0244087 [gene] locus=scaffold114785_1:1:678:- [Lack 3'-end] codon-table.11"]
["pigPIG-031_GL0171674 [gene] locus=scaffold97864_2:29:1135:- [Lack 5'-end] codon-table.11"]

["pigPIG-037_GL0047500 [gene] locus=scaffold88886_2:1:936:+ [Lack 5'-end] codon-table.11"]
["pigPIG-091_GL0066511 [gene] locus=scaffold155169_1:5965:6960:+ [Complete] codon-table.11"]
["pigPIG-123_GL0179481 [gene] locus=scaffold109245_2:3:665:+ [Lack both ends] codon-table.11"]
["pigSYZ-426B_GL0182759 [gene] locus=scaffold167211_1:3:542:+ [Lack both ends] codon-table.11"]
["pigSYZ-441B_GL0127622 [gene] locus=scaffold100124_1:2:562:+ [Lack both ends] codon-table.11"]
["pigZXZ-3B_GL0023913 [gene] locus=scaffold94759_2:1:606:- [Lack 3'-end] codon-table.11"]
["pigZXZ-8B_GL0155172 [gene] locus=scaffold121846_4:3:635:- [Lack both ends] codon-table.11"]
["pigZXZ-8B_GL0175471 [gene] locus=scaffold148983_2:2:424:- [Lack 3'-end] codon-table.11"]
["rumen0081_GL0148410_1 [gene] locus=scaffold391561_1:1:657:+[Lack both ends"]
["rumen0081_GL0415391_1 [gene] locus=scaffold1981889_2:1:516:-[Lack 3'-end"]
["rumen0081_GL0880584_1 [gene] locus=scaffold1025676_4:1:582:-[Lack both ends"]
["rumen0081_GL0914779_1 [gene] locus=scaffold559002_3:2076:3092:-[Complete]"]
["rumen0081_GL1763932_1 [gene] locus=scaffold843398_10:1498:2511:+[Complete]"]
["rumen0081_GL1968913_1 [gene] locus=scaffold1870805_1:2933:4003:-[Complete]"]
["rumen0081_GL2018936_1 [gene] locus=scaffold443506_2:1:972:+[Lack 5'-end"]
["rumen100058_GL0182296_1 [gene] locus=C59144964_1:74:715:+[Lack 3'-end"]
["rumen100058_GL0420621_1 [gene] locus=scaffold679606_2:1:717:+[Lack both ends"]
["rumen100058_GL0673369_1 [gene] locus=scaffold2677682_3:2:967:+[Lack 5'-end"]
["rumen100058_GL0752386_1 [gene] locus=scaffold2669260_1:3:608:+[Lack 5'-end"]
["rumen100058_GL0795452_1 [gene] locus=scaffold940039_6:3:542:-[Lack both ends"]
["rumen100058_GL1196038_1 [gene] locus=scaffold3288648_1:2:472:+[Lack 5'-end"]
["rumen100058_GL1413184_1 [gene] locus=scaffold186345_4:334:1347:-[Complete]"]
["rumen100058_GL1598357_1 [gene] locus=scaffold963304_1:1:561:+[Lack both ends"]
["rumen100058_GL1774012_1 [gene] locus=scaffold11065_2:14031:15044:+[Complete]"]
["rumen100058_GL1927446_1 [gene] locus=scaffold3059409_2:1:441:+[Lack 5'-end"]
["rumen100058_GL1952703_1 [gene] locus=scaffold2267543_1:85:783:-[Lack 5'-end"]
["rumen100058_GL2027952_1 [gene] locus=scaffold1493619_1:259:873:+[Lack 3'-end"]
["rumen100058_GL2251448_1 [gene] locus=scaffold1642429_11:3693:4700:-[Complete]", "rumen2009040_GL0894487_1 [gene] locus=scaffold3058227_1:263:1270:-[Complete]", "rumen2009040_GL0926795_1 [gene] locus=scaffold16901_2:313:1320:-[Complete]"]
["rumen100058_GL2253244_1 [gene] locus=scaffold2919524_3:1:636:+[Lack 5'-end"]
["rumen100058_GL2866962_1 [gene] locus=scaffold2199901_2:2281:3213:-[Complete]"]
["rumen100058_GL2876265_1 [gene] locus=scaffold935118_1:350:1336:-[Complete]", "rumen7049_GL1880481_1 [gene] locus=scaffold937463_1:1098:2084:+[Complete]", "rumen7049_GL2581625_1 [gene] locus=scaffold742976_2:1011:1997:-[Complete]"]
["rumen100058_GL3345981_1 [gene] locus=scaffold653675_3:179:925:-[Lack 5'-end"]
["rumen100058_GL3545252_1 [gene] locus=scaffold3268156_1:99:986:+[Lack 3'-end"]
["rumen100058_GL3606733_1 [gene] locus=scaffold3171313_2:2:721:+[Lack 5'-end"]
["rumen100058_GL3608591_1 [gene] locus=scaffold3059409_1:2249:2845:+[Lack 3'-end"]
["rumen100058_GL3802860_1 [gene] locus=scaffold105156_2:1:978:-[Lack 3'-end"]
["rumen2009040_GL0393603_1 [gene] locus=scaffold2886108_1:1:843:+[Lack 5'-end"]
["rumen2009040_GL0401932_1 [gene] locus=scaffold1563128_1:7065:8075:+[Complete]", "rumen2009040_GL1971060_1 [gene] locus=scaffold517671_1:656:1666:+[Complete]"]

["rumen2009040_GL0467795_1 [gene] locus=scaffold1551842_1:15:950:-[Complete]"]
["rumen2009040_GL0611515_1 [gene] locus=scaffold2319591_3:44:643:-[Lack 5'-end]"]
["rumen2009040_GL0632016_1 [gene] locus=scaffold2094132_1:3:686:-[Lack both ends]"]
["rumen2009040_GL0831155_4 [gene] locus=scaffold2323784_4:1:657:+[Lack both ends]"]
["rumen2009040_GL0865524_1 [gene] locus=C54003323_1:2:673:+[Lack both ends]"]
["rumen2009040_GL1053484_1 [gene] locus=scaffold3004335_1:2:991:-[Lack 3'-end]"]
["rumen2009040_GL1184095_1 [gene] locus=scaffold216471_1:1072:2076:+[Complete]"]
["rumen2009040_GL1244108_1 [gene] locus=scaffold836717_2:1:699:-[Lack 3'-end]"]
["rumen2009040_GL1647791_1 [gene] locus=scaffold701553_1:370:909:-[Lack 5'-end]"]
["rumen2009040_GL1719144_1 [gene] locus=scaffold441258_4:771:1565:-[Lack 5'-end]"]
["rumen2009040_GL1778089_1 [gene] locus=scaffold808100_2:1913:2893:+[Complete]"]
["rumen2009040_GL1928979_1 [gene] locus=scaffold648133_1:678:1652:-[Complete]"]
["rumen2009040_GL2041390_1 [gene] locus=scaffold519822_4:1:714:-[Lack both ends]"]
["rumen2009040_GL2064696_1 [gene] locus=scaffold24403_5:1142:1984:+[Lack 3'-end]"]
["rumen2009040_GL2209993_1 [gene] locus=scaffold2901289_2:1:474:-[Lack 3'-end]"]
["rumen2009040_GL2322489_1 [gene] locus=scaffold2669843_1:1:645:+[Lack both ends]"]
["rumen2009040_GL2768667_1 [gene] locus=scaffold1906587_1:2:526:-[Lack both ends]"]
["rumen2009040_GL2790716_1 [gene] locus=scaffold2580700_1:769:1767:+[Complete]"]
["rumen2009040_GL2934385_1 [gene] locus=scaffold953067_10:2237:3001:-[Lack 5'-end]"]
["rumen2009040_GL3422701_1 [gene] locus=scaffold3031986_2:477:1478:+[Complete]"]
["rumen3042_GL0013013_1 [gene] locus=scaffold109084_2:686:1792:-[Complete]"]
["rumen3042_GL0523502_1 [gene] locus=scaffold734776_6:1041:2147:-[Complete]"]
["rumen3042_GL0074138_1 [gene] locus=scaffold473778_1:409:879:+[Lack 3'-end]"]
["rumen3042_GL0275810_1 [gene] locus=scaffold1062555_2:30:770:-[Lack 5'-end]"]
["rumen3042_GL0321068_1 [gene] locus=scaffold393578_4:355:906:+[Lack 3'-end]"]
["rumen3042_GL0324243_1 [gene] locus=scaffold2171383_3:1:789:+[Lack 5'-end]"]
["rumen3042_GL0374639_1 [gene] locus=scaffold1459401_3:1:612:-[Lack both ends]"]
["rumen3042_GL0508326_1 [gene] locus=scaffold903167_2:3:503:-[Lack 3'-end]"]
["rumen3042_GL0635709_1 [gene] locus=scaffold1801982_1:1:690:-[Lack 3'-end]"]
["rumen3042_GL0699078_1 [gene] locus=scaffold2436159_2:637:1731:+[Complete]"]
["rumen3042_GL0826681_1 [gene] locus=scaffold957001_1:3:812:-[Lack 3'-end]"]
["rumen3042_GL1258686_1 [gene] locus=scaffold829964_3:653:1666:+[Complete]"]
["rumen3042_GL1616734_1 [gene] locus=scaffold984813_2:1184:1885:+[Lack 3'-end]"]
["rumen3042_GL1714555_1 [gene] locus=scaffold966246_6:2:550:+[Lack both ends]"]
["rumen3042_GL1743074_1 [gene] locus=scaffold1491757_2:108:1103:+[Complete]"]
["rumen3042_GL1977907_1 [gene] locus=scaffold711712_1:1:618:-[Lack 3'-end]"]
["rumen3042_GL1978410_1 [gene] locus=scaffold1184793_2:2:919:+[Lack 5'-end]"]
["rumen3042_GL2064520_1 [gene] locus=scaffold2550855_1:6107:7144:+[Complete]"]
["rumen3042_GL2331231_1 [gene] locus=scaffold70346_2:2:766:+[Lack 5'-end]"]
["rumen3042_GL2352900_1 [gene] locus=scaffold1672082_1:3:785:+[Lack 5'-end]"]
["rumen3042_GL2538555_1 [gene] locus=scaffold1897435_2:3:650:-[Lack both ends]"]
["rumen3042_GL2542398_1 [gene] locus=scaffold2103164_1:16:1098:+[Complete]"]
["rumen3042_GL2567092_1 [gene] locus=scaffold678778_2:163:1221:-[Complete]"]

["rumen3042_GL2580748_1 [gene] locus=scaffold1683391_1:1:543:-[Lack 3'-end]"]
["rumen3042_GL2639737_1 [gene] locus=C50992643_1:63:656:-[Lack 5'-end]"]
["rumen3042_GL2775128_1 [gene] locus=scaffold1387699_3:505:1011:-[Lack 5'-end]"]
["rumen3042_GL2824803_1 [gene] locus=scaffold1193901_2:172:708:-[Lack 5'-end]"]
["rumen552_GL0505066_1 [gene] locus=scaffold602548_6:3:968:-[Lack 3'-end]"]
["rumen552_GL0845075_1 [gene] locus=scaffold1019407_1:355:744:-[Lack 5'-end]"]
["rumen552_GL1002912_1 [gene] locus=scaffold1095106_1:3:938:-[Lack both ends]"]
["rumen552_GL1352490_1 [gene] locus=scaffold265239_5:3:509:-[Lack both ends]"]
["rumen552_GL1604742_1 [gene] locus=scaffold770560_4:151:1170:-[Lack 5'-end]"]
["rumen552_GL1727067_1 [gene] locus=scaffold755005_1:1:648:-[Lack 3'-end]"]
["rumen553_GL0455875_1 [gene] locus=scaffold46235_12:2554:3519:-[Complete]"]
["rumen553_GL0523540_1 [gene] locus=scaffold268121_2:1:612:-[Lack 3'-end]"]
["rumen554_GL0223422_1 [gene] locus=scaffold1470618_1:875:1390:+[Lack 3'-end]"]
["rumen554_GL0395216_1 [gene] locus=scaffold549399_1:1:477:-[Lack 3'-end]"]
["rumen554_GL0530969_1 [gene] locus=scaffold1614689_1:1:1086:-[Lack both ends]"]
["rumen554_GL0877945_1 [gene] locus=scaffold649645_2:2209:3324:+[Complete]"]
["rumen554_GL0966680_1 [gene] locus=scaffold2097347_2:1978:2913:+[Lack 3'-end]"]
["rumen554_GL1884248_1 [gene] locus=C39576505_1:2:571:+[Lack both ends]"]
["rumen554_GL1951062_1 [gene] locus=scaffold298222_2:1624:2670:-[Complete]"]
["rumen554_GL2035250_1 [gene] locus=scaffold536606_2:2:1060:+[Lack 5'-end]"]
["rumen554_GL2508113_1 [gene] locus=scaffold922117_5:734:1816:+[Lack 3'-end]"]
["rumen2009040_GL2686975_1 [gene] locus=C55695877_1:932:2017:-[Complete]"]
["rumen554_GL3164790_1 [gene] locus=scaffold208848_5:3:506:+[Lack both ends]"]
["rumen555_GL0157448_1 [gene] locus=scaffold207468_2:1005:2069:+[Complete]"]
["rumen3042_GL2771554_1 [gene] locus=scaffold30042_1:290:1354:-[Complete]"]
["rumen555_GL1109709_1 [gene] locus=scaffold1574979_1:2:469:-[Lack 3'-end]"]
["rumen583_GL0006884_1 [gene] locus=scaffold343648_2:12922:13914:+[Complete]"]
["rumen583_GL0502344_1 [gene] locus=scaffold339082_1:30623:31666:-[Complete]"]
["rumen583_GL0706440_1 [gene] locus=scaffold252626_1:808:1818:+[Complete]"]
["rumen7049_GL0308010_1 [gene] locus=scaffold2052315_1:188:796:-[Lack 5'-end]"]
["rumen7049_GL0385144_1 [gene] locus=C51642093_1:3:482:+[Lack 5'-end]"]
["rumen7049_GL1452498_1 [gene] locus=scaffold1929342_3:2:595:-[Lack both ends]"]
["rumen7049_GL1729428_1 [gene] locus=scaffold1174407_2:1067:2062:+[Complete]"]
["rumen7049_GL2188481_1 [gene] locus=scaffold886512_2:481:1353:+[Lack 3'-end]"]
["rumen7049_GL2671781_1 [gene] locus=scaffold1096931_1:1:762:-[Lack both ends]"]
["rumen7049_GL2771811_1 [gene] locus=scaffold2214772_3:127:768:-[Lack 5'-end]"]

## UC2

["Ncazy AOC93887.1 Beta-1", "4-mannooligosaccharide phosphorylase [Flavobacterium anhuiense]"]
"cazy AWK04528.1 glycosidase [Flavobacterium sp. HYN0056]"]
"cazy AXB56708.1 glycosidase [Flavobacterium sp. HYN0086]"]
"cazy 146152354 gb ABQ03208.1 protein of unknown function [Flavobacterium johnsoniae UW101]"]
["Ncazy AOE53425.1 glycosidase [Flavobacterium psychrophilum]"]

"cazy AWH83856.1 glycosidase [Flavobacterium sp. HYN0059]", "cazygi 947266270 gb ALM49808.1  glycosidase [Flavobacterium psychrophilum]"
"cazygi 1005374128 gb AMP99903.1  Glycosidase [Pedobacter cryoconitis]"
"cazygi 1008902684 gb AMR34349.1  glycosidase [Mucilaginibacter sp. PAMC 26640]"
"cazygi 1012312438 gb AMS30679.1  hypothetical protein AEM38_01165 [Hyphomonadaceae bacterium UKL 13-1]"
"cazygi 1015455903 gb AMV37685.1  Beta-1-, "4-mannooligosaccharide phosphorylase [Planctomyces sp. SH-PL62]"
"cazygi 1027796686 emb CUT14050.1  COG2152 predicted glycoside hydrolase [Bradyrhizobium sp.]"
"cazygi 1027804947 emb CUU17819.1  COG2152 predicted glycoside hydrolase CDS [Bradyrhizobium sp.]"
"cazygi 1028501711 gb ANE82221.1  glycosidase [Mycobacterium sp. YC-RL4]"
"cazygi 1033841697 gb ANH82550.1  glycosidase [Niabella sp. BS26]"
"cazygi 1034245045 gb ANI38080.1  glycosidase [Mycobacterium vaccae 95051]"
"cazygi 1035533153 gb ANJ27972.1  glycosylase [Agromyces sp. AR33]"
"cazygi 1047841245 gb ANW65006.1  glycosidase [Mycobacterium sp. dj-10]"
"cazygi 1050304164 gb ANZ40523.1  hypothetical protein BBK82_35480 [Lentzea sp. DHS C013]"
"cazygi 158107806 gb ABW10003.1  glycosidase PH1107-related [Frankia sp. EAN1pec]"
"cazygi 255344342 gb ACU03668.1  glycosidase PH1107-related [Pedobacter heparinus DSM 2366]"
"cazygi 256039487 gb ACU63031.1  glycosidase PH1107-related [Chitinophaga pinensis DSM 2588]"
"cazygi 312129304 ref ADQ16291.1  glycosidase related protein [Leadbetterella byssophila DSM 17132]"
"cazygi 32443503 emb CAD72945.1  conserved hypothetical protein [Rhodopirellula baltica SH 1]"
"cazygi 324972906 gb ADY51890.1  glycosidase related protein [Pseudopedobacter saltans DSM 12145]"
"cazygi 326550293 gb ADZ78678.1  glycosidase related protein [Sphingobacterium sp. 21]"
"cazygi 381359447 dbj BAL76277.1  hypothetical protein S23_30710 [Bradyrhizobium sp. S23321]"
"cazygi 381374982 dbj BAL91800.1  hypothetical protein AMIS_65800 [Actinoplanes missouriensis 431]"
"cazygi 381386098 dbj BAM02914.1  hypothetical protein PSMK_07550 [Phycisphaera mikurensis NBRC 102666]"
"cazygi 383801350 gb AFH48430.1  Putative glycosylase [Ignavibacterium album JCM 16511]"
"cazygi 384066316 emb CCG99526.1  glycosidase PH1107-related protein [Fibrella aestuarina BUZ 2]"
"cazygi 390611914 gb AFM13066.1  glycosidase related protein [Turneriella parva DSM 21527]"
"cazygi 399230158 gb AFP37651.1  Glycosidase PH1107-related protein [Mycobacterium smegmatis str. MC2 155]"
"cazygi 430016148 gb AGA27862.1  putative glycosylase [Singulisphaera acidiphila DSM 18658]"
"cazygi 430736185 gb AGA60122.1  glycoside hydrolase [Aminobacter sp. Gsoil204]"
"cazygi 456358657 dbj BAM93102.1  hypothetical protein S58_71370 [Bradyrhizobium oligotrophicum S58]"
"cazygi 469480061 gb AGH50286.1  glycosidase [Sphingomonas sp. MM-1]"
"cazygi 469480931 gb AGH51156.1  glycosidase PH1107-like protein [Sphingomonas sp. MM-1]"
"cazygi 469481522 gb AGH51613.1  hypothetical protein G432_19610 (plasmid) [Sphingomonas sp. MM-1]"
"cazygi 492008597 gb AGL19917.1  PH1107-like glycosidase [Actinoplanes sp. N902-109]"
"cazygi 510024552 emb CCW36629.1  Predicted glycosylase [Chthonomonas calidirosea T49]"
"cazygi 537742677 emb CDF80320.1  conserved hypothetical protein [Formosa agariphila KMM 3901]"
"cazygi 556037616 gb AGZ44863.1  glycosidase [Actinoplanes friuliensis DSM 7358]"
"cazygi 565684332 gb AHC24192.1  glycosidase [Mycobacterium neoaurum VKM Ac-1815D]", "cazygi 1003099503 gb AMO04816.1  glycosidase [Mycobacterium sp. NRRL B-3805]"
"cazygi 569545415 gb AHE57032.1  hypothetical protein NX02_27230 [Sphingomonas sanxanigenens DSM 19645 = NX02]"
"cazygi 573476715 gb AHF93726.1  glycosidase [Opitutaceae bacterium TAV5]"
"cazygi 610423367 gb AHW60571.1  glycosidase [Draconibacterium orientale]"

<p>["cazy 676328648 gb AIM37149.1  glycosidase [Sphingobacterium sp. ML3W]",  "cazy 672715095 emb CDS94603.1  Glycosidase [Sphingobacterium sp. PM2-P1-29]"]</p>
<p>["cazy 695171782 gb AIT07872.1  glycosidase [Sphingomonas taxii]"]</p>
<p>["cazy 698182875 gb AIT82398.1  glycosidase (plasmid) [Novosphingobium pentaromatorans US6-1]"]</p>
<p>["cazy 698948887 gb AIU13081.1  glycosidase [Mycobacterium smegmatis]",  "cazy 698957170 gb AIU19705.1  glycosidase [Mycobacterium smegmatis]",  "cazy 777215303 emb CKH15398.1  glycosidase [Mycobacterium smegmatis]"]</p>
<p>["cazy 821325234 gb AKH18715.1  glycosidase (plasmid) [Sphingomonas sanxanigenens DSM 19645 = NX02]"]</p>
<p>["cazy 821325377 gb AKH18858.1  glycosidase (plasmid) [Sphingomonas sanxanigenens DSM 19645 = NX02]"]</p>
<p>["cazy 821325385 gb AKH18866.1  glycosidase (plasmid) [Sphingomonas sanxanigenens DSM 19645 = NX02]"]</p>
<p>["cazy 828180910 gb AKK26145.1  glycosidase [Mycobacterium sp. EPA45]"]</p>
<p>["cazy 998165786 gb AMK22950.1  glycosidase PH1107-like protein [Sphingobium sp. TKS]"]</p>
<p>["cazy 998617162 dbj BAU53095.1  Beta-1", "4-mannooligosaccharide phosphorylase [Mucilaginibacter gotjawali]"]</p>
<p>["cazy AOG00709.1 hypothetical protein BSY18_2886 [Blastomonas sp. RAC04]"]</p>
<p>["cazy AOG08893.1 hypothetical protein BSY240_1987 [Agrobacterium sp. RAC06]"]</p>
<p>["cazy AOH84130.1 glycosidase [Sphingomonas panacis]",  "cazy API58243.1 glycosidase [Sphingomonas sp. JJ-A5]",  "cazy APR52417.1 glycosidase [Sphingomonas koreensis]",  "cazy APX67239.1 glycosidase [Sphingomonas sp. LK11]",  "cazy AUW56965.1 glycosidase [Sphingobium sp. SCG-1]",  "cazy AXJ96986.1 glycosidase [Sphingomonas sp. FARSPH]",  "cazy 695170294 gb AIT06384.1  glycosidase [Sphingomonas taxii]"]</p>
<p>["cazy AOH86817.1 glycosidase [Sphingomonas panacis]"]</p>
<p>["cazy AOM76044.1 glycosidase [Pedobacter steynii]"]</p>
<p>["cazy AOO80560.1 glycosidase [Bosea vaviloviae]"]</p>
<p>["cazy AOR80665.1 glycosidase (plasmid) [Novosphingobium resinovorum]",  "cazy AXB78745.1 glycosidase [Novosphingobium sp. P6W]",  "cazy BBC70930.1 glycosidase [Altererythrobacter sp. B11]"]</p>
<p>["cazy AOW22449.1 glycosidase [Sphingomonas melonis TY]",  "cazy ATI55837.1 glycosidase [Sphingomonas melonis]",  "cazy 1026262148 gb ANC86520.1  glycosidase [Sphingomonas sp. NIC1]",  "cazy 695171404 gb AIT07494.1  glycosidase [Sphingomonas taxii]"]</p>
<p>["cazy AOW23127.1 glycosidase [Sphingomonas melonis TY]",  "cazy ATI56558.1 glycosidase [Sphingomonas melonis]",  "cazy 1026262798 gb ANC87170.1  glycosidase [Sphingomonas sp. NIC1]"]</p>
<p>["cazy APF17754.1 putative glycosyl hydrolase", "GH43/DUF377 family [Caldithrix abyssi DSM 13497]"]</p>
<p>["cazy APG11330.1 glycosidase [Bradyrhizobium japonicum]",  "cazy APO52757.1 glycosidase [Bradyrhizobium diazoefficiens]",  "cazy AWM01740.1 glycosidase [Bradyrhizobium sp. 2 39S1MB]",  "cazy AWM08039.1 glycosidase [Bradyrhizobium sp. 3 85S1MB]",  "cazy AWO92058.1 glycosidase [Bradyrhizobium diazoefficiens]",  "cazy SHG41007.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Bradyrhizobium erythropleii]",  "cazy SHI07349.1 Predicted glycosyl hydrolase",</p>

"cazy 806932017 dbj BAR63019.1  hypothetical protein NK6_9885 [Bradyrhizobium diazoefficiens]", "cazy 1027481022 gb AND90349.1  glycosidase [Bradyrhizobium diazoefficiens USDA 110]", "cazy 736035080 gb AJA61541.1  glycosidase [Bradyrhizobium japonicum]", "cazy 627784905 gb AHY54122.1  hypothetical protein BJS_01507 [Bradyrhizobium japonicum SEMIA 5079]", "cazy 659656081 emb CDN49126.1  Glycosidase PH1107-related [Neorhizobium galegae bv. orientalis str. HAMB1 540]", "cazy 1002735159 gb AMN39076.1  glycosidase [Rhodoplanes sp. Z2-YC6860]"
["cazy APR55329.1 glycosidase (plasmid) [Sphingomonas koreensis]", "cazy BAV66555.1 hypothetical protein SCLO_2002220 (plasmid) [Sphingobium cloacae]", "cazy 821325209 gb AKH18690.1  glycosidase (plasmid) [Sphingomonas sanxanigenens DSM 19645 = NX02]"]
["cazy APR55450.1 glycosidase (plasmid) [Sphingomonas koreensis]", "cazy ARR57397.1 glycosidase (plasmid) [Sphingomonas wittichii DC-6]", "cazy ATE67775.1 glycosidase (plasmid) [Rhizorhabdus dicambivorans]", "cazy ATP19300.1 glycosidase [Sphingobium yanoikuyae]", "cazy 821325336 gb AKH18817.1  glycosidase (plasmid) [Sphingomonas sanxanigenens DSM 19645 = NX02]"]
["cazy APU98171.1 glycosidase [Sphingobacterium sp. B29]"]
["cazy APW72948.1 glycosidase", "partial [Sphingopyxis granulii]"]
["cazy APW73724.1 glycosidase [Sphingopyxis granulii]", "cazy APZ97389.1 glycosidase [Sphingopyxis sp. QXT-31]", "cazy AVA14877.1 glycosidase [Sphingopyxis sp. MG]", "cazy 991912921 gb AMG76131.1  Glycosidase", "-related protein [Sphingopyxis granulii]", "cazy 938157195 gb ALJ13556.1  glycosidase [Sphingopyxis macrogoltabida]", "cazy 1015407695 gb AMU88997.1  glycosidase [Sphingopyxis macrogoltabida]", "cazy 937289312 gb ALH79858.1  glycosidase [Sphingopyxis macrogoltabida]", "cazy 924525793 gb ALC11957.1  glycosidase [Sphingopyxis sp. 113P3]", "cazy 1015414355 gb AMU96148.1  glycosidase [Sphingopyxis terrae NBRC 15098]"]
["cazy APX66063.1 glycosidase [Sphingomonas sp. LK11]"]
["cazy APZ94250.1 Beta-1", "4-mannooligosaccharide phosphorylase [Fuerstia marisgermanicae]"]
["cazy APZ99995.1 glycosidase [Sphingopyxis sp. QXT-31]", "cazy 734571881 gb AJA09097.1  glycosidase [Sphingopyxis fribergensis]", "cazy 1015412072 gb AMU93865.1  glycosidase [Sphingopyxis terrae NBRC 15098]"]
["cazy AQG78080.1 glycosidase [Spirosoma montaniterrae]", "cazy ARK10959.1 glycosidase [Fibrella sp. ES10-3-2-2]"]
["cazy AQR74295.1 glycosidase [Sphingomonas sp. LM7]", "cazy ARR54224.1 glycosidase [Sphingomonas wittichii DC-6]", "cazy 761899411 gb AJP73780.1  glycosidase [Sphingomonas hengshuiensis]"]
["cazy ARS28226.1 hypothetical protein KC8_13165 [Sphingomonas sp. KC8]", "cazy BAV66381.1 hypothetical protein SCLO_2000480 (plasmid) [Sphingobium cloacae]"]
["cazy ARS39725.1 glycosidase [Sphingobacteriaceae bacterium GW460-11-11-14-LB5]", "cazy ATP55320.1 glycosidase [Pedobacter ginsengisoli]"]
["cazy ARU17145.1 glycosidase [Croceiococcus marinus]", "cazy 831209727 gb AKM11563.1  glycosidase [Croceiococcus naphthovorans]"]
["cazy ARU18462.1 glycosidase (plasmid) [Croceiococcus marinus]"]
["cazy ASB47878.1 glycosidase [Alkalitalea saponilacus]"]
["cazy ASR50966.1 glycosidase [Blastomonas fulva]"]



["cazy ASR56941.1 hypothetical protein CBP52_12735 [Cellulomonas sp. PSBB021]"]
["cazy ASU33243.1 glycosidase [Mucilagibacter sp. BJC16-A31]"]
["cazy ASY46536.1 glycosidase (plasmid) [Sphingobium hydrophobicum]", "cazy ATP21746.1 glycosidase (plasmid) [Sphingobium yanoikuyae]", "cazy BBE00152.1 glycosidase (plasmid) [Sphingobium amiense]"]
["cazy ASZ12424.1 glycosidase [Chitinophaga sp. MD30]"]
["cazy ATC63143.1 glycosidase [Verrucomicrobia bacterium]"]
["cazy ATE67300.1 glycosidase [Rhizorhabdus dicambivorans]"]
["cazy ATL49030.1 glycosidase [Chitinophaga caeni]"]
["cazy ATO86111.1 glycosylase [Actinoplanes sp. SE50]", "cazy SDT78711.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Actinoplanes derwentensis]", "cazy SLM03525.1 glycosylase [Actinoplanes sp. SE50/110]"]
["cazy ATQ44096.1 glycosidase [Caulobacter mirabilis]"]
["cazy AUD04817.1 glycosidase [Spirosoma pollinicola]", "cazy gij283815376 gb ADB37214.1  glycosidase PH1107-related protein [Spirosoma linguale DSM 74]", "cazy gij808693885 gb AKD54724.1  glycosidase [Spirosoma radiotolerans]"]
["cazy AUG56797.1 Beta-1", "4-mannooligosaccharide phosphorylase [Hungateiclostridium saccincola]"]
["cazy AUN32396.1 glycosidase [Niveispirillum cyanobacterium]"]
["cazy AUP80405.1 glycosidase [Flavivirga eckloniae]"]
["cazy AVA14706.1 glycosidase [Sphingopyxis sp. MG]", "cazy BBA74232.1 glycosidase PH1107-like protein [Ochrobactrum sp. PW1]", "cazy gij698182550 gb AIT82074.1  glycosidase (plasmid) [Novosphingobium pentaromativorans US6-1]", "cazy gij991911667 gb AMG74877.1  Glycoside hydrolase [Sphingopyxis granuli]", "cazy gij938157149 gb ALJ13510.1  glycosidase [Sphingopyxis macrogoltabida]", "cazy gij1015407733 gb AMU89035.1  glycosidase [Sphingopyxis macrogoltabida]"]
["cazy AVR45112.1 glycosidase [Gramella sp. SH35]"]
["cazy AWG26450.1 glycosidase [Flavobacterium kingsejongii]"]
["cazy AXG14456.1 glycosidase-like protein [Intrasporangium calvum]"]
["cazy AXJ96197.1 glycosidase [Sphingomonas sp. FARSPH]"]
["cazy AXK78571.1 glycosidase [Mycolicibacterium neoaurum]"]
["cazy AXO32969.1 putative glycoside hydrolase [Micromonospora sp. B006]"]
["cazy AXP81818.1 Beta-1-2C4-mannooligosaccharide phosphorylase [Mariniflexile sp. TRM1-10]"]
["cazy AYJ84568.1 glycosidase (plasmid) [Sphingomonas sp. YZ-8]"]
["cazy AYJ85823.1 glycosidase [Sphingomonas sp. YZ-8]"]
["cazy AYJ86812.1 glycosidase [Sphingomonas sp. YZ-8]"]
["cazy AYL97076.1 glycosidase [Mucilagibacter sp. HYN0043]"]
["cazy AYO75858.1 glycosidase (plasmid) [Sphingobium yanoikuyae]"]
["cazy BAV66533.1 hypothetical protein SCLO_2002000 (plasmid) [Sphingobium cloacae]"]
["cazy BAX80033.1 glycosidase [Marinifilaceae bacterium SPP2]"]
["cazy BBA14119.1 Glycosidase [Petrimonas sp. IBARAKI]", "cazy SCM55110.1", "4-beta-mannosyl-N-acetylglucosamine phosphorylase (ECO:0000303 PubMed:23943617) [Petrimonas mucosa]"]
["cazy BBB08500.1 glycosidase [Sphingopyxis sp. EG6]"]
["cazy BBC73503.1 glycosidase [Altererythrobacter sp. B11]"]

["cazy BBD02204.1 hypothetical protein YGS_C2P0217 [Sphingobium sp. YG1]"]
["cazy BBD98211.1 glycosidase [Sphingobium amiense]"]
["cazy BBF81586.1 predicted glycoside hydrolase [Asticcacaulis excentricus]"]
["cazy SBV32411.1 conserved protein of unknown function [uncultured Sphingopyxis sp.]"]
["cazy SBV34065.1 conserved protein of unknown function [uncultured Sphingopyxis sp.]"]
["cazy SCD20035.1 Glycosyl hydrolase family 43 [Proteiniphilum saccharofermentans]"]
["cazy SCE81998.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Micromonospora coriariae]"]
["cazy SCG16578.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Micromonospora echinofusca]"]
["cazy SCG71427.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Micromonospora zamorensis]"]
["cazy SCG77273.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Micromonospora inositola], "cazy 556034428 gb AGZ41675.1  glycosidase [Actinoplanes friuliensis DSM 7358]"]
["cazy SDJ47152.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Bradyrhizobium ottawaense], "cazy SDR93691.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Bradyrhizobium canariense], "cazy SHK72495.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Bradyrhizobium lablabi]"]
["cazy SDM92606.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Afipia sp. GAS231]"]
["cazy SDR71326.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Actinopolymorpha singaporensis]"]
["cazy SDS41644.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Mucilaginibacter mallensis]"]
["cazy SDT42454.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Friedmanniella luteola]"]
["cazy SDT97486.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Verrucomicrobium sp. GAS474]"]
["cazy SHL05964.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Bradyrhizobium lablabi]"]
["cazy SNV48420.1 Domain of uncharacterised function (DUF377) [Sphingobacterium mizutaii]"]

### UC3

["cazy 1016919455 gb AMY11887.1  Beta-1", "4-mannooligosaccharide phosphorylase [Acidobacteria bacterium DSM 100886]"]
["cazy 1027788893 emb CUS04732.1  conserved protein of unknown function [Ardenticatena]"]
["cazy 159889857 gb ABX02937.1  glycosidase PH1107-related [Herpetosiphon aurantiacus DSM 785]"]
["cazy 19916824 gb AAM06210.1  conserved hypothetical protein [Methanosarcina acetivorans C2A]"]
["cazy 20517637 gb AAM25746.1  predicted glycosylase [Caldanaerobacter subterraneus subsp. tengcongensis MB4], "cazy 694167300 gb AIS53471.1  beta-1", "4-mannooligosaccharide phosphorylase [Thermoanaerobacter kivui]"]
["cazy 20907595 gb AAM32640.1  conserved protein [Methanosarcina mazei Go], "cazy 805367849 gb AKB64961.1  hypothetical protein MSMAS_1765 [Methanosarcina mazei S-6], "cazy 805364371 gb AKB61645.1  hypothetical protein MSMA_P_1660 [Methanosarcina mazei SarPi], "cazy 452101355 gb AGF98295.1  hypothetical protein MmTuc01_3026 [Methanosarcina mazei Tuc01], "cazy 805360882 gb AKB40671.1  hypothetical protein MSMAW_1680 [Methanosarcina mazei WWM610]"]
["cazy 222455536 gb ACM59798.1  glycosidase PH1107-related [Caldicellulosiruptor besicii DSM 6725], "cazy 311778212 gb ADQ07698.1  glycosidase related protein [Caldicellulosiruptor hydrothermalis 108], "cazy 312180843 gb ADQ41013.1  glycosidase related protein [Caldicellulosiruptor kristjanssonii I77R1B], "cazy 312203467 gb ADQ46794.1  glycosidase related protein [Caldicellulosiruptor kronotskyensis 2002], "cazy 343964401 gb AEM73548.1  glycosidase related protein [Caldicellulosiruptor lactoaceticus 6A], "cazy 302574154 gb ADL41945.1  glycosidase related protein [Caldicellulosiruptor obsidiansis OB47], "cazy 311774639 gb ADQ04126.1  glycosidase related protein [Caldicellulosiruptor owensensis OL], "cazy 145409466 gb ABP66470.1  glycosidase"," PH1107-related protein [Caldicellulosiruptor saccharolyticus DSM 8903]"]
["cazy 256357926 gb ACU71423.1  glycosidase PH1107-related [Catenuispora acidiphila DSM 44928]"]

["cazygi 256362862 gb ACU76359.1  glycosidase PH1107-related [Catenuispora acidiphila DSM 44928]"]
["cazygi 262335690 gb ACY49487.1  glycosidase PH1107-related protein [Rhodothermus marinus DSM 4252]", "cazygi 345113684 gb AEN74516.1  glycosidase related protein [Rhodothermus marinus SG0.5JP17-172]"]
["cazygi 283437935 gb ADB16377.1  glycosidase PH1107-related protein [Pirellula staleyii DSM 6068]"]
["cazygi 289182776 gb ADC90020.1  glycosidase PH1107-related protein [Thermocrinis albus DSM 14484]"]
["cazygi 290570138 gb ADD43103.1  glycosidase PH1107-related protein [Stackebrandtia nassauensis DSM 44728]"]
["cazygi 290754977 dbj BAI81354.1  conserved hypothetical protein [Deferribacter desulfuricans SSM1]"]
["cazygi 297165045 gb ADI14756.1  glycosidase-related protein [Truepera radiovictrix DSM 17093]"]
["cazygi 309749954 gb ADO84614.1  glycosidase PH1107-related protein (plasmid) [Ilyobacter polytropus DSM 2926]"]
["cazygi 333749895 gb AEF95002.1  glycosidase related protein [Desulfotomaculum nigrificans CO-1-SRB]"]
["cazygi 359825205 gb AEV67978.1  putative glycosylase [[Clostridium] clariflavum DSM 19732]"]
["cazygi 374851343 dbj BAL54306.1  glycosidase [uncultured prokaryote]"]
["cazygi 390624871 gb AFM26078.1  putative glycosylase [Desulfomonile tiedjei DSM 6799]"]
["cazygi 395811041 gb AFN73790.1  Glycosidase [Melioribacter roseus P3M-2]"]
["cazygi 409171345 gb AFV25220.1  hypothetical protein Mpsy_3021 [Methanolobus psychrophilus R15]"]
["cazygi 409171348 gb AFV25223.1  hypothetical protein Mpsy_3024 [Methanolobus psychrophilus R15]"]
["cazygi 488451852 gb AGK98554.1  putative glycosylase [Clostridium pasteurianum BC1]"]
["cazygi 573473034 gb AHF90045.1  glycosidase [Opitutaceae bacterium TAV5]"]
["cazygi 673066667 emb CDZ24022.1  glycosidase-like protein [[Clostridium] cellulosi]"]
["cazygi 763683253 gb AJQ25503.1  glycosidase related protein [Pelosinus fermentans JBW45]"]
["cazygi 805336947 gb AKB18229.1  hypothetical protein MSWHS_1366 [Methanosarcina sp. WWM596]"]
["cazygi 805340529 gb AKB21554.1  hypothetical protein MSWH1_1283 [Methanosarcina sp. WH1]", "cazygi 19916827 gb AAM06213.1  conserved hypothetical protein [Methanosarcina acetivorans C2A]"]
["cazygi 805352552 gb AKB32867.1  hypothetical protein MSSIH_2177 [Methanosarcina siciliae HI350]"]
["cazygi 805356935 gb AKB37006.1  hypothetical protein MSSAC_2416 [Methanosarcina siciliae C2J]", "cazygi 805352369 gb AKB32684.1  hypothetical protein MSSIH_1994 [Methanosarcina siciliae HI350]", "cazygi 805348346 gb AKB28968.1  hypothetical protein MSSIT_2249 [Methanosarcina siciliae T4/M]", "cazygi 805348139 gb AKB28761.1  hypothetical protein MSSIT_2042 [Methanosarcina siciliae T4/M]", "cazygi 19916327 gb AAM05768.1  conserved hypothetical protein [Methanosarcina acetivorans C2A]"]
["cazygi 805357115 gb AKB37186.1  hypothetical protein MSSAC_2596 [Methanosarcina siciliae C2J]"]
["cazygi 805358024 gb AKB38095.1  hypothetical protein MSSAC_3505 [Methanosarcina siciliae C2J]", "cazygi 80533708 gb AKB15341.1  hypothetical protein MSTHC_1023 [Methanosarcina thermophila CHTI-55]", "cazygi 805332062 gb AKB14015.1  hypothetical protein MSTHT_2257 [Methanosarcina thermophila TM-1]"]
["cazygi 805377250 gb AKB73322.1  hypothetical protein MSLAZ_0061 [Methanosarcina lacustris Z-7289]"]
["cazygi 805378839 gb AKB74911.1  hypothetical protein MSLAZ_1650 [Methanosarcina lacustris Z-7289]", "cazygi 805340853 gb AKB21878.1  hypothetical protein MSWH1_1607 [Methanosarcina sp. WH1]", "cazygi 805337275 gb AKB18557.1  hypothetical protein MSWHS_1694 [Methanosarcina sp. WWM596]", "cazygi 805385618 gb AKB81199.1  hypothetical protein MSBR3_0621 [Methanosarcina barkeri 3]"]
["cazygi 805382850 gb AKB78727.1  hypothetical protein MSHOH_2244 [Methanosarcina horonobensis HB-1 = JCM 15518]"]
["cazygi 805383064 gb AKB78941.1  hypothetical protein MSHOH_2458 [Methanosarcina horonobensis HB-1 = JCM 15518]"]
["cazygi 805383132 gb AKB79009.1  hypothetical protein MSHOH_2526 [Methanosarcina horonobensis HB-1 = JCM 15518]"]
["cazygi 805383620 gb AKB79497.1  hypothetical protein MSHOH_3014 [Methanosarcina horonobensis HB-1 = JCM 15518]"]
["cazygi 805386140 gb AKB81721.1  hypothetical protein MSBR3_1143 [Methanosarcina barkeri 3]"]

<p>["cazygi 805395560 gb AKB46392.1  hypothetical protein MSKOL_0615 [Methanosarcina sp. Kolksee]",</p> <p>"cazygi 805330281 gb AKB12234.1  hypothetical protein MSTHT_0476 [Methanosarcina thermophila TM-1]",</p> <p>"cazygi 805391804 gb AKB42902.1  hypothetical protein MSVAZ_0633 [Methanosarcina vacuolata Z-761]"</p>
<p>["cazygi 827039147 gb AKJ63706.1  putative glycoside hydrolase [Verrucomicrobia bacterium L21-Fru-AB]"</p>
<p>["cazygi 827397648 gb AKJ37809.1  glycoside hydrolase GH130 family [Methanosarcina barkeri CM1]",</p> <p>"cazygi 805404860 gb AKB54666.1  hypothetical protein MSBRM_1668 [Methanosarcina barkeri MS]",</p> <p>"cazygi 805400966 gb AKB51486.1  hypothetical protein MSBRW_2233 [Methanosarcina barkeri str. Wiesmoor]",</p> <p>"cazygi 805382254 gb AKB78131.1  hypothetical protein MSHOH_1648 [Methanosarcina horonobensis HB-1 = JCM 15518]",</p> <p>"cazygi 805374689 gb AKB71059.1  hypothetical protein MSMAC_1169 [Methanosarcina mazei C16]",</p> <p>"cazygi 805374875 gb AKB71245.1  hypothetical protein MSMAC_1355 [Methanosarcina mazei C16]",</p> <p>"cazygi 20907400 gb AAM32467.1  conserved protein [Methanosarcina mazei Go1]",</p> <p>"cazygi 805371788 gb AKB68522.1  hypothetical protein MSMAL_1979 [Methanosarcina mazei LYC]",</p> <p>"cazygi 805371248 gb AKB67982.1  hypothetical protein MSMAL_1439 [Methanosarcina mazei LYC]",</p> <p>"cazygi 805368039 gb AKB65151.1  hypothetical protein MSMAS_1955 [Methanosarcina mazei S-6]",</p> <p>"cazygi 805364558 gb AKB61832.1  hypothetical protein MSMAP_1847 [Methanosarcina mazei SarPi]",</p> <p>"cazygi 452101160 gb AGF98100.1  hypothetical protein MmTuc01_2818 [Methanosarcina mazei Tuc01]",</p> <p>"cazygi 805361070 gb AKB40859.1  hypothetical protein MSMAW_1868 [Methanosarcina mazei WWM610]",</p> <p>"cazygi 805396668 gb AKB47500.1  hypothetical protein MSKOL_1723 [Methanosarcina sp. Kolksee]",</p> <p>"cazygi 805392925 gb AKB44023.1  hypothetical protein MSVAZ_1754 [Methanosarcina vacuolata Z-761]",</p> <p>"cazygi 805408088 gb AKB57251.1  hypothetical protein MSBR2_0735 [Methanosarcina barkeri 227]"</p>
<p>["cazygi 85722651 gb ABC77594.1  hypothetical cytosolic protein [Syntrophus aciditrophicus SB]"</p>
<p>["cazygi 921146216 dbj BAS29302.1  glycosidase [Limnochorda pilosa]"</p>
<p>["cazygi 973198458 gb ALX07675.1  glycosidase related protein [Ruminiclostridium thermocellum AD2]",</p> <p>"cazygi 125715815 gb ABN54307.1  glycosidase related protein [Ruminiclostridium thermocellum ATCC 27405]",</p> <p>"cazygi 316939711 gb ADU73745.1  glycosidase related protein [Ruminiclostridium thermocellum DSM 1313]",</p> <p>"cazygi 1046311829 gb ANV5417.1  glycosidase related protein [Ruminiclostridium thermocellum DSM 2360]"</p>
<p>["cazy AOP33799.1 glycosidase [Leptospira alstonii]"</p>
<p>["cazy APF17755.1 putative glycosyl hydrolase", "GH43/DUF377 family [Caldithrix abyssi DSM 13497]"</p>
<p>["cazy APF19181.1 putative glycosyl hydrolase", "GH43/DUF377 family [Caldithrix abyssi DSM 13497]"</p>
<p>["cazy APZ94252.1 Beta-1", "4-mannooligosaccharide phosphorylase [Fuerstia marisgermanicae]"</p>
<p>["cazy AQO6985.1 Beta-1", "4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium SM-Chi-D1]"</p>
<p>["cazy AQO75139.1 hypothetical protein [uncultured bacterium]"</p>
<p>["cazy AQT67267.1 Beta-1", "4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium ST-NAGAB-D1]"</p>
<p>["cazy AQT69233.1 Beta-1", "4-mannooligosaccharide phosphorylase [Phycisphaerae bacterium ST-NAGAB-D1]"</p>
<p>["cazy ARU40590.1 glycosidase [Armatimonadetes bacterium Uphv1-Ar1]"</p>
<p>["cazy AVM45738.1 glycosidase [Victivallales bacterium CCUG 44730]",</p> <p>"humangut340101.Vvad_PD1643 [Complete]:- codon-table.11]"</p>
<p>["cazy AVM46485.1 glycosidase [Victivallales bacterium CCUG 44730]"</p>
<p>["cazy AWB09627.1 putative glycosyl hydrolase", "GH43/DUF377 family [Thermodesulfobium acidiphilum]",</p> <p>"cazygi 332178210 gb AEE13899.1  glycosidase related protein [Thermodesulfobium narugense DSM 14796]"</p>
<p>["cazy AWB09634.1 putative glycosyl hydrolase", "GH43/DUF377 family [Thermodesulfobium acidiphilum]",</p> <p>"cazygi 332178216 gb AEE13905.1  glycosidase related protein [Thermodesulfobium narugense DSM 14796]"</p>
<p>["cazy AXC09803.1 putative glycoside hydrolase [Acidobacteriaceae bacterium SBC82]"</p>

<p>["cazy AYK13833.1 glycosidase [Methanosarcina flavescens]",</p> <p>"cazy BAW29818.1 conserved hypothetical protein [Methanosarcina thermophila]",</p> <p>"cazygi 827397862 gb AKJ38023.1  glycoside hydrolase GH130 family [Methanosarcina barkeri CM1]",</p> <p>"cazygi 805404638 gb AKB54444.1  hypothetical protein MSBRM_1446 [Methanosarcina barkeri MS]",</p> <p>"cazygi 72397404 gb AAZ71677.1  conserved hypothetical protein [Methanosarcina barkeri str. Fusaro]",</p> <p>"cazygi 805400684 gb AKB51204.1  hypothetical protein MSBRW_1951 [Methanosarcina barkeri str. Wiesmoor]",</p> <p>"cazygi 940663404 gb ALK06238.1  glycosidase [Methanosarcina sp. 795]",</p> <p>"cazygi 805396749 gb AKB47581.1  hypothetical protein MSKOL_1804 [Methanosarcina sp. Kolksee]",</p> <p>"cazygi 805332992 gb AKB14625.1  hypothetical protein MSTHC_0307 [Methanosarcina thermophila CHTI-55]",</p> <p>"cazygi 805330219 gb AKB12172.1  hypothetical protein MSTHT_0414 [Methanosarcina thermophila TM-1]",</p> <p>"cazygi 805392998 gb AKB44096.1  hypothetical protein MSVAZ_1827 [Methanosarcina vacuolata Z-761]",</p> <p>"cazygi 805408310 gb AKB57473.1  hypothetical protein MSBR2_0957 [Methanosarcina barkeri 227]"</p>
<p>["cazy AYK14555.1 glycosidase [Methanosarcina flavescens]"]</p>
<p>["cazy AYK15987.1 glycosidase [Methanosarcina flavescens]",</p> <p>"cazy BAW29922.1 conserved hypothetical protein [Methanosarcina thermophila]",</p> <p>"cazygi 805385660 gb AKB81241.1  hypothetical protein MSBR3_0663 [Methanosarcina barkeri 3]",</p> <p>"cazygi 827397595 gb AKJ37756.1  glycoside hydrolase GH130 family [Methanosarcina barkeri CM1]",</p> <p>"cazygi 805404919 gb AKB54725.1  hypothetical protein MSBRM_1727 [Methanosarcina barkeri MS]",</p> <p>"cazygi 72397752 gb AAZ72025.1  conserved hypothetical protein [Methanosarcina barkeri str. Fusaro]",</p> <p>"cazygi 805400332 gb AKB50852.1  hypothetical protein MSBRW_1599 [Methanosarcina barkeri str. Wiesmoor]",</p> <p>"cazygi 940663319 gb ALK06153.1  glycosidase [Methanosarcina sp. 795]",</p> <p>"cazygi 805396382 gb AKB47214.1  hypothetical protein MSKOL_1437 [Methanosarcina sp. Kolksee]",</p> <p>"cazygi 805332930 gb AKB14563.1  hypothetical protein MSTHC_0245 [Methanosarcina thermophila CHTI-55]",</p> <p>"cazygi 805392665 gb AKB43763.1  hypothetical protein MSVAZ_1494 [Methanosarcina vacuolata Z-761]",</p> <p>"cazygi 805408031 gb AKB57194.1  hypothetical protein MSBR2_0678 [Methanosarcina barkeri 227]"</p>
<p>["cazy BAW29060.1 conserved hypothetical protein [Methanosarcina thermophila]"]</p>
<p>["cazy SCD20033.1 Glycosyl hydrolase family 43 [Proteiniphilum saccharofermentans]",</p> <p>"cazygi 50877343 emb CAG37183.1  conserved hypothetical protein [Desulfotalea psychrophila Lsv54]"</p>
<p>["cazy SDE97465.1 Predicted glycosyl hydrolase"," GH43/DUF377 family [Terriglobus roseus]"]</p>
<p>["humangut158499257-stool2_revised_scaffold72074_1_gene141523 strand:+ start:690 stop:1607 length:918 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut159571453-stool2_revised_C1123888_1_gene199483 strand:+ start:362 stop:928 length:567 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]</p>
<p>["humangut160400887-stool1_revised_C1477000_1_gene247217 strand:- start:446 stop:1270 length:825 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]</p>
<p>["humangut340101.Vvad_PD1241 [Complete]:- codon-table.11"]</p>
<p>["humangut340101.Vvad_PD2400 [Complete]:- codon-table.11"]</p>
<p>["humangut764062976-stool1_revised_scaffold23685_2_gene105148 strand:+ start:4207 stop:5172 length:966 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangut764062976-stool1_revised_scaffold27403_3_gene37791 strand:- start:76 stop:1032 length:957 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]</p>
<p>["humangutMH0169_GL0139631 [gene] locus=scaffold64081_2:2:439:+ [Lack 5'-end] codon-table.11"]</p>
<p>["humangutMH0193_GL0131665 [gene] locus=scaffold32408_2:358:924:+ [Lack 3'-end] codon-table.11"]</p>
<p>["humangutMH0262_GL0072459 [gene] locus=scaffold88337_1:263:739:+ [Lack 3'-end] codon-table.11"]</p>

["humangutMH0309_GL0085017 [gene] locus=scaffold22344_10:439:1359:- [Complete] codon-table.11"]
["humangutMH0354_GL0034140 [gene] locus=scaffold11732_2:2405:3403:+ [Complete] codon-table.11", "pigEYZ-353B_GL0113613 [gene] locus=scaffold101503_1:566:1564:+ [Complete] codon-table.11", "rumen552_GL0643663_1 [gene] locus=scaffold1113893_1:2767:3765:-[Complete]"]
["humangutMH0373_GL0093988 [gene] locus=scaffold47371_4:64:1038:- [Complete] codon-table.11", "humangut764062976-stool1_revised_scaffold9809_2_gene2100 strand:- start:3175 stop:4149 length:975 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangutMH0406_GL0074073 [gene] locus=scaffold65977_5:374:904:+ [Lack 3'-end] codon-table.11"]
["humangutMH0409_GL0192637 [gene] locus=scaffold117421_1:1:468:- [Lack 3'-end] codon-table.11"]
["humangutMH0428_GL0177607 [gene] locus=scaffold57726_11:1695:2264:- [Lack 5'-end] codon-table.11"]
["humangutO2_UC40-1_GL0040994 [gene] locus=scaffold18544_1:2:892:+ [Lack 5'-end] codon-table.11"]
["humangutO2_UC58-0_GL0161340 [gene] locus=scaffold17208_5:228:1049:- [Lack 5'-end] codon-table.11"]
["humangutT2D-51A_GL0093383 [gene] locus=scaffold93772_1:2:556:- [Lack both ends] codon-table.11"]
["humangutV1_CD15-3_GL0040164 [gene] locus=scaffold49695_3:2:484:+ [Lack 5'-end] codon-table.11"]
["humangutV1_FI04_GL0203609 [gene] locus=scaffold17882_4:1:831:- [Lack 3'-end] codon-table.11"]
["humangutV1_FI14_GL0222358 [gene] locus=scaffold137474_3:3308:4282:- [Complete] codon-table.11", "cazygi 281315545 gb EFA99573.1  glycosidase PH1107-related protein [Victivallis vadensis ATCC BAA-548]"]
["pigDB-515B_GL0232700 [gene] locus=scaffold150890_7:564:1295:- [Lack 5'-end] codon-table.11"]
["pigPIG-109_GL0047844 [gene] locus=C1990877_1:1:483:- [Lack 3'-end] codon-table.11"]
["rumen100058_GL0983401_1 [gene] locus=scaffold3190690_1:24:965:+[Complete]"]
["rumen3042_GL0702297_1 [gene] locus=scaffold35316_6:241:1191:-[Complete]"]
["rumen3042_GL0999342_1 [gene] locus=scaffold80553_1:1918:2763:+[Lack 3'-end]"]
["rumen553_GL0472450_1 [gene] locus=scaffold411084_3:1515:2471:+[Complete]"]
["rumen554_GL0240044_1 [gene] locus=scaffold1516873_2:6503:7441:+[Complete]"]
["rumen7049_GL0107992_1 [gene] locus=scaffold2024283_2:43:975:+[Complete]"]

## UC4

["humangut158256496-stool1_revised_scaffold18980_2_gene38785 strand:+ start:341 stop:1132 length:792 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut764487809-stool1_revised_scaffold4689_2_gene42041 strand:+ start:6929 stop:7918 length:990 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11", "rumen553_GL0826154_1 [gene] locus=scaffold435537_1:3775:4764:-[Complete]"]
["humangutDLF004_GL0016933 [gene] locus=scaffold19599_3:8945:9850:+ [Complete] codon-table.11"]
["humangutDLM008_GL0061961 [gene] locus=scaffold44391_5:188:1057:- [Lack 5'-end] codon-table.11"]
["humangutED50A_GL0000867 [gene] locus=scaffold25008_1:46810:47682:- [Complete] codon-table.11"]
["humangutMH0011_GL0029022 [gene] locus=scaffold7568_3:2672:3619:- [Complete] codon-table.11"]
["humangutMH0096_GL0061141 [gene] locus=scaffold22077_6:4857:5867:- [Complete] codon-table.11"]
["humangutMH0101_GL0067829 [gene] locus=scaffold4763_8:26:1069:- [Complete] codon-table.11"]
["humangutMH0138_GL0002739 [gene] locus=scaffold19519_1:3272:4231:+ [Complete] codon-table.11"]
["humangutMH0189_GL0091319 [gene] locus=scaffold110197_1:1:651:- [Lack 3'-end] codon-table.11"]
["humangutMH0229_GL0107614 [gene] locus=scaffold25401_13:56:1099:+ [Complete] codon-table.11"]
["humangutMH0233_GL0013042 [gene] locus=scaffold9523_29:3585:4604:+ [Complete] codon-table.11"]
["humangutMH0233_GL0013043 [gene] locus=scaffold9523_29:4595:5641:+ [Complete] codon-table.11",

"humangutMH0372_GL0056056 [gene] locus=scaffold81346_1:7107:8153:+ [Complete] codon-table.11"
"humangutMH0233_GL0013044 [gene] locus=scaffold9523_29:5665:6690:+ [Complete] codon-table.11"
"humangutMH0238_GL0120931 [gene] locus=scaffold18048_4:1:933:- [Lack 3'-end] codon-table.11"
"humangutMH0276_GL0165020 [gene] locus=scaffold116114_1:580:1617:- [Complete] codon-table.11"
"humangutMH0297_GL0042092 [gene] locus=scaffold24105_11:560:1507:- [Complete] codon-table.11"
"humangutMH0326_GL0077808 [gene] locus=scaffold34917_6:2:562:+ [Lack 5'-end] codon-table.11"
"humangutMH0432_GL0017216 [gene] locus=scaffold74274_2:677:1486:- [Complete] codon-table.11"
"humangutMH0435_GL0128647 [gene] locus=scaffold48848_1:16702:17736:- [Complete] codon-table.11"
"humangutMH0441_GL0072164 [gene] locus=scaffold106162_2:2:508:+ [Lack 5'-end] codon-table.11"
"humangutMH0454_GL0224663 [gene] locus=scaffold167705_1:236:1120:- [Complete] codon-table.11"
"humangutN037A_GL0076705 [gene] locus=scaffold96827_1:5901:6863:+ [Complete] codon-table.11"
"humangutO2.UC12-2_GL0019987 [gene] locus=scaffold36507_5:3:1058:+ [Lack 5'-end] codon-table.11"
"humangutO2.UC18-1_GL0145511 [gene] locus=scaffold115526_2:805:1779:- [Complete] codon-table.11"
"humangutT2D-2A_GL0003884 [gene] locus=scaffold30816_1:16212:17159:+ [Complete] codon-table.11"
"humangutT2D-52A_GL0026708 [gene] locus=scaffold15908_6:203:1180:- [Complete] codon-table.11"
"humangutV1.CD6-0-PT_GL0147720 [gene] locus=scaffold69971_1:1:807:- [Lack 3'-end] codon-table.11"
"humangutV1.FI02_GL0025090 [gene] locus=scaffold94077_2:2:880:- [Lack 3'-end] codon-table.11"
"humangutV1.F114_GL0038492 [gene] locus=scaffold50057_15:4786:5721:- [Complete] codon-table.11"
"mouse10_GL0091524 [gene] locus=C802032_1:5542:6492:+ [Complete] codon-table.11"
"mouse3-3_GL0099932 [gene] locus=scaffold6365_18:4177:5181:- [Complete] codon-table.11"
"pigPIG-011_GL0184940 [gene] locus=scaffold11862_1:595:1548:+ [Complete] codon-table.11",
"pigPIG-039_GL0245309 [gene] locus=scaffold203270_1:210:1163:- [Complete] codon-table.11"
"pigPIG-017_GL0015599 [gene] locus=scaffold31147_1:1:624:- [Lack both ends] codon-table.11"
"pigPIG-099_GL0057693 [gene] locus=scaffold18816_2:414:1427:- [Complete] codon-table.11"
"pigPIG_197_GL0235305 [gene] locus=scaffold185672_1:2:748:+ [Lack 5'-end] codon-table.11"
"rumen0081_GL0027620_1 [gene] locus=scaffold536563_4:510:2939:- [Complete]"
"rumen0081_GL1034664_1 [gene] locus=scaffold1911713_1:79:1101:- [Complete]"
"rumen0081_GL1803283_1 [gene] locus=scaffold257285_1:3:1214:- [Lack both ends]"
"rumen0081_GL2504083_1 [gene] locus=scaffold96095_1:1488:2501:- [Complete]"
"rumen100058_GL0373208_1 [gene] locus=scaffold2313431_1:2:523:- [Lack both ends]"
"rumen100058_GL1078658_1 [gene] locus=scaffold177350_4:1:927:+ [Lack 5'-end]"
"rumen100058_GL1435802_1 [gene] locus=scaffold1536970_3:2:619:+ [Lack both ends]"
"rumen100058_GL1531659_1 [gene] locus=scaffold1737296_1:1703:2590:- [Complete]"
"rumen100058_GL2234764_1 [gene] locus=scaffold2839642_2:5632:6543:+ [Complete]"
"rumen100058_GL2690309_1 [gene] locus=scaffold247893_2:798:1784:- [Complete]"
"rumen100058_GL3224210_1 [gene] locus=scaffold1847454_2:2:1045:+ [Lack 5'-end]"
"rumen2009040_GL0393904_1 [gene] locus=scaffold1386324_1:2515:3567:+ [Complete]"
"rumen2009040_GL0435555_1 [gene] locus=scaffold22983_2:27115:28026:- [Complete]"
"rumen2009040_GL0597183_1 [gene] locus=scaffold1642628_1:108:1010:+ [Complete]",
"rumen7049_GL0623453_1 [gene] locus=scaffold46047_2:3:905:+ [Lack 5'-end]"
"rumen2009040_GL0734912_1 [gene] locus=scaffold3035117_1:3:830:- [Lack both ends]"
"rumen2009040_GL1002494_1 [gene] locus=scaffold2437775_1:2:2122:- [Lack both ends]"
"rumen2009040_GL2571825_1 [gene] locus=scaffold768466_11:487:1413:- [Complete]"

["rumen2009040_GL3531709_1 [gene] locus=scaffold1886671_1:2142:2930:-[Complete]"]
["rumen3042_GL0041832_1 [gene] locus=scaffold1574742_2:1:1044:+[Lack 5'-end]"]
["rumen3042_GL0756330_1 [gene] locus=scaffold1795046_1:808:1719:-[Lack 5'-end]"]
["rumen3042_GL1432874_1 [gene] locus=scaffold2032861_1:2:634:+[Lack 5'-end]"]
["rumen3042_GL1702200_1 [gene] locus=C52378453_1:3:986:-[Lack 3'-end]"]
["rumen552_GL0306419_1 [gene] locus=scaffold372819_1:1160:12134:+[Complete]"]
["rumen552_GL0725128_1 [gene] locus=scaffold25472_4:71:943:+[Lack 3'-end]"]
["rumen552_GL0980381_1 [gene] locus=scaffold844410_1:8463:9398:-[Complete]"]
["rumen552_GL1270477_1 [gene] locus=C21838829_1:1:843:+[Lack both ends]"]
["rumen552_GL1612692_1 [gene] locus=scaffold222006_1:5081:6076:-[Complete]"]
["rumen553_GL0125182_1 [gene] locus=scaffold31694_2:2:787:-[Lack both ends]"]
["rumen553_GL0195818_1 [gene] locus=scaffold297294_2:52:1029:-[Complete]"]
["rumen553_GL0432390_1 [gene] locus=scaffold311754_6:810:1688:-[Complete]"]
["rumen554_GL0058843_1 [gene] locus=scaffold2186748_1:1:1608:-[Lack 3'-end]"]
["rumen554_GL0242537_1 [gene] locus=C39321293_1:1:537:+[Lack both ends]"]
["rumen554_GL0767578_1 [gene] locus=scaffold692326_7:242:1228:+[Complete]"]
["rumen554_GL1013538_1 [gene] locus=scaffold867912_4:1:882:-[Lack 3'-end]"]
["rumen554_GL1726577_1 [gene] locus=scaffold343966_3:1:531:-[Lack both ends]"]
["rumen554_GL2509294_1 [gene] locus=scaffold1971782_2:3:932:-[Lack 3'-end]"]
["rumen555_GL0472243_1 [gene] locus=scaffold232364_3:1509:3149:+[Lack 3'-end]"]
["rumen555_GL1429890_1 [gene] locus=scaffold1399540_1:80073:82535:+[Complete]"]
["rumen555_GL1580868_1 [gene] locus=scaffold7995_4:1113:2063:+[Complete]"]
["rumen555_GL1941667_1 [gene] locus=scaffold624502_1:1:930:-[Lack 3'-end]"]
["rumen555_GL2055061_1 [gene] locus=scaffold426608_1:3:542:-[Lack both ends]"]
["rumen555_GL2075599_1 [gene] locus=scaffold1570648_1:3117:4145:-[Complete]"]
["rumen583_GL0511310_1 [gene] locus=scaffold35205_7:5214:6182:+[Complete]"]
["rumen7049_GL0076584_1 [gene] locus=C53231994_1:302:1351:-[Complete]"]
["rumen7049_GL0127006_1 [gene] locus=scaffold1138997_2:3:734:+[Lack both ends]"]
["rumen7049_GL0214725_1 [gene] locus=scaffold1751583_1:1745:2773:+[Complete]"]
["rumen7049_GL0472254_1 [gene] locus=scaffold846035_1:3:1142:-[Lack both ends]"]
["rumen7049_GL0484382_1 [gene] locus=scaffold1272497_2:3:637:6123:-[Complete]"]
["rumen7049_GL0871356_1 [gene] locus=scaffold12802_1:1:1062:-[Lack 3'-end]"]
["rumen7049_GL2287543_1 [gene] locus=scaffold459179_2:1:669:+[Lack both ends]"]
["rumen7049_GL2483910_1 [gene] locus=scaffold1417062_1:1673:2695:-[Lack 5'-end]"]

## UC5

["cazygi 1001868162 gb AMM34648.1  glycosidase [Sinomonas atrocyanea]"]
["cazygi 1008898328 gb AMR29993.1  glycosidase [Mucilaginibacter sp. PAMC 26640]"]
["cazygi 1008898478 gb AMR30143.1  glycosidase [Mucilaginibacter sp. PAMC 26640]"]
["cazygi 1042050605 gb ANP72493.1  glycosidase [Cryobacterium arcticum]"]
["cazygi 116612543 gb ABK05267.1  glycosidase", " PH1107-related protein [Arthrobacter sp. FB24]"]
["cazygi 283808896 gb ADB30735.1  glycosidase PH1107-related protein [Kribbella flavida DSM 17836]"]



["cazy 344036218 gb AEM81943.1  glycosidase related protein [Streptomyces violaceusniger Tu 4113]"
["cazy 430014651 gb AGA26365.1  putative glycosylase [Singulisphaera acidiphila DSM 18658]"
["cazy 430015464 gb AGA27178.1  putative glycosylase [Singulisphaera acidiphila DSM 18658]"
["cazy 910742044 dbj BAS11444.1  beta-1", "4-mannooligosaccharide phosphorylase [Arthrobacter sp. Hiyo4]"
["cazy 910746572 dbj BAS15971.1  beta-1", "4-mannooligosaccharide phosphorylase [Arthrobacter sp. Hiyo8]"
["cazy 91802586 gb ABE64959.1  glycosidase", " PH1107-related (plasmid) [Nitrobacter hamburgensis X14]"
["cazy 927296265 gb ALE07716.1  glycosidase [Arthrobacter sp. ERGS1:01]"
["cazy 941977275 gb ALL08704.1  glycosidase [Pedobacter sp. PACM 27299]"
["cazy 971341525 gb ALV41709.1  glycosidase [Pseudarthrobacter sulfonivorans]"
["cazy AQP47186.1  glycosidase [Tessaracoccus aquimaris]"
["cazy AQU71430.1  glycosidase [Streptomyces niveus]"
["cazy ARC55674.1 1", "4-beta-mannosyl-N-acetylglucosamine phosphorylase [Frondehabitans sp. 762G35]", "cazy SDH28511.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 197AMF]", "cazy SDJ09728.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 466MF]", "cazy SDJ60848.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 157MF]", "cazy SDN30974.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 509MF]", "cazy SEM90328.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 467MF]", "cazy SFM34653.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 98AMF]", "cazy 1029984076 gb ANF30333.1  glycosidase [Leifsonia xylif]"
["cazy ARJ03840.1  glycosidase [Cnubacter physcomitrella]", "cazy AWB90245.1  glycosidase [Salinibacterium sp. CGMCC 1.16371]", "cazy AXH34393.1  glycosidase [Humibacter sp. BT305]", "cazy SDH54002.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Microbacterium pygmaeum]"
["cazy ARU52422.1  glycosidase [Cellulosimicrobium cellulans]"
["cazy ASD21953.1  glycosidase [Cryobacterium sp. LW097]", "cazy SDT27368.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Jiangella sp. DSM 45060]"
["cazy ATL88355.1  putative glycosidase [Streptomyces malaysiensis]", "cazy AUA08447.1  Beta-1", "4-mannooligosaccharide phosphorylase [Streptomyces sp. M56]", "cazy 521355665 gb AGP53982.1  hypothetical protein M271_11925 [Streptomyces rapamycinicus NRRL 5491]" "cazy 822597516 gb AKH86411.1  glycosidase [Streptomyces sp. CNQ-509]"
["cazy AVH60180.1  glycosidase [Streptomyces dengpaensis]", "cazy AVH60610.1  glycosidase [Streptomyces dengpaensis]", "cazy AWW41409.1  glycosidase [Streptomyces sp. ZFG47]", "cazy AWZ03955.1  glycosidase [Streptomyces sp. ICC4]", "cazy AWZ11467.1  glycosidase [Streptomyces sp. ICC1]"
["cazy AWB88056.1  glycosidase [Mycetocola sp. 449]"
["cazy SCF17406.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Micromonospora viridifaciens]"
["cazy SCY64477.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Microbacterium sp. LKL04]", "cazy 545576718 gb AGW41830.1  glycosidase-related protein [Leifsonia xylif subsp. cynodontis DSM 46306]", "cazy 323273515 dbj BAJ73660.1  predicted glycosylase [Microbacterium testaceum StLB037]"
["cazy SDH07407.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 197AMF]", "cazy SDJ32740.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 466MF]", "cazy SDK47187.1  Predicted glycosyl hydrolase", " GH43/DUF377 family [Leifsonia sp. 157MF]"

"cazy SDN53817.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Leifsonia sp. 509MF]",
"cazy SEB07343.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Leifsonia sp. 21MFCrub1.1]",
"cazy SEN56279.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Leifsonia sp. 467MF]",
"cazy SFM73071.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Leifsonia sp. 98AMF]"
["cazy SDP38023.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Nakamurella panacisegetis]"]
["cazy SDS31711.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Friedmanniella luteola]"
["cazy SDS49464.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Agromyces flavus]"
["cazy SDS60844.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Mucilagibacter mallensis]"
["cazy SDT01232.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Actinopolymorpha singaporensis]"
["cazy SDU66583.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Jiangella alkaliphila]"
["cazy SDV02219.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Friedmanniella sagamiharensis]"
["cazy SEA91313.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Leifsonia sp. 21MFCrub1.1]"

## UC6

["humangut158499257-stool2_revised_scaffold72385_2_gene82008 strand:- start:4781 stop:5743 length:963 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11",  "humangut160400887-stool1_revised_C1502255_1_gene51724 strand:+ start:328 stop:1290 length:963 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangut159227541-stool2_revised_scaffold7276_1_gene122964 strand:- start:8251 stop:9252 length:1002 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["humangutMH0142_GL0034722 [gene] locus=scaffold9349_11:2:613:+ [Lack both ends] codon-table.11"]
["humangutMH0197_GL0140065 [gene] locus=scaffold35217_1:127:1110:- [Lack 5'-end] codon-table.11"]
["humangutMH0262_GL0139398 [gene] locus=scaffold85419_2:464:1021:- [Lack 5'-end] codon-table.11"]
["humangutMH0318_GL0049685 [gene] locus=scaffold118166_3:2:568:+ [Lack 5'-end] codon-table.11"]
["humangutMH0336_GL0012146 [gene] locus=scaffold109992_1:2:1000:- [Lack 3'-end] codon-table.11"]
["humangutMH0346_GL0101425 [gene] locus=scaffold14559_10:1:672:+ [Lack 5'-end] codon-table.11"]
["humangutMH0346_GL0103563 [gene] locus=C1364741_1:3:557:- [Lack both ends] codon-table.11"]
["humangutMH0409_GL0096961 [gene] locus=scaffold22078_3:531:1487:+ [Complete] codon-table.11"]
["humangutMH0409_GL0137711 [gene] locus=scaffold120846_1:2:1210:+ [Lack 5'-end] codon-table.11"]
["humangutMH0454_GL0227900 [gene] locus=scaffold62405_1:3:617:+ [Lack both ends] codon-table.11"]
["humangutO2_UC40-1_GL0171371 [gene] locus=scaffold40152_4:210:845:+ [Lack 3'-end] codon-table.11"]
["humangutO2_UC40-1_GL0222073 [gene] locus=scaffold34346_1:2:622:+ [Lack both ends] codon-table.11"]
["humangutO2_UC47-1_GL0051376 [gene] locus=scaffold80731_1:3458:4300:- [Complete] codon-table.11"]
["humangutO2_UC52-0_GL0022652 [gene] locus=scaffold28367_2:644:1597:- [Complete] codon-table.11"]
["humangutO2_UC58-0_GL0126372 [gene] locus=scaffold45505_2:3:575:- [Lack both ends] codon-table.11"]
["humangutV1_FI14_GL0104269 [gene] locus=scaffold85970_10:338:1297:- [Complete] codon-table.11"]
["humangutV1_UC59-0_GL0148453 [gene] locus=scaffold69280_1:2:601:+ [Lack 5'-end] codon-table.11"]
["pigPIG_113_GL0207321 [gene] locus=scaffold195580_2:3286:4218:+ [Complete] codon-table.11"]
["rumen0081_GL2480971_1 [gene] locus=scaffold1973809_4:2:604:-[Lack 3'-end]"]
["rumen3042_GL0125898_1 [gene] locus=scaffold342906_4:1502:2467:-[Complete]"]
["rumen3042_GL1087710_1 [gene] locus=scaffold2375413_1:1:507:-[Lack both ends]"]
["rumen3042_GL1135338_1 [gene] locus=scaffold2541626_1:2906:3877:-[Complete]"]
["rumen3042_GL1910308_1 [gene] locus=scaffold2307581_1:1:609:-[Lack both ends]"]

["rumen3042_GL2776489_1 [gene] locus=scaffold1309776_2:2:853:+[Lack 5'-end]"]
["rumen3042_GL2791217_1 [gene] locus=scaffold1001623_4:394:1302:+[Lack 3'-end]"]
["rumen554_GL0416144_1 [gene] locus=scaffold1978920_1:1946:2905:+[Complete]"]
["rumen554_GL2903134_1 [gene] locus=scaffold597931_9:1172:1801:+[Lack 3'-end]"]
["rumen7049_GL0087913_1 [gene] locus=C53044636_1:187:1155:+[Lack 3'-end]"]
["rumen7049_GL0628403_1 [gene] locus=C51084884_1:2:499:-[Lack both ends]"]

## UC7

["cazygi 378569207 gb AFC29517.1  hypothetical protein PM3016_2635 [Paenibacillus mucilaginosus 3016], "cazygi 384090260 gb AFH61696.1  hypothetical protein B2K_13370 [Paenibacillus mucilaginosus K02], "cazygi 336297832 gb AEI40935.1  conserved hypothetical protein [Paenibacillus mucilaginosus KNP414]"]
["cazygi 573474722 gb AHF91733.1  hypothetical protein OPIT5_17390 [Opitutaceae bacterium TAV5]"]
["cazygi 686517651 gb AIQ28352.1  hypothetical protein P40081_09285 [Paenibacillus sp. FSL P4-0081]"]
["cazygi 686537905 gb AIQ48603.1  hypothetical protein R70723_23855 [Paenibacillus sp. FSL R7-0273], "cazygi 686543392 gb AIQ54089.1  hypothetical protein R70331_22850 [Paenibacillus sp. FSL R7-0331]"]
["cazygi 686546435 gb AIQ57131.1  hypothetical protein PBOR_09450 [Paenibacillus borealis], "cazygi 686529384 gb AIQ40083.1  hypothetical protein R50912_08590 [Paenibacillus sp. FSL R5-0912]"]
["humangut340101.Vvad_PD3074 [Complete]:- codon-table.11"]
["humangutMH0189_GL0091337 [gene] locus=scaffold66450_2:12028:13188:+ [Complete] codon-table.11"]
["humangutMH0206_GL0063663 [gene] locus=scaffold45456_2:2:736:+ [Lack both ends] codon-table.11"]
["humangutMH0431_GL0078632 [gene] locus=scaffold30057_3:3:620:+ [Lack 5'-end] codon-table.11"]
["humangutO2_UC29-1_GL0090695 [gene] locus=scaffold46262_2:1:762:- [Lack 3'-end] codon-table.11"]
["humangutO2_UC41-0_GL0042946 [gene] locus=scaffold31328_15:3:1133:- [Lack 3'-end] codon-table.11"]
["mouseG1-8A_GL0038729 [gene] locus=scaffold17912_1:1303:2508:- [Complete] codon-table.11"]
["pigPIG-042_GL0086388 [gene] locus=scaffold104638_3:889:1515:- [Lack 5'-end] codon-table.11"]
["pigPIG-046_GL0013240 [gene] locus=scaffold81578_4:125:1333:- [Complete] codon-table.11"]
["pigPIG-046_GL0176179 [gene] locus=scaffold14074_9:823:1977:+ [Complete] codon-table.11"]
["pigPIG-076_GL0179006 [gene] locus=scaffold125115_1:179:814:+ [Lack 3'-end] codon-table.11"]
["rumen0081_GL2147510_1 [gene] locus=scaffold1507797_2:605:1633:+[Lack 3'-end]"]
["rumen0081_GL2215322_1 [gene] locus=scaffold643617_3:2:916:+[Lack both ends]"]
["rumen3042_GL0867394_1 [gene] locus=scaffold1159051_2:399:1604:-[Complete]"]
["rumen3042_GL1213105_1 [gene] locus=scaffold828639_5:2:1075:-[Lack 3'-end]"]
["rumen3042_GL2237420_1 [gene] locus=scaffold311030_1:3:950:+[Lack 5'-end]"]
["rumen552_GL1306643_1 [gene] locus=scaffold643874_3:1:612:-[Lack 3'-end]"]
["rumen552_GL1309865_1 [gene] locus=scaffold231265_1:961:2169:+[Complete]"]
["rumen552_GL1412182_1 [gene] locus=scaffold1105037_1:309:1238:+[Lack 3'-end]"]
["rumen554_GL2480060_1 [gene] locus=scaffold874753_1:498:1718:-[Complete]"]
["rumen583_GL0634395_1 [gene] locus=scaffold581_1:303:1229:-[Lack 5'-end]"]
["rumen583_GL0642444_1 [gene] locus=scaffold88451_1:5910:7130:+[Complete]"]
["rumen7049_GL1849370_1 [gene] locus=scaffold855161_2:1027:2397:+[Complete]"]
["rumen7049_GL2458338_1 [gene] locus=scaffold2170225_1:1:621:+[Lack both ends]"]

## UC8

"Ncazy AOC96266.1 Beta-1", "4-mannooligosaccharide phosphorylase [Flavobacterium anhuiense]", "cazy AXB59105.1 pesticidal protein Cry7Aa [Flavobacterium sp. HYN0086]"
"cazygi 1012308368 gb AMS26787.1  pesticidal protein Cry7Aa [Bacteroidetes bacterium UKL13-3]"
"cazygi 146156290 gb ABQ07144.1  protein of unknown function [Flavobacterium johnsoniae UW101]"
"cazygi 146156465 gb ABQ07319.1  protein of unknown function [Flavobacterium johnsoniae UW101]"
"cazygi 312444444 gb ADQ80800.1  glycosidase related protein [Paludibacter propionigenes WB4]"
"cazygi 324972948 gb ADY51932.1  glycosidase related protein [Pseudopedobacter saltans DSM 12145]"
"cazygi 332336403 gb AEE53504.1  glycosidase related protein [Haliscomenobacter hydrossis DSM 1100]"
"cazygi 674273058 dbj BAP32451.1  glycosidase [Chryseobacterium sp. StRB126]"
"cazygi 941975621 gb ALL07050.1  pesticidal protein Cry7Aa [Pedobacter sp. PACM 27299]", "cazygi 941974835 gb ALL06264.1  pesticidal protein Cry7Aa [Pedobacter sp. PACM 27299]"
"cazygi 998616991 dbj BAU52924.1  Beta-1", "4-mannooligosaccharide phosphorylase [Mucilaginibacter gotjawali]"
"cazy AQW94859.1 pesticidal protein Cry7Aa [Elizabethkingia anophelis]", "cazy AQX07818.1 pesticidal protein Cry7Aa [Elizabethkingia ursingii]", "cazy AQX83981.1 pesticidal protein Cry7Aa [Elizabethkingia bruuniana]", "cazy ATL43456.1 pesticidal protein Cry7Aa [Elizabethkingia miricola]", "cazygi 769872902 gb AJW65144.1  Beta-1", "4-mannooligosaccharide phosphorylase [Elizabethkingia miricola]"
"cazy ARV12310.1 pesticidal protein Cry7Aa [Gilvibacter sp. SZ-19]"
"cazy ARV14799.1 pesticidal protein Cry7Aa [Polaribacter sp. SA4-12]"
"cazy ASS50864.1 pesticidal protein Cry7Aa [Candidatus Fluvicola riflensis]"
"cazy ASU33050.1 pesticidal protein Cry7Aa [Mucilaginibacter sp. BJC16-A31]"
"cazy AWA30851.1 pesticidal protein Cry7Aa [Flavobacterium sp. HYN0048]", "cazy AWI26887.1 pesticidal protein Cry7Aa [Flavobacterium sp. HYN0049]"
"cazy AXE18829.1 pesticidal protein Cry7Aa [Runella sp. HYN0085]", "cazy SHH93191.1 Probable glycosidase", "PH1107-related protein [Flavobacterium psychrophilum]"
"cazy SCD21651.1 Glycosyl hydrolase family 43 [Proteiniphilum saccharofermentans]"
"humangutMH0085_GL0052975 [gene] locus=scaffold24144_1:588:1619:+ [Complete] codon-table.11", "humangutMH0110_GL0077006 [gene] locus=scaffold25166_3:30539:31570:- [Complete] codon-table.11", "humangutMH0267_GL0191591 [gene] locus=scaffold8389_4:5151:6182:- [Complete] codon-table.11", "humangutDLM002_GL0028684 [gene] locus=scaffold4301_12:573:1604:- [Complete] codon-table.11", "humangutT2D-26A_GL0071593 [gene] locus=scaffold15549_4:116691:117722:+ [Complete] codon-table.11", "mouseG1-2A_GL0069908 [gene] locus=scaffold51256_3:291:1322:+ [Complete] codon-table.11"
"humangutMH0101_GL0058946 [gene] locus=C907273_1:3:740:- [Lack both ends] codon-table.11"
"humangutMH0250_GL0227047 [gene] locus=scaffold5499_8:2:520:+ [Lack 5'-end] codon-table.11"
"humangutMH0267_GL0216388 [gene] locus=scaffold43994_9:6461:7495:- [Complete] codon-table.11"
"mouseGroup2-5A_GL0073689 [gene] locus=scaffold45925_7:279:1193:+ [Lack 3'-end] codon-table.11"

## UC9

"cazygi 384069514 emb CCH02724.1  hypothetical protein FAES_4725 [Fibrella aestuarina BUZ 2]"
"cazygi 469478590 gb AGH48815.1  glycosidase related protein [Sphingomonas sp. MM-1]"
"cazygi 761899770 gb AJP74139.1  glycosidase [Sphingomonas hengshuiensis]"
"cazy AOH86025.1 glycosidase [Sphingomonas panacis]", "cazy ATY32282.1 glycosidase [Sphingomonas sp. Cra20]"

["cazy AOW22975.1 glycosidase [Sphingomonas melonis TY]", "cazy ATI56389.1 glycosidase [Sphingomonas melonis]", "cazy 1026262635 gb ANC87007.1  glycosidase [Sphingomonas sp. NIC1]", "cazy 695171035 gb AIT07125.1  glycosidase [Sphingomonas taxii]"]
["cazy API59475.1 glycosidase [Sphingomonas sp. JJ-A5]"]
["cazy APR51401.1 glycosidase [Sphingomonas koreensis]", "cazy APZ97396.1 glycosidase [Sphingopyxis sp. QXT-31]", "cazy 938157188 gb ALJ13549.1  glycosidase [Sphingopyxis macrogoltabida]", "cazy 1015407702 gb AMU89004.1  glycosidase [Sphingopyxis macrogoltabida]", "cazy 937289309 gb ALH79855.1  glycosidase [Sphingopyxis macrogoltabida]"]
["cazy APX66178.1 glycosidase [Sphingomonas sp. LK11]"]
["cazy AQR74940.1 glycosidase [Sphingomonas sp. LM7]", "cazy 761898906 gb AJP73275.1  glycosidase [Sphingomonas hengshuiensis]", "cazy 569540496 gb AHE52113.1  hypothetical protein NX02_01755 [Sphingomonas sanxanigenens DSM 19645 = NX02]"]
["cazy ATE66422.1 glycosidase [Rhizorhabdus dicambivorans]"]
["cazy ATQ44417.1 glycosidase [Caulobacter mirabilis]"]
["cazy ATY33401.1 glycosidase [Sphingomonas sp. Cra20]"]
["cazy AUN32391.1 glycosidase [Niveispirillum cyanobacterium]", "cazy BBD98208.1 glycosidase [Sphingobium amiense]"]
["cazy AUW56966.1 glycosidase [Sphingobium sp. SCG-1]"]
["cazy AXB80036.1 glycosidase (plasmid) [Novosphingobium sp. P6W]", "cazy 1015414349 gb AMU96142.1  glycosidase [Sphingopyxis terrae NBRC 15098]"]
["cazy AXJ95617.1 glycosidase [Sphingomonas sp. FARSPH]"]
["cazy SBV34078.1 conserved protein of unknown function [uncultured Sphingopyxis sp.]"]

### Small meta-nodes

["cazy 206739935 gb ACI18993.1  conserved hypothetical protein [Dictyoglomus thermophilum H-6-12]"]
["cazy 262335691 gb ACY49488.1  glycosidase PH1107-related protein [Rhodothermus marinus DSM 4252]", "cazy 345113685 gb AEN74517.1  glycosidase related protein [Rhodothermus marinus SG0.5JP17-172]"]
["cazy 217336150 gb ACK41943.1  glycosidase PH1107-related [Dictyoglomus turgidum DSM 6724]"]
["cazy 837353939 gb AKM83974.1  Glycosidase-related protein [Candidatus Campbellbacteria bacterium GW2011_OD1_34_28]"]
["cazy 837348939 gb AKM78124.1  Glycosidase-related protein [Candidatus Wolfebacteria bacterium GW2011_GWB1_47_1]"]
["cazy 837348940 gb AKM78125.1  Glycosidase-related protein [Candidatus Wolfebacteria bacterium GW2011_GWB1_47_1]"]
["cazy AQS34661.1 hypothetical protein [uncultured bacterium]"]
["cazy 311224651 gb ADP77507.1  glycosidase PH1107-related protein [Methanothermus fervidus DSM 2088]"]
["rumen3042_GL2596963_1 [gene] locus=scaffold1257999_2:824:2365:-[Complete]"]
["cazy 837353937 gb AKM83972.1  Glycosidase-related protein [Candidatus Campbellbacteria bacterium GW2011_OD1_34_28]"]
["cazy 114338472 gb ABI69320.1  conserved hypothetical protein [Syntrophomonas wolfei subsp. wolfei str. Goettingen G311]"]
["cazy BAX79955.1 hypothetical protein ALGA_1579 [Marinifilaceae bacterium SPP2]"]
["cazy 262333470 gb ACY47267.1  glycosidase PH1107-related protein [Rhodothermus marinus DSM 4252]", "cazy 345111471 gb AEN72303.1  glycosidase related protein [Rhodothermus marinus SG0.5JP17-172]"]
["mouseGroup2-1A_GL0053921 [gene] locus=scaffold35316_5:532:1638:+ [Complete] codon-table.11"]
["cazy ARA94165.1 glycosidase [Rhodothermaceae bacterium RA]"]

["cazy AVH57250.1 hypothetical protein C4B68_17345 [Streptomyces dengaensis]"]
["cazy 573475668 gb AHF92679.1  glycosidase [Opitutaceae bacterium TAV5]"]
["cazy 1001868161 gb AMM34647.1  hypothetical protein SA2016_3993 [Sinomonas atrocyanea]"]
["cazy 359383778 emb CCE79694.1  PISO_001778 [Milleromyces farinosa CBS 7064]", "cazy 359465278 emb CCE88983.1  PISO_001778 [Milleromyces farinosa CBS 7064]"]
["cazy SGZ51348.1 C1C11C00000001274 [[Candida] intermedia], "cazy SGZ52548.1 C1C11C00000000424 [[Candida] intermedia]"]
["cazy 199433069 emb CAG88529.2  DEHA2E21890p [Debaryomyces hansenii CBS767]"]
["cazy 256558512 gb ACU84359.1  predicted glycosylase [Brachybacterium faecium DSM 4810]"]
["cazy 262333469 gb ACY47266.1  glycosidase PH1107-related protein [Rhodothermus marinus DSM 4252], "cazy 345111470 gb AEN72302.1  glycosidase related protein [Rhodothermus marinus SG0.5JP17-172]"]
["cazy 149387617 gb ABN67904.2  glycosidase [Scheffersomyces stipitis CBS 6054]"]
["cazy 223645453 emb CAX40110.1  glycosyl hydrolase", "putative [Candida dubliniensis CD36]", "cazy 380353874 emb CCG23386.1  hypothetical protein CORT_0D05470 [Candida orthopsilosis], "cazy 354546163 emb CCE42892.1  hypothetical protein CPAR2_205350 [Candida parapsilosis], "cazy AOW31291.1 hypothetical protein CAALFM_CR05750WA [Candida albicans SC5314]"]
["cazy SDH28525.1 protein of unknown function [Leifsonia sp. 197AMF], "cazy SDJ09705.1 protein of unknown function [Leifsonia sp. 466MF], "cazy SDJ60880.1 protein of unknown function [Leifsonia sp. 157MF], "cazy SDN30956.1 protein of unknown function [Leifsonia sp. 509MF], "cazy SEA91288.1 protein of unknown function [Leifsonia sp. 21MFCrub1.1], "cazy SEM90351.1 protein of unknown function [Leifsonia sp. 467MF], "cazy SFM34619.1 protein of unknown function [Leifsonia sp. 98AMF]"]
["cazy 1029984077 gb ANF30334.1  hypothetical protein A0130_00330 [Leifsonia xyli]"]
["mouse4-1_GL0005498 [gene] locus=scaffold49332_1:2611:3633:+ [Complete] codon-table.11"]
["humangutMH0257_GL0045417 [gene] locus=scaffold23966_1:17250:18269:- [Complete] codon-table.11"]
["cazy 973720559 gb ALX65937.1  glycosylase [Microbacterium sp. XT11]"]
["humangutV1_CD40-0_GL0193429 [gene] locus=scaffold27959_4:5026:6036:+ [Complete] codon-table.11", "cazy 757810268 dbj BAQ31053.1  putative glycoside hydrolase [Bifidobacterium scardovii JCM 12489 = DSM 13734]"]
["cazy 1032525890 emb SBN62434.1  Predicted glycosyl hydrolase", "GH43/DUF377 family [Curtobacterium sp. 9128]"]
["cazy ARA94161.1 glycosidase [Rhodothermaceae bacterium RA]"]
["cazy AQY03092.1 glycosylase [Microbacterium foliorum]"]
["cazy ATG50115.1 glycosylase [Brachybacterium sp. VM2412]"]
["cazy APH46442.1 glycosylase [Microbacterium sp. 1.5R]"]
["cazy AQS34659.1 hypothetical protein [uncultured bacterium]"]
["cazy 229566671 gb ACQ80522.1  glycosidase PH1107-related protein [Beutenbergia cavernae DSM 12333]"]
["humangutMH0220_GL0080902 [gene] locus=scaffold7359_33:439:1410:+ [Complete] codon-table.11"]
["humangut340101.Vvad_PD3403 [Complete]:- codon-table.11"]
["cazy SDT30597.1 Predicted glycosyl hydrolase", "GH43/DUF377 family [Microlunatus solii]"]
["pigBHZ-5B_GL0031827 [gene] locus=scaffold140501_1:35:988:- [Complete] codon-table.11"]
["rumen553_GL0683180_1 [gene] locus=scaffold402048_1:74:1024:- [Complete]"]
["humangutMH0003_GL0030005 [gene] locus=scaffold37737_2:359:1309:+ [Complete] codon-table.11"]
["mouse4-8_GL0036406 [gene] locus=scaffold81080_1:8580:9527:- [Complete] codon-table.11"]

["cazygi 914700676 gb AKV88118.1  glycosylase [Microbacterium sp. CGR1]"]
["cazy CED90748.1 Predicted glycosylase [Actinomyces succinicurminis]"]
["humangut159227541-stool2_revised_scaffold19850_2_gene29414 strand:+ start:431 stop:1351 length:921 start_codon:yes stop_codon:yes gene_type:complete [Complete] codon-table.11"]
["cazy APX34598.1 glycosylase [Brachybacterium sp. P6-10-X1]"]
["rumen555_GL0214116_1 [gene] locus=scaffold696522_5:2230:3135:+[Complete]"]
["cazy AQS34660.1 hypothetical protein [uncultured bacterium]"]
["humangutMH0346_GL0078767 [gene] locus=scaffold75005_3:3:851:- [Lack 3'-end] codon-table.11"]
["pigPIG-028_GL0192965 [gene] locus=scaffold117322_5:2:823:+ [Lack both ends] codon-table.11"]
["humangutNOF010_GL0029537 [gene] locus=scaffold17487_9:5760:6572:- [Complete] codon-table.11"]
["humangutMH0197_GL0122548 [gene] locus=scaffold137058_2:2:811:+ [Lack 5'-end] codon-table.11"]
["pigBMZ-9B_GL0044137 [gene] locus=scaffold102243_1:74:853:- [Lack 5'-end] codon-table.11"]
["humangutN074A_GL0016438 [gene] locus=scaffold976_1:5783:6538:+ [Complete] codon-table.11"]
["pigPIG-028_GL0224767 [gene] locus=scaffold117322_3:3:743:+ [Lack 5'-end] codon-table.11"]
["humangutMH0409_GL0098559 [gene] locus=scaffold9315_2:569:1300:- [Lack 5'-end] codon-table.11"]
["humangutMH0318_GL0061353 [gene] locus=scaffold94357_2:3:713:- [Lack 3'-end] codon-table.11"]
["mouseMC-0-1_GL0056371 [gene] locus=scaffold45214_1:1:684:- [Lack 3'-end] codon-table.11"]
["humangutV1_UC59-0_GL0081196 [gene] locus=scaffold51068_2:1:681:+ [Lack 5'-end] codon-table.11"]
["humangutMH0281_GL0008336 [gene] locus=scaffold27025_1:1:630:- [Lack both ends] codon-table.11"]
["humangutMH0447_GL0179870 [gene] locus=scaffold66916_2:2:613:- [Lack 3'-end] codon-table.11"]
["pigPIG-028_GL0070410 [gene] locus=scaffold117322_4:2:577:+ [Lack both ends] codon-table.11"]
["mouseGroup2-4A_GL0108517 [gene] locus=scaffold91072_2:1:510:+ [Lack both ends] codon-table.11"]
["pigPIG-015_GL0249704 [gene] locus=scaffold190176_1:3:506:- [Lack both ends] codon-table.11"]
["pigZXZ-10B_GL0280819 [gene] locus=scaffold133522_1:1:504:- [Lack both ends] codon-table.11"]
["pigZXZ-1B_GL0233238 [gene] locus=scaffold56240_1:2:502:+ [Lack 5'-end] codon-table.11"]
["pigPIG_174_GL0095238 [gene] locus=scaffold190388_3:2:499:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-107A_GL0038210 [gene] locus=scaffold26835_2:2356:2832:+ [Complete] codon-table.11"]
["humangutO2_UC47-1_GL0100437 [gene] locus=scaffold29550_4:1017:1484:- [Lack 5'-end] codon-table.11"]
["humangutV1_UC55-4_GL0013856 [gene] locus=scaffold83934_1:38518:38973:+ [Complete] codon-table.11"]
["rumen100058_GL0865693_1 [gene] locus=scaffold2253014_2:368:802:+[Lack 3'-end]"]
["rumen2009040_GL0847873_1 [gene] locus=scaffold1230346_2:212:610:+[Lack 3'-end]";
"rumen7049_GL0372540_1 [gene] locus=scaffold719587_1:245:643:+[Lack 3'-end]"]
["cazygi 297144786 gb ADI01543.1  glycosidase-related protein [Syntrophothermus lipocalidus DSM 12680]"]
["cazygi 297145773 gb ADI02530.1  glycosidase-related protein [Syntrophothermus lipocalidus DSM 12680]"]
["cazygi 409106947 gb AFV13072.1  glycosylase-like protein [Thermaetogenium phaeum DSM 12270]"]
["cazy CCP27154.1 Glycosidase related protein [Tepidanaerobacter acetatoydians Re1],
"cazygi 332697821 gb AEE92278.1  glycosidase related protein [Tepidanaerobacter acetatoydians Re1]"]
["cazygi 302200862 gb ADL08432.1  glycosidase related protein [Thermosediminibacter oceani DSM 16646]"]
["cazygi 432179615 emb CCP26588.1  Glycosidase related protein [Tepidanaerobacter acetatoydians Re1]"]
["cazygi 114338368 gb ABI69216.1  glycosylase-like protein [Syntrophomonas wolfei subsp. wolfei str. Goettingen G311]"]
["cazygi 332697340 gb AEE91797.1  glycosidase related protein [Tepidanaerobacter acetatoydians Re1]"]
["cazygi 332700025 gb AEE96966.1  glycosidase related protein [Mahella australiensis 50-1 BON]"]
["cazy AYO32279.1 glycosidase [Thermoanaerobacteriales bacterium SK-G1]"]

["cazygi 332700567 gb AEE97508.1  glycosidase related protein [Mahella australiensis 50-1 BON]"]
["humangutMH0369_GL0053907 [gene] locus=scaffold3527_4:66957:70382:- [Complete] codon-table.11"]

## Singletons

["cazy AWH84733.1 hypothetical protein HYN59_06180 [Flavobacterium sp. HYN0059]"]
["cazy AWI66994.1 Glycosyl hydrolase family 130", " partial [Chytridiomycota sp. NHY-2018]"]
["cazygi 256361128 gb ACU74625.1  glycosidase PH1107-related [Catenuispora acidiphila DSM 44928]"]
["cazygi 256362158 gb ACU75655.1  glycosidase PH1107-related [Catenuispora acidiphila DSM 44928]"]
["cazygi 288894249 gb ADC65786.1  glycosidase PH1107-related protein [Ferroglobus placidus DSM 10642]"]
["cazygi 311224650 gb ADP77506.1  glycosidase PH1107-related protein [Methanothermobacter fervidus DSM 2088]"]
["cazygi 395812064 gb AFN74813.1  glycosidase PH1107-related protein [Melioribacter roseus P3M-2]"]
["cazygi 441473635 emb CCQ23389.1  Undefined function [Listeria monocytogenes N53-1]"]
["cazygi 575462748 gb AHG93799.1  glycosidase related protein (plasmid) [Gemmatirosa kalamazoonesis]"]
["cazygi 663075780 gb AIE87935.1  glycosidase like protein [Fimbriimonas ginsengisoli Gsoil 348]"]
["cazygi 686529468 gb AIQ40167.1  hypothetical protein R50912_09100 [Paenibacillus sp. FSL R5-0912]"]
["cazygi 805357112 gb AKB37183.1  hypothetical protein MSSAC_2593 [Methanosarcina sicilliae C2J]"]
["cazygi 910742045 dbj BAS11445.1  glycosidase PH1107-related [Arthrobacter sp. Hiyo4]"]
["cazygi 910746573 dbj BAS15972.1  L-arabinose transport system permease protein AraQ [Arthrobacter sp. Hiyo8]"]
["cazygi 941938696 gb ALL00674.1  putative glycosylase [Pyrodicticum delaneyi]"]
["cazygi 948529002 gb ALM76546.1  hypothetical protein TBCH5v1_2658 [Thermococcus barophilus]"]
["cazygi 948529004 gb ALM76548.1  hypothetical protein TBCH5v1_2660 [Thermococcus barophilus]"]
["cazygi 961671808 gb ALS92213.1  protein of unknown function (DUF377)", " partial [uncultured bacterium]"]
["humangut158458797-stool1_revised_C1329368_1_gene123209 strand:- start:1 stop:450 length:450 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut158479027-stool1_revised_scaffold1100_2_gene58535 strand:- start:14782 stop:15147 length:366 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut158479027-stool1_revised_scaffold18864_1_gene136702 strand:+ start:2 stop:247 length:246 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut158499257-stool1_revised_C1407643_1_gene167372 strand:- start:1 stop:354 length:354 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut158802708-stool1_revised_scaffold20396_1_gene173909 strand:+ start:142 stop:570 length:429 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut159247771-stool1_revised_C639626_1_gene39863 strand:+ start:3 stop:347 length:345 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut159247771-stool1_revised_C699412_1_gene62056 strand:+ start:1102 stop:1380 length:279 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut159268001-stool1_revised_C1012689_1_gene118452 strand:+ start:1 stop:291 length:291 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut159571453-stool2_revised_scaffold24542_1_gene69618 strand:+ start:2 stop:355 length:354 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]



["humangut160400887-stool1_revised_C1333607_1_gene208705 strand:+ start:2 stop:244 length:243 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut160400887-stool1_revised_C1423142_1_gene31428 strand:+ start:3 stop:308 length:306 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut160400887-stool1_revised_scaffold13211_1_gene86925 strand:- start:227 stop:610 length:384 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut160582958-stool1_revised_C587123_1_gene4656 strand:+ start:333 stop:563 length:231 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut160765029-stool1_revised_C967610_1_gene119236 strand:- start:380 stop:520 length:141 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut508703490-stool1_revised_scaffold13815_1_gene2495 strand:+ start:2 stop:346 length:345 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut763496533-stool2_revised_C1050883_1_gene24509 strand:- start:217 stop:564 length:348 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut763496533-stool2_revised_scaffold33035_1_gene29300 strand:+ start:493 stop:792 length:300 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut764062976-stool1_revised_scaffold25949_3_gene131258 strand:+ start:3 stop:1970 length:1968 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut764224817-stool1_revised_scaffold11534_1_gene7253 strand:+ start:3 stop:257 length:255 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut764447348-stool1_revised_C417161_1_gene108174 strand:- start:2 stop:355 length:354 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut764588959-stool1_revised_C721118_1_gene46911 strand:- start:189 stop:545 length:357 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangut764588959-stool1_revised_scaffold32622_1_gene138004 strand:- start:2 stop:340 length:339 start_codon:yes stop_codon:no gene_type:incomplete [Lack 3'-end] codon-table.11"]
["humangut809635352-stool1_revised_scaffold12936_1_gene102208 strand:+ start:1 stop:144 length:144 start_codon:no stop_codon:yes gene_type:incomplete [Lack 5'-end] codon-table.11"]
["humangutDOF007_GL0046180 [gene] locus=scaffold3151_10:1097:1441:+ [Lack 3'-end] codon-table.11"]
["humangutDOF008_GL0049325 [gene] locus=scaffold5558_25:2:304:+ [Lack 5'-end] codon-table.11"]
["humangutDOM012_GL0002710 [gene] locus=scaffold5297_3:985:1194:- [Lack 5'-end] codon-table.11"]
["humangutDOM012_GL0017444 [gene] locus=scaffold24111_2:322:624:- [Complete] codon-table.11"]
["humangutDOM025_GL0036051 [gene] locus=scaffold18744_1:1:867:- [Lack both ends] codon-table.11"]
["humangutED11A_GL0002445 [gene] locus=scaffold18900_1:676:852:- [Lack 5'-end] codon-table.11"]
["humangutHT14A_GL0076475 [gene] locus=scaffold20905_1:1:345:+ [Lack 5'-end] codon-table.11", "rumen554_GL0550693_1 [gene] locus=scaffold1139629_4:1182:1526:-[Lack 5'-end]"]
["humangutMH0010_GL0040027 [gene] locus=scaffold12470_4:1147:1725:+ [Complete] codon-table.11"]
["humangutMH0014_GL0001393 [gene] locus=C1167635_1:786:1820:+ [Complete] codon-table.11"]
["humangutMH0016_GL0077462 [gene] locus=scaffold6606_1:577:930:- [Lack 5'-end] codon-table.11"]
["humangutMH0024_GL0009042 [gene] locus=C684765_1:908:1084:- [Lack 5'-end] codon-table.11"]
["humangutMH0046_GL0044530 [gene] locus=scaffold6969_15:676:891:- [Lack 5'-end] codon-table.11"]
["humangutMH0055_GL0027772 [gene] locus=scaffold12333_3:922:1296:+ [Lack 3'-end] codon-table.11"]
["humangutMH0072_GL0008226 [gene] locus=scaffold2833_3:873:1034:+ [Lack 3'-end] codon-table.11"]

["humangutMH0077_GL0057517 [gene] locus=C1128509_1:1122:1352:+ [Lack 3'-end] codon-table.11"]
["humangutMH0098_GL0007885 [gene] locus=scaffold20250_3:379:690:- [Lack 5'-end] codon-table.11"]
["humangutMH0121_GL0011395 [gene] locus=scaffold70_1:305:634:+ [Lack 3'-end] codon-table.11"]
["humangutMH0123_GL0022321 [gene] locus=scaffold41860_5:1206:1553:+ [Lack 3'-end] codon-table.11"]
["humangutMH0128_GL0082326 [gene] locus=scaffold20314_9:3:368:- [Lack 3'-end] codon-table.11"]
["humangutMH0143_GL0081219 [gene] locus=scaffold4032_2:202:567:+ [Lack 3'-end] codon-table.11"]
["humangutMH0143_GL0124264 [gene] locus=scaffold4032_5:2:364:+ [Lack 5'-end] codon-table.11"]
["humangutMH0168_GL0057763 [gene] locus=scaffold3169_3:335:559:- [Lack 5'-end] codon-table.11"]
["humangutMH0168_GL0103270 [gene] locus=scaffold113052_1:1:369:- [Lack 3'-end] codon-table.11"]
["humangutMH0189_GL0168280 [gene] locus=scaffold38117_1:364:708:+ [Lack 3'-end] codon-table.11", "rumen7049_GL2839234_1 [gene] locus=C52385712_1:3:347:-[Lack 3'-end]"]
["humangutMH0196_GL0117325 [gene] locus=scaffold58671_1:675:1052:+ [Lack 3'-end] codon-table.11"]
["humangutMH0197_GL0038811 [gene] locus=scaffold62716_1:2:382:- [Lack 3'-end] codon-table.11"]
["humangutMH0197_GL0107836 [gene] locus=scaffold92544_4:3:197:+ [Lack 5'-end] codon-table.11"]
["humangutMH0197_GL0182739 [gene] locus=scaffold92544_2:700:915:+ [Lack 3'-end] codon-table.11"]
["humangutMH0229_GL0028465 [gene] locus=scaffold41588_5:2:295:+ [Lack 5'-end] codon-table.11"]
["humangutMH0233_GL0074858 [gene] locus=scaffold20373_4:3:365:+ [Lack 5'-end] codon-table.11", "humangutMH0419_GL0062472 [gene] locus=scaffold36938_7:153:515:- [Lack 5'-end] codon-table.11"]
["humangutMH0233_GL0123407 [gene] locus=scaffold46519_5:124:747:+ [Lack 3'-end] codon-table.11"]
["humangutMH0243_GL0001251 [gene] locus=scaffold15770_16:1:267:- [Lack 3'-end] codon-table.11"]
["humangutMH0243_GL0017421 [gene] locus=scaffold15249_9:2:349:- [Lack 3'-end] codon-table.11"]
["humangutMH0245_GL0009488 [gene] locus=scaffold19950_15:9189:9509:- [Lack 5'-end] codon-table.11", "rumen0081_GL0391993_1 [gene] locus=scaffold938228_1:1:321:+[Lack 5'-end]"]
["humangutMH0250_GL0085360 [gene] locus=scaffold5947_4:438:698:+ [Lack 3'-end] codon-table.11"]
["humangutMH0251_GL0101220 [gene] locus=scaffold50228_1:3:221:+ [Lack 5'-end] codon-table.11"]
["humangutMH0257_GL0166458 [gene] locus=scaffold38642_1:1:516:- [Lack both ends] codon-table.11"]
["humangutMH0260_GL0057638 [gene] locus=scaffold85160_13:1670:2227:+ [Lack 3'-end] codon-table.11"]
["humangutMH0260_GL0139297 [gene] locus=scaffold87671_2:2:355:+ [Lack 5'-end] codon-table.11"]
["humangutMH0260_GL0141136 [gene] locus=scaffold35061_1:342:668:+ [Lack 3'-end] codon-table.11"]
["humangutMH0262_GL0133865 [gene] locus=scaffold12319_12:315:683:+ [Lack 3'-end] codon-table.11"]
["humangutMH0276_GL0235251 [gene] locus=scaffold127463_2:1:486:- [Lack 3'-end] codon-table.11"]
["humangutMH0286_GL0158074 [gene] locus=scaffold35417_3:1:318:+ [Lack 5'-end] codon-table.11"]
["humangutMH0293_GL0011214 [gene] locus=scaffold75357_2:3:242:+ [Lack 5'-end] codon-table.11"]
["humangutMH0303_GL0015638 [gene] locus=scaffold17511_14:314:628:- [Lack 5'-end] codon-table.11"]
["humangutMH0303_GL0051007 [gene] locus=scaffold35829_13:244:636:- [Lack 5'-end] codon-table.11"]
["humangutMH0303_GL0160402 [gene] locus=scaffold17511_16:2:517:- [Lack 3'-end] codon-table.11"]
["humangutMH0318_GL0061354 [gene] locus=scaffold94357_2:736:963:- [Lack 5'-end] codon-table.11"]
["humangutMH0318_GL0139096 [gene] locus=scaffold65132_1:170:538:+ [Lack 3'-end] codon-table.11"]
["humangutMH0318_GL0202644 [gene] locus=scaffold63258_1:3:449:+ [Lack 5'-end] codon-table.11"]
["humangutMH0318_GL0207266 [gene] locus=scaffold14436_8:2:265:+ [Lack 5'-end] codon-table.11"]
["humangutMH0329_GL0021822 [gene] locus=scaffold126498_1:2:628:+ [Lack both ends] codon-table.11"]
["humangutMH0329_GL0082370 [gene] locus=scaffold111403_3:3:599:- [Lack 3'-end] codon-table.11"]
["humangutMH0329_GL0138621 [gene] locus=scaffold112733_7:2946:3245:+ [Complete] codon-table.11"]

["humangutMH0329_GL0149676 [gene] locus=scaffold113332_2:481:819:+ [Lack 3'-end] codon-table.11"]
["humangutMH0346_GL0110027 [gene] locus=scaffold89974_1:572:1072:+ [Lack 3'-end] codon-table.11"]
["humangutMH0346_GL0162467 [gene] locus=scaffold7702_18:670:897:- [Lack 5'-end] codon-table.11"]
["humangutMH0357_GL0064342 [gene] locus=scaffold81132_2:187:504:+ [Lack 3'-end] codon-table.11"]
["humangutMH0357_GL0140850 [gene] locus=scaffold4369_2:3:269:+ [Lack 5'-end] codon-table.11"]
["humangutMH0368_GL0068373 [gene] locus=scaffold10102_6:475:855:- [Lack 5'-end] codon-table.11"]
["humangutMH0369_GL0047535 [gene] locus=scaffold9102_1:250:777:+ [Lack 3'-end] codon-table.11"]
["humangutMH0382_GL0027958 [gene] locus=scaffold35103_2:2:232:+ [Lack 5'-end] codon-table.11", "rumen100058_GL3102479_1 [gene] locus=scaffold2198624_3:2:232:+[Lack 5'-end]"]
["humangutMH0385_GL0104250 [gene] locus=scaffold749_13:1209:1442:- [Lack 5'-end] codon-table.11"]
["humangutMH0385_GL0132644 [gene] locus=scaffold53331_2:210:1139:- [Complete] codon-table.11"]
["humangutMH0389_GL0107452 [gene] locus=scaffold109432_4:19720:19914:+ [Complete] codon-table.11"]
["humangutMH0389_GL0171050 [gene] locus=scaffold47280_6:204:575:+ [Lack 3'-end] codon-table.11"]
["humangutMH0393_GL0009257 [gene] locus=scaffold37165_5:629:892:- [Lack 5'-end] codon-table.11"]
["humangutMH0398_GL0051839 [gene] locus=scaffold105642_5:2047:2310:- [Lack 5'-end] codon-table.11"]
["humangutMH0399_GL0082759 [gene] locus=scaffold58178_1:1:1032:+ [Lack 5'-end] codon-table.11"]
["humangutMH0403_GL0206053 [gene] locus=scaffold84639_2:1:243:+ [Lack 5'-end] codon-table.11"]
["humangutMH0404_GL0066200 [gene] locus=scaffold3587_12:3:341:+ [Lack 5'-end] codon-table.11"]
["humangutMH0411_GL0081080 [gene] locus=scaffold53319_5:3:443:- [Lack 3'-end] codon-table.11"]
["humangutMH0411_GL0204994 [gene] locus=scaffold53319_3:414:707:- [Lack 5'-end] codon-table.11"]
["humangutMH0412_GL0016753 [gene] locus=scaffold136420_1:1:192:+ [Lack 5'-end] codon-table.11"]
["humangutMH0412_GL0070194 [gene] locus=scaffold134926_1:1:318:- [Lack 3'-end] codon-table.11"]
["humangutMH0415_GL0122360 [gene] locus=scaffold36551_3:881:1219:+ [Lack 3'-end] codon-table.11"]
["humangutMH0419_GL0186502 [gene] locus=scaffold36938_4:1:384:- [Lack 3'-end] codon-table.11"]
["humangutMH0426_GL0166470 [gene] locus=scaffold4251_4:3:458:- [Lack 3'-end] codon-table.11"]
["humangutMH0436_GL0106385 [gene] locus=scaffold23900_2:1:240:- [Lack 3'-end] codon-table.11"]
["humangutMH0437_GL0089863 [gene] locus=scaffold41065_3:1248:1613:+ [Lack 3'-end] codon-table.11"]
["humangutMH0437_GL0259147 [gene] locus=scaffold34459_6:24138:26636:+ [Complete] codon-table.11"]
["humangutMH0439_GL0237845 [gene] locus=scaffold70555_6:1:318:- [Lack 3'-end] codon-table.11"]
["humangutMH0442_GL0069732 [gene] locus=scaffold131865_2:248:592:+ [Lack 3'-end] codon-table.11"]
["humangutMH0445_GL0174357 [gene] locus=scaffold92326_1:147:512:- [Lack 5'-end] codon-table.11"]
["humangutMH0447_GL0051147 [gene] locus=scaffold66916_1:873:1235:- [Lack 5'-end] codon-table.11"]
["humangutMH0447_GL0078042 [gene] locus=scaffold63630_3:608:1192:- [Complete] codon-table.11"]
["humangutMH0447_GL0220358 [gene] locus=scaffold83071_3:1:240:+ [Lack 5'-end] codon-table.11"]
["humangutMH0447_GL0236530 [gene] locus=scaffold29789_17:2:226:- [Lack 3'-end] codon-table.11"]
["humangutMH0447_GL0236531 [gene] locus=scaffold29789_17:216:776:- [Complete] codon-table.11"]
["humangutMH0454_GL0021889 [gene] locus=scaffold4028_4:230:589:- [Lack 5'-end] codon-table.11"]
["humangutMH0457_GL0039335 [gene] locus=scaffold43943_10:2:289:+ [Lack 5'-end] codon-table.11"]
["humangutMH0457_GL0154021 [gene] locus=scaffold178004_6:1:1287:+ [Lack 5'-end] codon-table.11"]
["humangutN020A_GL0010815 [gene] locus=C849507_1:3:425:- [Lack 3'-end] codon-table.11"]
["humangutN038A_GL0084844 [gene] locus=scaffold49879_2:1:282:- [Lack 3'-end] codon-table.11"]
["humangutNLF007_GL0037795 [gene] locus=scaffold12704_35:333:578:- [Lack 5'-end] codon-table.11"]
["humangutNLM010_GL0060849 [gene] locus=scaffold6721_1:3:347:- [Lack 3'-end] codon-table.11"]

["humangutNLM024_GL0004802 [gene] locus=scaffold1090_2:1:276:- [Lack 3'-end] codon-table.11", "rumen552_GL1342428_1 [gene] locus=C21370228_1:329:604:+[Lack 3'-end]"]
["humangutNOF008_GL0005032 [gene] locus=scaffold40245_1:2903:3022:- [Lack 5'-end] codon-table.11"]
["humangutNOM023_GL0012275 [gene] locus=scaffold8794_8:1:324:+ [Lack 5'-end] codon-table.11"]
["humangutNOM026_GL0020969 [gene] locus=scaffold6339_15:2:511:- [Lack both ends] codon-table.11"]
["humangutO2.UC14-1_GL0075951 [gene] locus=scaffold10916_1:2:145:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC18-2_GL0006426 [gene] locus=scaffold89177_7:617:913:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC18-2_GL0143529 [gene] locus=scaffold89177_9:1216:1545:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC29-1_GL0030376 [gene] locus=scaffold18749_4:2146:2517:+ [Complete] codon-table.11"]
["humangutO2.UC3-2_GL0091900 [gene] locus=scaffold18465_13:2:166:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC4-2_GL0090005 [gene] locus=scaffold56944_3:857:1201:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC40-1_GL0224539 [gene] locus=scaffold141934_3:537:728:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC44-2_GL0263974 [gene] locus=scaffold37118_14:3:200:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC47-1_GL0175948 [gene] locus=scaffold31155_5:2:343:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC48-1_GL0066184 [gene] locus=scaffold21500_4:1:450:- [Lack 3'-end] codon-table.11"]
["humangutO2.UC48-1_GL0146576 [gene] locus=scaffold45801_4:3:140:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC50-2_GL0004976 [gene] locus=scaffold96327_2:325:573:- [Lack 5'-end] codon-table.11"]
["humangutO2.UC53-0_GL0142653 [gene] locus=scaffold126471_1:2:493:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC53-0_GL0249722 [gene] locus=scaffold129671_3:228:545:+ [Lack 3'-end] codon-table.11"]
["humangutO2.UC58-0_GL0006881 [gene] locus=scaffold101956_4:2:553:+ [Lack 5'-end] codon-table.11"]
["humangutO2.UC58-0_GL0106275 [gene] locus=scaffold101956_3:1074:1481:+ [Lack 3'-end] codon-table.11"]
["humangutO2.UC58-0_GL0110180 [gene] locus=scaffold45318_2:577:825:- [Lack 5'-end] codon-table.11"]
["humangutSZEY-10A_GL0038183 [gene] locus=scaffold20329_1:3:218:+ [Lack 5'-end] codon-table.11", "rumen552_GL0949102_1 [gene] locus=scaffold370500_1:618:833:-[Lack 5'-end]", "rumen2009040_GL2301131_1 [gene] locus=scaffold1554320_1:446:661:-[Lack 5'-end]"]
["humangutSZEY-22A_GL0033591 [gene] locus=scaffold5290_2:3:209:- [Lack 3'-end] codon-table.11"]
["humangutSZEY-62A_GL0089677 [gene] locus=scaffold78306_1:1:522:+ [Lack both ends] codon-table.11"]
["humangutT2D-108A_GL0017687 [gene] locus=scaffold86502_1:97:564:- [Lack 5'-end] codon-table.11"]
["humangutT2D-118A_GL0042792 [gene] locus=C396885_1:1:177:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-177A_GL0047681 [gene] locus=scaffold4254_3:16671:17177:+ [Lack 3'-end] codon-table.11"]
["humangutT2D-203A_GL0056743 [gene] locus=scaffold78733_1_2:3:212:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-34A_GL0107992 [gene] locus=scaffold9114_7:3:401:- [Lack 3'-end] codon-table.11"]
["humangutT2D-48A_GL0030912 [gene] locus=scaffold15415_8:1:348:+ [Lack 5'-end] codon-table.11"]
["humangutT2D-51A_GL0083700 [gene] locus=scaffold82597_2:2:409:- [Lack 3'-end] codon-table.11"]
["humangutV1.CD43-0_GL0114439 [gene] locus=scaffold11857_7:3:188:+ [Lack 5'-end] codon-table.11"]
["humangutV1.CD51-0_GL0063834 [gene] locus=scaffold13102_6:1:552:- [Lack both ends] codon-table.11"]
["humangutV1.CD6-0-PT_GL0094869 [gene] locus=scaffold73099_1:1:333:- [Lack 3'-end] codon-table.11"]
["humangutV1.FI14_GL0207273 [gene] locus=scaffold65910_4:1:234:+ [Lack 5'-end] codon-table.11"]
["humangutV1.FI16_GL0209695 [gene] locus=C1703249_1:3:326:+ [Lack 5'-end] codon-table.11"]
["humangutV1.UC11-5_GL0005806 [gene] locus=scaffold5864_3:3:254:+ [Lack 5'-end] codon-table.11", "mouseG1-5A_GL0120335 [gene] locus=scaffold84034_10:1:252:+ [Lack 5'-end] codon-table.11", "rumen555_GL0927358_1 [gene] locus=scaffold603547_4:491:742:-[Lack 5'-end]"]
["humangutV1.UC11-5_GL0089600 [gene] locus=scaffold45835_1:82:504:- [Lack 5'-end] codon-table.11"]

["humangutV1_UC41-0_GL0015005 [gene] locus=scaffold57083_3:712:993:- [Lack 5'-end] codon-table.11"]
["humangutV1_UC41-0_GL0113065 [gene] locus=scaffold57083_5:1:294:- [Lack 3'-end] codon-table.11"]
["humangutV1_UC49-1_GL0105266 [gene] locus=scaffold56477_1:176:547:- [Lack 5'-end] codon-table.11", "rumen100058_GL1141971_1 [gene] locus=scaffold2010358_2:1:372:+ [Lack 5'-end]"]
["humangutV1_UC49-1_GL0196061 [gene] locus=scaffold56477_3:3:344:- [Lack 3'-end] codon-table.11", "pigPIG-035_GL0055410 [gene] locus=scaffold86648_3:1:342:- [Lack 3'-end] codon-table.11"]
["humangutV1_UC52-0_GL0033844 [gene] locus=scaffold38680_1:3:275:+ [Lack 5'-end] codon-table.11"]
["humangutV1_UC52-0_GL0076910 [gene] locus=scaffold58297_4:724:1050:- [Lack 5'-end] codon-table.11"]
["humangutV1_UC52-1_GL0217357 [gene] locus=scaffold71732_5:3:323:- [Lack 3'-end] codon-table.11"]
["humangutV1_UC58-0_GL0010265 [gene] locus=C1344929_1:2:373:- [Lack 3'-end] codon-table.11"]
["humangutV1_UC63-0_GL0226429 [gene] locus=scaffold90032_1:1:135:+ [Lack 5'-end] codon-table.11"]
["humangutV1_UC64-0_GL0075621 [gene] locus=scaffold98556_3:292:516:- [Lack 5'-end] codon-table.11"]
["mouse1-1_GL0096491 [gene] locus=scaffold3628_1:197:583:- [Lack 5'-end] codon-table.11", "rumen100058_GL1762176_1 [gene] locus=C59653100_1:474:860:- [Lack 5'-end]"]
["mouse1-1_GL0117991 [gene] locus=scaffold46637_1:1:474:+ [Lack 5'-end] codon-table.11"]
["mouse1-7_GL0135936 [gene] locus=scaffold5470_3:2:421:- [Lack 3'-end] codon-table.11"]
["mouse1A-dyr4-07_GL0070331 [gene] locus=scaffold24038_1:66:335:- [Complete] codon-table.11"]
["mouse29_GL0000723 [gene] locus=scaffold79796_1:3074:3502:+ [Complete] codon-table.11"]
["mouse2A-dyr14-07_GL0041658 [gene] locus=scaffold64604_2:3:305:- [Lack 3'-end] codon-table.11"]
["mouse2A-dyr16-07_GL0084188 [gene] locus=scaffold27478_6:539:766:+ [Lack 3'-end] codon-table.11"]
["mouse3-5_GL0087646 [gene] locus=scaffold51054_3:3:377:- [Lack 3'-end] codon-table.11"]
["mouse31_GL0041785 [gene] locus=scaffold38423_1:2:343:- [Lack 3'-end] codon-table.11"]
["mouse31_GL0087261 [gene] locus=scaffold9451_3:719:940:+ [Lack 3'-end] codon-table.11", "rumen553_GL0862616_1 [gene] locus=scaffold105027_1:2:223:- [Lack 3'-end]"]
["mouse4-6_GL0101804 [gene] locus=scaffold2035_6:417:704:+ [Lack 3'-end] codon-table.11"]
["mouse5-8_GL0019899 [gene] locus=scaffold87431_2:271:636:+ [Lack 3'-end] codon-table.11"]
["mouse54_GL0000607 [gene] locus=scaffold73491_1:1:270:+ [Lack 5'-end] codon-table.11"]
["mouse6-1_GL0059324 [gene] locus=scaffold17903_6:36:635:+ [Complete] codon-table.11"]
["mouse6-5_GL0028346 [gene] locus=C1005479_1:315:644:- [Lack 5'-end] codon-table.11"]
["mouse8_GL0140135 [gene] locus=scaffold4385_3:1391:1759:+ [Lack 3'-end] codon-table.11"]
["mouse8-6_GL0006984 [gene] locus=scaffold62741_3:3:650:+ [Lack both ends] codon-table.11"]
["mouseG1-5A_GL0072854 [gene] locus=scaffold45912_7:1:324:+ [Lack 5'-end] codon-table.11"]
["mouseG1-5A_GL0120334 [gene] locus=scaffold84034_7:431:763:+ [Lack 3'-end] codon-table.11"]
["mouseGroup2-3A_GL0026299 [gene] locus=scaffold9194_6:843:1259:- [Lack 5'-end] codon-table.11"]
["mouseGroup2-6A_GL0092520 [gene] locus=scaffold78815_3:370:654:- [Lack 5'-end] codon-table.11"]
["mouseGroup2-7A_GL0056368 [gene] locus=scaffold30847_2:444:593:- [Lack 5'-end] codon-table.11"]
["mouseGroup2-7A_GL0123938 [gene] locus=scaffold75360_2:198:527:- [Lack 5'-end] codon-table.11"]
["mouseGroup2-8A_GL0028086 [gene] locus=scaffold15469_9:3:557:+ [Lack 5'-end] codon-table.11"]
["mouseGroup2-8A_GL0143788 [gene] locus=scaffold118207_6:544:834:+ [Complete] codon-table.11"]
["mouseMC-0-1_GL0090641 [gene] locus=scaffold79734_1:411:653:- [Lack 5'-end] codon-table.11"]
["mouseMC-6-1_GL0109569 [gene] locus=scaffold75917_2:1644:1898:+ [Lack 3'-end] codon-table.11"]
["mouseMC-6-2_GL0023171 [gene] locus=scaffold13217_1:478:747:- [Lack 5'-end] codon-table.11"]
["mouseMC-6-4_GL0116751 [gene] locus=scaffold82976_1:2:316:+ [Lack 5'-end] codon-table.11"]

["mouseMH-6-4_GL0057792 [gene] locus=scaffold29094_5:789:1085:+ [Lack 3'-end] codon-table.11"]
["mouseMH-6-5_GL0187250 [gene] locus=C1421343_1:1:360:+ [Lack 5'-end] codon-table.11"]
["mouseS-Fe12_GL0047612 [gene] locus=scaffold96729_4:2:394:+ [Lack 5'-end] codon-table.11"]
["mouseS-Fe20_GL0143757 [gene] locus=scaffold40175_6:2563:3003:- [Complete] codon-table.11"]
["pigBHZ-2B_GL0081036 [gene] locus=scaffold158413_1:595:804:- [Lack 5'-end] codon-table.11"]
["pigBHZ-2B_GL0184861 [gene] locus=C1791472_1:181:501:+ [Lack 3'-end] codon-table.11"]
["pigBMZ-11B_GL0030146 [gene] locus=C730619_1:2:388:+ [Lack 5'-end] codon-table.11"]
["pigBMZ-3B_GL0023917 [gene] locus=scaffold31904_2:2:400:+ [Lack 5'-end] codon-table.11", "rumen553_GL0697729_1 [gene] locus=scaffold294515_1:3:401:+[Lack 5'-end]", "rumen3042_GL2826746_1 [gene] locus=scaffold613841_8:2:400:+[Lack 5'-end]"]
["pigDB-510B_GL0107434 [gene] locus=scaffold13970_4:144:503:+ [Lack 3'-end] codon-table.11", "rumen3042_GL1813635_1 [gene] locus=scaffold1263564_1:3:362:-[Lack 3'-end]"]
["pigDB-511B_GL0113845 [gene] locus=scaffold143693_1:214:594:+ [Lack 3'-end] codon-table.11"]
["pigDB-515B_GL0054726 [gene] locus=scaffold16049_1:3:374:+ [Lack 5'-end] codon-table.11"]
["pigDB-537B_GL0163431 [gene] locus=scaffold101887_1:414:515:- [Lack 5'-end] codon-table.11"]
["pigEYZ-120B_GL0206302 [gene] locus=scaffold237029_2:664:1104:+ [Lack 3'-end] codon-table.11"]
["pigEYZ-120B_GL0294049 [gene] locus=C2860800_1:1:333:+ [Lack 5'-end] codon-table.11"]
["pigEYZ-120B_GL0321485 [gene] locus=scaffold14870_2:605:1066:+ [Lack 3'-end] codon-table.11"]
["pigEYZ-160B_GL0065439 [gene] locus=scaffold127538_2:720:986:- [Lack 5'-end] codon-table.11"]
["pigEYZ-183B_GL0093119 [gene] locus=C1902746_1:3:254:+ [Lack 5'-end] codon-table.11", "rumen554_GL1357027_1 [gene] locus=scaffold2116913_3:2:253:+[Lack 5'-end]"]
["pigEYZ-254B_GL0138696 [gene] locus=scaffold130898_3:2:316:- [Lack 3'-end] codon-table.11"]
["pigEYZ-468B_GL0121204 [gene] locus=scaffold111554_2:202:528:+ [Lack 3'-end] codon-table.11"]
["pigEYZ-566B_GL0058282 [gene] locus=scaffold23378_1:7685:8092:- [Lack 5'-end] codon-table.11", "rumen554_GL1394829_1 [gene] locus=scaffold115438_7:2:409:+[Lack 5'-end]"]
["pigEYZ-652B_GL0098387 [gene] locus=C2233085_1:299:505:- [Lack 5'-end] codon-table.11"]
["pigEYZ-652B_GL0150164 [gene] locus=scaffold176952_1:340:543:- [Lack 5'-end] codon-table.11"]
["pigPIG_111_GL0240613 [gene] locus=scaffold123134_4:3144:3302:- [Lack 5'-end] codon-table.11"]
["pigPIG_113_GL0122499 [gene] locus=scaffold108127_1:865:1062:- [Lack 5'-end] codon-table.11"]
["pigPIG_114_GL0134963 [gene] locus=scaffold102660_1:880:1083:- [Lack 5'-end] codon-table.11"]
["pigPIG_117_GL0145015 [gene] locus=scaffold262986_2:3:164:+ [Lack 5'-end] codon-table.11"]
["pigPIG_118_GL0313249 [gene] locus=scaffold186655_1:3:362:- [Lack 3'-end] codon-table.11"]
["pigPIG_127_GL0070920 [gene] locus=scaffold109974_2:1:435:+ [Lack 5'-end] codon-table.11"]
["pigPIG_132_GL0135900 [gene] locus=scaffold90934_2:1:426:- [Lack 3'-end] codon-table.11"]
["pigPIG_133_GL0231348 [gene] locus=C2983132_1:272:571:- [Lack 5'-end] codon-table.11", "rumen7049_GL2519477_1 [gene] locus=scaffold2250314_2:506:805:-[Lack 5'-end]"]
["pigPIG_138_GL0147636 [gene] locus=scaffold177634_3:1109:1411:+ [Lack 3'-end] codon-table.11"]
["pigPIG_152_GL0249489 [gene] locus=scaffold32872_1:644:913:- [Lack 5'-end] codon-table.11"]
["pigPIG_153_GL0162516 [gene] locus=scaffold159393_2:1:258:- [Lack 3'-end] codon-table.11"]
["pigPIG_157_GL0088951 [gene] locus=scaffold224945_1:3:311:- [Lack 3'-end] codon-table.11"]
["pigPIG_160_GL0213499 [gene] locus=scaffold180689_2:2:646:- [Lack both ends] codon-table.11"]
["pigPIG_167_GL0264842 [gene] locus=scaffold193421_1:1:246:+ [Lack 5'-end] codon-table.11"]
["pigPIG_184_GL0157776 [gene] locus=scaffold229490_1:2:301:+ [Lack 5'-end] codon-table.11"]

["pigPIG_186_GL0004825 [gene] locus=scaffold84602_2:1:255:+ [Lack 5'-end] codon-table.11"]
["pigPIG_197_GL0218858 [gene] locus=scaffold215673_2:1575:1871:+ [Lack 3'-end] codon-table.11"]
["pigPIG_208_GL0173811 [gene] locus=scaffold85110_4:2:358:+ [Lack 5'-end] codon-table.11"]
["pigPIG-001_GL0117069 [gene] locus=scaffold122346_3:381:635:+ [Lack 3'-end] codon-table.11"]
["pigPIG-003_GL0222283 [gene] locus=scaffold84423_1:2:424:- [Lack 3'-end] codon-table.11"]
["pigPIG-006_GL0020498 [gene] locus=scaffold142627_2:1:360:+ [Lack 5'-end] codon-table.11"]
["pigPIG-008_GL0016749 [gene] locus=scaffold22564_7:1:771:- [Lack both ends] codon-table.11"]
["pigPIG-011_GL0020761 [gene] locus=scaffold113987_5:996:1316:- [Complete] codon-table.11"]
["pigPIG-011_GL0170241 [gene] locus=scaffold104732_2:2:334:+ [Lack 5'-end] codon-table.11"]
["pigPIG-012_GL0163005 [gene] locus=scaffold150081_4:2:130:+ [Lack 5'-end] codon-table.11", "rumen100058_GL1209970_1 [gene] locus=scaffold1419203_3:1609:1737:-[Lack 5'-end]"]
["pigPIG-015_GL0265072 [gene] locus=scaffold151874_1:594:878:- [Lack 5'-end] codon-table.11"]
["pigPIG-017_GL0112081 [gene] locus=scaffold153992_2:2:184:+ [Lack 5'-end] codon-table.11"]
["pigPIG-018_GL0111462 [gene] locus=scaffold133034_2:2:349:+ [Lack 5'-end] codon-table.11"]
["pigPIG-018_GL0195533 [gene] locus=scaffold111815_1:1:258:+ [Lack 5'-end] codon-table.11"]
["pigPIG-018_GL0199020 [gene] locus=scaffold112197_1:3:227:+ [Lack 5'-end] codon-table.11"]
["pigPIG-019_GL0028926 [gene] locus=scaffold60304_1:3:299:- [Lack 3'-end] codon-table.11"]
["pigPIG-024_GL0024416 [gene] locus=scaffold47495_8:2:241:+ [Lack 5'-end] codon-table.11"]
["pigPIG-026_GL0092700 [gene] locus=scaffold85874_1:2:250:+ [Lack 5'-end] codon-table.11"]
["pigPIG-028_GL0034422 [gene] locus=scaffold158936_1:3:167:+ [Lack 5'-end] codon-table.11"]
["pigPIG-028_GL0090129 [gene] locus=scaffold31169_2:134:742:+ [Lack 3'-end] codon-table.11"]
["pigPIG-031_GL0019289 [gene] locus=scaffold127176_2:1:372:+ [Lack 5'-end] codon-table.11"]
["pigPIG-031_GL0041678 [gene] locus=scaffold4042_9:2030:2251:+ [Lack 3'-end] codon-table.11"]
["pigPIG-031_GL0116372 [gene] locus=scaffold104719_3:1:183:+ [Lack 5'-end] codon-table.11"]
["pigPIG-032_GL0055991 [gene] locus=scaffold55164_1:2:340:- [Lack 3'-end] codon-table.11"]
["pigPIG-033_GL0076027 [gene] locus=scaffold141581_1:1:318:- [Lack 3'-end] codon-table.11"]
["pigPIG-033_GL0130815 [gene] locus=scaffold105326_1:3:224:+ [Lack 5'-end] codon-table.11", "rumen554_GL2776972_1 [gene] locus=scaffold1334142_4:399:620:-[Lack 5'-end]"]
["pigPIG-033_GL0147033 [gene] locus=C1668203_1:641:904:+ [Lack 3'-end] codon-table.11"]
["pigPIG-034_GL0023999 [gene] locus=scaffold14305_4:1:369:+ [Lack 5'-end] codon-table.11"]
["pigPIG-034_GL0176454 [gene] locus=scaffold64564_1:3:389:- [Lack 3'-end] codon-table.11"]
["pigPIG-035_GL0022304 [gene] locus=scaffold79779_2:646:996:+ [Lack 3'-end] codon-table.11"]
["pigPIG-035_GL0080528 [gene] locus=scaffold100050_2:3:326:- [Lack 3'-end] codon-table.11"]
["pigPIG-035_GL0145693 [gene] locus=scaffold86648_8:2:337:- [Lack 3'-end] codon-table.11"]
["pigPIG-035_GL0158671 [gene] locus=scaffold57862_2:1:261:+ [Lack 5'-end] codon-table.11"]
["pigPIG-036_GL0072983 [gene] locus=C1974901_1:38:415:- [Complete] codon-table.11"]
["pigPIG-038_GL0106270 [gene] locus=scaffold24360_3:1177:1434:- [Lack 5'-end] codon-table.11"]
["pigPIG-041_GL0102979 [gene] locus=scaffold68019_2:13259:13489:- [Complete] codon-table.11"]
["pigPIG-041_GL0102980 [gene] locus=scaffold68019_2:13470:13904:- [Complete] codon-table.11"]
["pigPIG-044_GL0196258 [gene] locus=scaffold21536_4:3:305:+ [Lack 5'-end] codon-table.11"]
["pigPIG-046_GL0080358 [gene] locus=scaffold13760_5:3:389:- [Lack 3'-end] codon-table.11"]
["pigPIG-046_GL0102775 [gene] locus=scaffold132270_2:324:650:+ [Lack 3'-end] codon-table.11"]
["pigPIG-046_GL0108704 [gene] locus=scaffold120671_1:1:135:+ [Lack 5'-end] codon-table.11"]

["pigPIG-046_GL0223004 [gene] locus=scaffold12098_1:1:366:+ [Lack 5'-end] codon-table.11"]
["pigPIG-063_GL0161198 [gene] locus=scaffold59817_4:603:791:- [Lack 5'-end] codon-table.11"]
["pigPIG-084_GL0114288 [gene] locus=scaffold145976_2:3:173:+ [Lack 5'-end] codon-table.11"]
["pigPIG-085_GL0149522 [gene] locus=scaffold101103_6:990:1346:+ [Lack 3'-end] codon-table.11"]
["pigPIG-087_GL0007883 [gene] locus=scaffold64475_2:325:717:- [Complete] codon-table.11"]
["pigPIG-089_GL0097410 [gene] locus=scaffold10150_1:3:641:- [Lack 3'-end] codon-table.11"]
["pigPIG-098_GL0154563 [gene] locus=scaffold87102_1:1:264:- [Lack 3'-end] codon-table.11"]
["pigPIG-102_GL0083633 [gene] locus=scaffold60087_1:466:786:- [Lack 5'-end] codon-table.11"]
["pigPIG-105_GL0069463 [gene] locus=scaffold22999_2:282:548:+ [Complete] codon-table.11"]
["pigPIG-106_GL0167568 [gene] locus=scaffold69983_1:2:253:- [Lack 3'-end] codon-table.11"]
["pigPIG-106_GL0188441 [gene] locus=scaffold67583_1:3:386:+ [Lack 5'-end] codon-table.11"]
["pigSYZ-388B_GL0022359 [gene] locus=scaffold25372_1:685:828:- [Lack 5'-end] codon-table.11"]
["pigSYZ-423B_GL0126391 [gene] locus=scaffold120838_3:1:411:+ [Lack 5'-end] codon-table.11"]
["pigSYZ-477B_GL0143256 [gene] locus=scaffold139826_2:3:356:- [Lack 3'-end] codon-table.11"]
["pigZXZ-8B_GL0060071 [gene] locus=scaffold198339_2:407:829:+ [Lack 3'-end] codon-table.11"]
["pigZXZ-8B_GL0212337 [gene] locus=scaffold26205_2:651:1016:+ [Lack 3'-end] codon-table.11"]
["rumen0081_GL0025168_1 [gene] locus=scaffold1981889_1:515:772:-[Lack 5'-end]"]
["rumen0081_GL0068449_1 [gene] locus=scaffold22173_6:2:277:+[Lack 5'-end]"]
["rumen0081_GL0492384_1 [gene] locus=scaffold57901_2:493:723:+[Lack 3'-end]"]
["rumen0081_GL0526665_1 [gene] locus=scaffold446716_3:4533:4832:-[Lack 5'-end]"]
["rumen0081_GL0555004_1 [gene] locus=scaffold908016_3:766:957:-[Lack 5'-end]", "rumen100058_GL3309303_1 [gene] locus=scaffold3233303_1:2:193:+[Lack 5'-end]"]
["rumen0081_GL0596527_1 [gene] locus=scaffold1846311_1:2:364:+[Lack 5'-end]"]
["rumen0081_GL0687396_1 [gene] locus=scaffold1598019_2:2:262:+[Lack 5'-end]"]
["rumen0081_GL0816418_1 [gene] locus=scaffold68961_6:2:292:+[Lack 5'-end]"]
["rumen0081_GL0822408_1 [gene] locus=scaffold860226_2:2:145:+[Lack 5'-end]"]
["rumen0081_GL0913246_1 [gene] locus=scaffold1430310_1:1:243:-[Lack 3'-end]", "rumen100058_GL0542887_1 [gene] locus=scaffold3134266_1:683:925:+[Lack 3'-end]"]
["rumen0081_GL0929565_1 [gene] locus=scaffold526150_2:2:352:-[Lack 3'-end]"]
["rumen0081_GL0929566_1 [gene] locus=scaffold526150_2:349:714:-[Lack 5'-end]", "rumen3042_GL0034857_1 [gene] locus=scaffold2452405_4:239:604:-[Lack 5'-end]"]
["rumen0081_GL0943521_1 [gene] locus=scaffold804545_8:2:265:+[Lack 5'-end]"]
["rumen0081_GL0960161_1 [gene] locus=C38002635_1:3:191:+[Lack 5'-end]"]
["rumen0081_GL0977653_1 [gene] locus=scaffold1075911_4:971:1300:-[Lack 5'-end]"]
["rumen0081_GL0978695_1 [gene] locus=scaffold951404_1:1011:1346:-[Lack 5'-end]"]
["rumen0081_GL1050938_1 [gene] locus=scaffold2002823_1:3:341:-[Lack 3'-end]"]
["rumen0081_GL1063997_1 [gene] locus=scaffold1650903_1:3:392:-[Lack 3'-end]"]
["rumen0081_GL1156168_1 [gene] locus=scaffold1810593_2:2:160:+[Lack 5'-end]"]
["rumen0081_GL1434169_1 [gene] locus=scaffold437330_3:1:273:+[Lack 5'-end]"]
["rumen0081_GL1469283_1 [gene] locus=scaffold538318_4:3:404:-[Lack 3'-end]"]
["rumen0081_GL1535099_1 [gene] locus=scaffold1995295_1:1:447:-[Lack 3'-end]"]
["rumen0081_GL1563107_1 [gene] locus=scaffold1292164_1:593:871:+[Lack 3'-end]"]
["rumen0081_GL1570278_1 [gene] locus=scaffold1723398_2:1:321:-[Lack 3'-end]"]



["rumen0081_GL1674201_1 [gene] locus=scaffold65194_4:303:590:-[Lack 5'-end]"]
["rumen0081_GL1763635_1 [gene] locus=scaffold1486654_1:177:515:+[Lack 3'-end]"]
["rumen0081_GL1980800_1 [gene] locus=scaffold556784_3:3:179:+[Lack 5'-end]"]
["rumen0081_GL1984450_1 [gene] locus=scaffold272372_1:462:740:-[Lack 5'-end]"]
["rumen0081_GL1985915_1 [gene] locus=scaffold156778_2:563:991:+[Lack 3'-end]"]
["rumen0081_GL2131252_1 [gene] locus=scaffold412998_6:2:406:+[Lack 5'-end]", "rumen100058_GL1739690_1 [gene] locus=scaffold1196121_1:1:405:+[Lack 5'-end]"]
["rumen0081_GL2169682_1 [gene] locus=scaffold922929_1:227:559:-[Lack 5'-end]"]
["rumen0081_GL2310984_1 [gene] locus=scaffold902722_1:3:287:-[Lack 3'-end]"]
["rumen0081_GL2316711_1 [gene] locus=scaffold1177913_1:1:348:+[Lack 5'-end]"]
["rumen0081_GL2352002_1 [gene] locus=scaffold1576824_2:1:435:+[Lack 5'-end]"]
["rumen0081_GL2352340_1 [gene] locus=scaffold1973809_3:3220:3549:-[Lack 5'-end]"]
["rumen0081_GL2530018_1 [gene] locus=scaffold845286_6:1022:1417:+[Lack 3'-end]"]
["rumen0081_GL2555062_1 [gene] locus=scaffold181403_1:2:397:-[Lack 3'-end]"]
["rumen100058_GL0022013_1 [gene] locus=scaffold3198607_2:646:1062:+[Lack 3'-end]"]
["rumen100058_GL0079653_1 [gene] locus=scaffold2482952_1:1:273:+[Lack 5'-end]"]
["rumen100058_GL0089784_1 [gene] locus=scaffold743560_1:2426:2731:-[Lack 5'-end]"]
["rumen100058_GL0099082_1 [gene] locus=scaffold656461_5:249:587:-[Lack 5'-end]"]
["rumen100058_GL0159734_1 [gene] locus=scaffold80811_4:1817:2188:+[Lack 3'-end]"]
["rumen100058_GL0181973_1 [gene] locus=scaffold744079_1:3:323:-[Lack 3'-end]", "rumen2009040_GL3528128_1 [gene] locus=scaffold1511778_1:1011:1331:+[Lack 3'-end]"]
["rumen100058_GL0286299_1 [gene] locus=scaffold1165601_2:3:545:+[Lack both ends]"]
["rumen100058_GL0322092_1 [gene] locus=scaffold1356170_1:1:312:+[Lack 5'-end]"]
["rumen100058_GL0431768_1 [gene] locus=C60004488_1:805:1029:+[Lack 3'-end]"]
["rumen100058_GL0531429_1 [gene] locus=scaffold1392407_4:1170:1460:+[Lack 3'-end]"]
["rumen100058_GL0534021_1 [gene] locus=scaffold3171351_1:3:368:-[Lack 3'-end]"]
["rumen100058_GL0586047_1 [gene] locus=scaffold2616239_2:3:365:-[Lack 3'-end]"]
["rumen100058_GL0631258_1 [gene] locus=C59445710_1:374:790:-[Lack 5'-end]"]
["rumen100058_GL0633342_1 [gene] locus=scaffold930924_1:1:255:-[Lack 3'-end]"]
["rumen100058_GL0644812_1 [gene] locus=scaffold2605206_3:423:692:+[Lack 3'-end]"]
["rumen100058_GL0677781_1 [gene] locus=scaffold1316226_5:2208:2555:+[Complete]"]
["rumen100058_GL0734503_1 [gene] locus=scaffold51761_2:2:247:+[Lack 5'-end]"]
["rumen100058_GL0752936_1 [gene] locus=scaffold1928015_3:2:304:+[Lack 5'-end]", "rumen3042_GL1281026_1 [gene] locus=scaffold2375079_2:2:304:+[Lack 5'-end]"]
["rumen100058_GL0766909_1 [gene] locus=scaffold22185_3:2:214:+[Lack 5'-end]"]
["rumen100058_GL0866875_1 [gene] locus=scaffold2432313_1:1:336:+[Lack 5'-end]"]
["rumen100058_GL0956944_1 [gene] locus=scaffold3332839_1:1:198:+[Lack 5'-end]"]
["rumen100058_GL1056175_1 [gene] locus=scaffold2252074_1:1:186:+[Lack 5'-end]", "rumen3042_GL0211651_1 [gene] locus=scaffold2125478_2:361:546:-[Lack 5'-end]"]
["rumen100058_GL1186590_1 [gene] locus=scaffold2712369_3:3:377:-[Lack 3'-end]"]
["rumen100058_GL1260280_1 [gene] locus=scaffold3242967_1:356:523:-[Lack 5'-end]"]
["rumen100058_GL1277341_1 [gene] locus=scaffold3134266_4:1:240:+[Lack 5'-end]"]
["rumen100058_GL1507542_1 [gene] locus=scaffold529438_4:894:1070:+[Lack 3'-end]"]

["rumen100058_GL1521442_1 [gene] locus=scaffold1325861_2:2:202:+[Lack 5'-end]"]
["rumen100058_GL1532997_1 [gene] locus=scaffold1512339_1:297:545:-[Lack 5'-end]"]
["rumen100058_GL1546047_1 [gene] locus=scaffold2351752_4:876:1211:+[Lack 3'-end]"]
["rumen100058_GL1583839_1 [gene] locus=scaffold2751180_1:685:888:+[Lack 3'-end]"]
["rumen100058_GL1599682_1 [gene] locus=scaffold1900018_3:3:287:-[Lack 3'-end]"]
["rumen100058_GL1612120_1 [gene] locus=scaffold2154041_1:1:354:+[Lack 5'-end]"]
["rumen100058_GL1643378_1 [gene] locus=scaffold1233893_1:1:210:+[Lack 5'-end]", "rumen100058_GL2885838_1 [gene] locus=scaffold2415619_1:1:210:+[Lack 5'-end]"]
["rumen100058_GL1659862_1 [gene] locus=scaffold2136811_1:1:405:+[Lack 5'-end]", "rumen2009040_GL0791826_1 [gene] locus=scaffold2466552_1:323:727:-[Lack 5'-end]", "rumen2009040_GL2914999_1 [gene] locus=scaffold985728_2:279:683:-[Lack 5'-end]"]
["rumen100058_GL1822836_1 [gene] locus=scaffold357672_3:160:537:+[Lack 3'-end]"]
["rumen100058_GL1901186_1 [gene] locus=scaffold2569265_1:1034:1315:+[Lack 3'-end]"]
["rumen100058_GL1964487_1 [gene] locus=scaffold3095996_1:1:219:-[Lack 3'-end]"]
["rumen100058_GL2029115_1 [gene] locus=scaffold1998067_1:2265:2435:-[Lack 5'-end]"]
["rumen100058_GL2036481_1 [gene] locus=scaffold940039_5:2802:3149:-[Lack 5'-end]"]
["rumen100058_GL2180073_1 [gene] locus=scaffold355308_4:138:506:-[Lack 5'-end]"]
["rumen100058_GL2222493_1 [gene] locus=scaffold1798464_1:576:890:+[Lack 3'-end]"]
["rumen100058_GL2260244_1 [gene] locus=scaffold466119_4:2838:3167:+[Lack 3'-end]"]
["rumen100058_GL2377314_1 [gene] locus=C58474256_1:368:601:-[Lack 5'-end]"]
["rumen100058_GL2821626_1 [gene] locus=scaffold148270_1:2:346:-[Lack 3'-end]"]
["rumen100058_GL2862569_1 [gene] locus=scaffold2358813_2:2:139:+[Lack 5'-end]"]
["rumen100058_GL2888023_1 [gene] locus=scaffold2352961_2:239:556:+[Lack 3'-end]"]
["rumen100058_GL2899304_1 [gene] locus=C59020242_1:373:687:+[Lack 3'-end]"]
["rumen100058_GL2959246_1 [gene] locus=scaffold1367024_1:3:380:-[Lack 3'-end]"]
["rumen100058_GL2995843_1 [gene] locus=scaffold3058537_1:2:532:-[Lack 3'-end]"]
["rumen100058_GL3043600_1 [gene] locus=scaffold2179793_1:1:360:+[Lack 5'-end]", "rumen2009040_GL0831966_1 [gene] locus=scaffold251460_6:286:645:-[Lack 5'-end]"]
["rumen100058_GL3091063_1 [gene] locus=scaffold8500_2:6213:6593:+[Lack 3'-end]"]
["rumen100058_GL3131347_1 [gene] locus=scaffold2092912_5:3:347:-[Lack 3'-end]"]
["rumen100058_GL3136593_1 [gene] locus=scaffold762324_1:1063:1398:-[Lack 5'-end]"]
["rumen100058_GL3179586_1 [gene] locus=scaffold1757812_3:2:319:+[Lack 5'-end]"]
["rumen100058_GL3403594_1 [gene] locus=scaffold3217913_1:3226:3615:+[Lack 3'-end]"]
["rumen100058_GL3461589_1 [gene] locus=scaffold2608196_1:3:326:-[Lack 3'-end]"]
["rumen100058_GL3582693_1 [gene] locus=scaffold2712369_1:3460:3768:-[Lack 5'-end]"]
["rumen100058_GL3616812_1 [gene] locus=scaffold3251965_1:1:366:+[Lack 5'-end]"]
["rumen100058_GL3622815_1 [gene] locus=scaffold1676918_1:2:574:-[Lack 3'-end]"]
["rumen100058_GL3735820_1 [gene] locus=scaffold2101219_2:272:643:+[Lack 3'-end]"]
["rumen100058_GL3736148_1 [gene] locus=scaffold2030091_1:425:664:-[Lack 5'-end]"]
["rumen2009040_GL0078744_1 [gene] locus=scaffold2896672_1:558:899:-[Lack 5'-end]", "rumen3042_GL0849564_1 [gene] locus=scaffold811678_1:886:1227:-[Lack 5'-end]"]
["rumen2009040_GL0091146_1 [gene] locus=scaffold2536092_2:145:534:-[Lack 5'-end]"]
["rumen2009040_GL0185634_1 [gene] locus=scaffold980264_1:645:959:-[Lack 5'-end]"]

["rumen2009040_GL0192501_1 [gene] locus=scaffold1137677_3:1163:1528:-[Lack 5'-end]", "rumen2009040_GL0883937_1 [gene] locus=scaffold951347_2:2:367:+[Lack 5'-end]"]
["rumen2009040_GL0217692_1 [gene] locus=scaffold2799247_1:1:369:-[Lack 3'-end]", "rumen2009040_GL1061855_1 [gene] locus=scaffold2664944_1:3:371:-[Lack 3'-end]"]
["rumen2009040_GL0240816_1 [gene] locus=scaffold993739_5:2:211:+[Lack 5'-end]"]
["rumen2009040_GL0388547_1 [gene] locus=scaffold1851692_1:2:283:+[Lack 5'-end]"]
["rumen2009040_GL0426471_1 [gene] locus=scaffold2986670_1:518:829:+[Lack 3'-end]", "rumen2009040_GL2875767_1 [gene] locus=scaffold838611_1:3:314:-[Lack 3'-end]"]
["rumen2009040_GL0462510_1 [gene] locus=scaffold1959291_1:1:378:+[Lack 5'-end]", "rumen2009040_GL3572450_1 [gene] locus=scaffold4938_2:1082:1459:-[Lack 5'-end]"]
["rumen2009040_GL0547865_1 [gene] locus=scaffold1675910_2:1:333:-[Lack 3'-end]"]
["rumen2009040_GL0608834_1 [gene] locus=scaffold2637331_1:1:360:-[Lack 3'-end]"]
["rumen2009040_GL0814568_1 [gene] locus=scaffold2576949_1:321:659:+[Lack 3'-end]"]
["rumen2009040_GL0879318_1 [gene] locus=scaffold2762198_1:769:1149:+[Lack 3'-end]", "rumen3042_GL0331167_1 [gene] locus=scaffold1631620_2:131:511:+[Lack 3'-end]"]
["rumen2009040_GL0939811_1 [gene] locus=scaffold568240_2:2:346:+[Lack 5'-end]"]
["rumen2009040_GL0950215_1 [gene] locus=scaffold1949330_2:434:667:+[Lack 3'-end]"]
["rumen2009040_GL0954223_1 [gene] locus=scaffold1387697_5:1:342:-[Lack 3'-end]"]
["rumen2009040_GL0984223_1 [gene] locus=scaffold1625450_1:289:630:+[Lack 3'-end]"]
["rumen2009040_GL0997165_1 [gene] locus=scaffold220049_1:1:348:+[Lack 5'-end]", "rumen2009040_GL3427521_1 [gene] locus=scaffold133033_4:317:664:-[Lack 5'-end]"]
["rumen2009040_GL1033074_1 [gene] locus=scaffold702423_1:3:341:-[Lack 3'-end]"]
["rumen2009040_GL1079553_1 [gene] locus=scaffold409690_4:223:504:+[Lack 3'-end]"]
["rumen2009040_GL1109961_1 [gene] locus=scaffold2635216_5:525:893:-[Lack 5'-end]"]
["rumen2009040_GL1260350_1 [gene] locus=scaffold142321_2:959:1072:-[Lack 5'-end]"]
["rumen2009040_GL1294987_1 [gene] locus=scaffold2114311_2:273:542:-[Lack 5'-end]"]
["rumen2009040_GL1327098_1 [gene] locus=scaffold2734079_1:1264:1644:-[Lack 5'-end]"]
["rumen2009040_GL1374063_1 [gene] locus=scaffold839853_4:3:356:-[Lack 3'-end]"]
["rumen2009040_GL1521253_1 [gene] locus=scaffold1250252_1:1:300:+[Lack 5'-end]"]
["rumen2009040_GL1598708_1 [gene] locus=scaffold571617_1:2:307:-[Lack 3'-end]"]
["rumen2009040_GL1679044_1 [gene] locus=scaffold1288072_1:523:870:-[Lack 5'-end]"]
["rumen2009040_GL1718379_1 [gene] locus=scaffold204805_1:1:261:+[Lack 5'-end]"]
["rumen2009040_GL1801902_1 [gene] locus=scaffold1839399_2:328:714:+[Lack 3'-end]"]
["rumen2009040_GL1938061_1 [gene] locus=scaffold2528382_1:1:207:+[Lack 5'-end]"]
["rumen2009040_GL1938873_1 [gene] locus=scaffold2716147_1:1:381:+[Lack 5'-end]"]
["rumen2009040_GL1951308_1 [gene] locus=scaffold2801546_1:2:289:-[Lack 3'-end]"]
["rumen2009040_GL2024789_1 [gene] locus=scaffold1742962_1:123:557:-[Lack 5'-end]"]
["rumen2009040_GL2159959_1 [gene] locus=scaffold1441602_1:2:358:+[Lack 5'-end]"]
["rumen2009040_GL2165755_1 [gene] locus=C53051945_1:305:541:-[Lack 5'-end]"]
["rumen2009040_GL2200785_1 [gene] locus=scaffold2372755_1:354:566:-[Lack 5'-end]"]
["rumen2009040_GL2286530_1 [gene] locus=scaffold1585469_1:377:790:+[Lack 3'-end]"]
["rumen2009040_GL2381555_1 [gene] locus=scaffold1472774_1:1:285:+[Lack 5'-end]"]
["rumen2009040_GL2400909_1 [gene] locus=scaffold27439_1:58:567:-[Lack 5'-end]"]

["rumen2009040_GL2500842_1 [gene] locus=scaffold2535259_1:360:572:-[Lack 5'-end]"]
["rumen2009040_GL2532651_1 [gene] locus=scaffold2404720_3:1:234:-[Lack 3'-end]"]
["rumen2009040_GL2535472_1 [gene] locus=scaffold1951967_1:295:558:-[Lack 5'-end]"]
["rumen2009040_GL2566513_1 [gene] locus=scaffold2998878_1:3:419:-[Lack 3'-end]"]
["rumen2009040_GL2582273_1 [gene] locus=scaffold992072_5:3:191:+[Lack 5'-end]"]
["rumen2009040_GL2672523_1 [gene] locus=scaffold701553_2:2:451:-[Lack 3'-end]"]
["rumen2009040_GL2756463_1 [gene] locus=scaffold939657_2:135:503:+[Lack 3'-end]"]
["rumen2009040_GL2758646_1 [gene] locus=scaffold938630_2:3:353:+[Lack 5'-end]"]
["rumen2009040_GL2773498_1 [gene] locus=scaffold1931446_6:1:234:+[Lack 5'-end]"]
["rumen2009040_GL2847452_1 [gene] locus=scaffold441258_5:2:331:-[Lack 3'-end]"]
["rumen2009040_GL2875492_1 [gene] locus=scaffold238312_3:2:367:-[Lack 3'-end]"]
["rumen2009040_GL3055096_1 [gene] locus=scaffold1333588_2:393:728:+[Lack 3'-end]"]
["rumen2009040_GL3082071_1 [gene] locus=scaffold2862968_2:1:390:+[Lack 5'-end]"]
["rumen2009040_GL3107942_1 [gene] locus=scaffold1798144_1:3:221:-[Lack 3'-end]"]
["rumen2009040_GL3155417_1 [gene] locus=scaffold1387697_3:410:706:-[Lack 5'-end]"]
["rumen2009040_GL3269873_1 [gene] locus=scaffold1148194_5:126:503:+[Lack 3'-end]"]
["rumen2009040_GL3276802_1 [gene] locus=scaffold448955_2:1:291:+[Lack 5'-end]"]
["rumen2009040_GL3326257_1 [gene] locus=scaffold2241552_1:144:581:+[Lack 3'-end]"]
["rumen2009040_GL3500042_1 [gene] locus=scaffold132598_3:200:535:-[Complete]"]
["rumen2009040_GL3501092_1 [gene] locus=scaffold2196175_1:756:1154:-[Complete]"]
["rumen2009040_GL3528901_1 [gene] locus=scaffold223775_1:839:1186:+[Lack 3'-end]"]
["rumen2009040_GL3531298_1 [gene] locus=scaffold2764935_1:2:391:-[Lack 3'-end]"]
["rumen2009040_GL3541435_1 [gene] locus=scaffold832351_2:2:370:-[Lack 3'-end]"]
["rumen2009040_GL3626590_1 [gene] locus=C53128917_1:355:549:-[Lack 5'-end]"]
["rumen2009040_GL3630757_1 [gene] locus=C53501220_1:1:312:+[Lack 5'-end]"]
["rumen3042_GL0059136_1 [gene] locus=scaffold695306_3:1587:1763:-[Lack 5'-end]"]
["rumen3042_GL0363961_1 [gene] locus=scaffold1314062_1:1:405:-[Lack 3'-end]"]
["rumen3042_GL0587160_1 [gene] locus=scaffold731980_1:1:492:+[Lack 5'-end]"]
["rumen3042_GL0822696_1 [gene] locus=scaffold1355477_3:1:390:+[Lack 5'-end]"]
["rumen3042_GL0833834_1 [gene] locus=scaffold2422269_1:1:363:+[Lack 5'-end]"]
["rumen3042_GL0846119_1 [gene] locus=scaffold1033519_1:3:260:-[Lack 3'-end]"]
["rumen3042_GL0860281_1 [gene] locus=scaffold804980_2:3:335:+[Lack 5'-end]"]
["rumen3042_GL0916107_1 [gene] locus=scaffold85108_1:6131:6484:+[Lack 3'-end]"]
["rumen3042_GL0946451_1 [gene] locus=scaffold1087221_6:1:282:-[Lack 3'-end]"]
["rumen3042_GL0955061_1 [gene] locus=scaffold2586303_1:3:455:-[Lack 3'-end]"]
["rumen3042_GL0981838_1 [gene] locus=scaffold1489189_1:2420:2575:-[Lack 5'-end]"]
["rumen3042_GL0994695_1 [gene] locus=scaffold2511542_1:1:372:+[Lack 5'-end]"]
["rumen3042_GL1081317_1 [gene] locus=scaffold63982_1:3:251:-[Lack 3'-end]"]
["rumen3042_GL1178291_1 [gene] locus=scaffold373936_3:208:525:+[Lack 3'-end]"]
["rumen3042_GL1208192_1 [gene] locus=scaffold10932_2:1:177:+[Lack 5'-end]"]
["rumen3042_GL1213106_1 [gene] locus=scaffold828639_5:1075:1281:-[Lack 5'-end]"]
["rumen3042_GL1361017_1 [gene] locus=scaffold1087221_4:293:802:-[Lack 5'-end]"]
["rumen3042_GL1469042_1 [gene] locus=scaffold1922261_1:1:471:+[Lack 5'-end]"]

["rumen3042_GL1494266_1 [gene] locus=scaffold15366_1:4080:4355:-[Lack 5'-end]"]
["rumen3042_GL1705099_1 [gene] locus=scaffold2401685_5:1:501:-[Lack 3'-end]"]
["rumen3042_GL1761385_1 [gene] locus=scaffold1369872_1:815:958:-[Lack 5'-end]"]
["rumen3042_GL1834328_1 [gene] locus=scaffold2313862_1:146:541:-[Lack 5'-end]"]
["rumen3042_GL1943551_1 [gene] locus=scaffold589701_1:1:243:+[Lack 5'-end]"]
["rumen3042_GL2029715_1 [gene] locus=scaffold1758679_2:1112:1279:-[Lack 5'-end]"]
["rumen3042_GL2082551_1 [gene] locus=scaffold1268850_4:5265:5447:-[Lack 5'-end]"]
["rumen3042_GL2090665_1 [gene] locus=scaffold1981975_1:656:916:+[Lack 3'-end]"]
["rumen3042_GL2136591_1 [gene] locus=scaffold1561710_1:1:279:+[Lack 5'-end]"]
["rumen3042_GL2147114_1 [gene] locus=scaffold586307_5:480:788:-[Lack 5'-end]"]
["rumen3042_GL2177302_1 [gene] locus=scaffold98686_2:2:385:-[Lack 3'-end]"]
["rumen3042_GL2281281_1 [gene] locus=scaffold157141_3:3:197:-[Lack 3'-end]"]
["rumen3042_GL2333249_1 [gene] locus=scaffold2580510_1:378:686:+[Lack 3'-end]"]
["rumen3042_GL2373089_1 [gene] locus=scaffold851029_1:1:201:+[Lack 5'-end]"]
["rumen3042_GL2400089_1 [gene] locus=scaffold2401685_4:432:857:-[Lack 5'-end]"]
["rumen3042_GL2613267_1 [gene] locus=scaffold1933295_1:3:242:-[Lack 3'-end]"]
["rumen3042_GL2658947_1 [gene] locus=scaffold1076797_1:2:367:+[Lack 5'-end]"]
["rumen552_GL0024812_1 [gene] locus=scaffold831033_1:3:341:+[Lack 5'-end]"]
["rumen552_GL0063210_1 [gene] locus=scaffold759128_1:3:410:-[Lack 3'-end]"]
["rumen552_GL0079101_1 [gene] locus=C21751169_1:569:781:+[Lack 3'-end]"]
["rumen552_GL0205558_1 [gene] locus=scaffold394049_1:3:509:+[Lack both ends]"]
["rumen552_GL0238773_1 [gene] locus=scaffold881856_1:1:180:+[Lack 5'-end]"]
["rumen552_GL0242063_1 [gene] locus=scaffold470503_2:1073:1399:-[Lack 5'-end]", "rumen2009040_GL2429135_1 [gene] locus=scaffold682176_2:1:327:+[Lack 5'-end]"]
["rumen552_GL0376701_1 [gene] locus=scaffold370500_3:3:314:-[Lack 3'-end]"]
["rumen552_GL0643184_1 [gene] locus=scaffold551232_2:1:264:+[Lack 5'-end]"]
["rumen552_GL0749241_1 [gene] locus=scaffold713861_6:2:379:-[Lack 3'-end]"]
["rumen552_GL0757863_1 [gene] locus=scaffold418765_1:1:231:+[Lack 5'-end]"]
["rumen552_GL1230559_1 [gene] locus=scaffold873417_1:782:994:-[Lack 5'-end]", "rumen100058_GL1267405_1 [gene] locus=scaffold73793_2:2:214:+[Lack 5'-end]"]
["rumen552_GL1343886_1 [gene] locus=scaffold209070_9:2:130:+[Lack 5'-end]"]
["rumen552_GL1372244_1 [gene] locus=scaffold634987_3:265:663:-[Lack 5'-end]"]
["rumen552_GL1470768_1 [gene] locus=scaffold255115_1:298:600:-[Lack 5'-end]"]
["rumen552_GL1680869_1 [gene] locus=scaffold745815_2:627:782:-[Lack 5'-end]"]
["rumen552_GL1709277_1 [gene] locus=C21710250_1:3:275:-[Lack 3'-end]"]
["rumen552_GL1712898_1 [gene] locus=scaffold949811_2:2:340:-[Lack 3'-end]"]
["rumen552_GL1748723_1 [gene] locus=C21253972_1:1:327:+[Lack 5'-end]"]
["rumen553_GL0082586_1 [gene] locus=scaffold44886_4:1009:1368:+[Lack 3'-end]"]
["rumen553_GL0098425_1 [gene] locus=scaffold319491_5:1:375:+[Lack 5'-end]"]
["rumen553_GL0160224_1 [gene] locus=scaffold69956_2:2:346:+[Lack 5'-end]"]
["rumen553_GL0202918_1 [gene] locus=scaffold274312_1:2:181:+[Lack 5'-end]"]
["rumen553_GL0490408_1 [gene] locus=scaffold372603_4:266:604:+[Lack 3'-end]"]
["rumen553_GL0543694_1 [gene] locus=scaffold194301_6:407:676:-[Lack 5'-end]"]

["rumen553_GL0553274_1 [gene] locus=C7637698_1:1574:1957:-[Lack 5'-end]"]
["rumen553_GL0562574_1 [gene] locus=scaffold392100_1:3:185:+[Lack 5'-end]", "rumen583_GL0702223_1 [gene] locus=scaffold303135_1:781:963:-[Lack 5'-end]"]
["rumen553_GL0665105_1 [gene] locus=scaffold46728_2:1479:1772:+[Complete]"]
["rumen553_GL0678607_1 [gene] locus=scaffold145208_1:211:585:+[Lack 3'-end]"]
["rumen553_GL0718529_1 [gene] locus=scaffold362985_2:3:404:+[Lack 5'-end]"]
["rumen553_GL0865556_1 [gene] locus=scaffold13571_2:1:372:-[Lack 3'-end]"]
["rumen553_GL0865807_1 [gene] locus=scaffold195522_3:2:337:+[Lack 5'-end]", "rumen552_GL0376702_1 [gene] locus=scaffold370500_3:304:639:-[Lack 5'-end]"]
["rumen553_GL0895254_1 [gene] locus=scaffold100021_2:2:349:+[Lack 5'-end]"]
["rumen554_GL0138870_1 [gene] locus=scaffold288892_1:2183:2407:-[Lack 5'-end]"]
["rumen554_GL0188842_1 [gene] locus=scaffold1360733_1:1145:1423:+[Lack 3'-end]"]
["rumen554_GL0365240_1 [gene] locus=scaffold1555248_1:1:246:+[Lack 5'-end]"]
["rumen554_GL0394083_1 [gene] locus=scaffold2148067_1:692:922:-[Lack 5'-end]"]
["rumen554_GL0397046_1 [gene] locus=scaffold679321_2:2:406:+[Lack 5'-end]", "rumen3042_GL1821535_1 [gene] locus=scaffold1264780_4:3:407:+[Lack 5'-end]"]
["rumen554_GL0410305_1 [gene] locus=scaffold1434111_2:1:207:+[Lack 5'-end]"]
["rumen554_GL0532025_1 [gene] locus=scaffold1503866_2:461:688:-[Lack 5'-end]"]
["rumen554_GL0907277_1 [gene] locus=scaffold2042893_9:3:305:+[Lack 5'-end]"]
["rumen554_GL1014034_1 [gene] locus=scaffold597931_10:1:285:+[Lack 5'-end]"]
["rumen554_GL1019426_1 [gene] locus=scaffold135260_1:3196:3411:-[Lack 5'-end]"]
["rumen554_GL1048462_1 [gene] locus=scaffold2076749_2:872:1165:+[Lack 3'-end]"]
["rumen554_GL1231103_1 [gene] locus=C40248868_1:241:708:+[Lack 3'-end]"]
["rumen554_GL1251878_1 [gene] locus=scaffold837034_2:2:190:+[Lack 5'-end]"]
["rumen554_GL1269965_1 [gene] locus=scaffold1279791_1:254:637:+[Lack 3'-end]"]
["rumen554_GL1400747_1 [gene] locus=scaffold357645_4:923:1123:-[Lack 5'-end]"]
["rumen554_GL1410982_1 [gene] locus=scaffold861386_5:540:947:-[Lack 5'-end]", "rumen2009040_GL2121181_1 [gene] locus=scaffold1829910_2:536:943:-[Lack 5'-end]"]
["rumen554_GL1541304_1 [gene] locus=scaffold519696_3:3:323:+[Lack 5'-end]", "rumen100058_GL1478275_1 [gene] locus=scaffold2792750_1:343:663:-[Lack 5'-end]"]
["rumen554_GL1657938_1 [gene] locus=scaffold1094179_2:369:686:+[Lack 3'-end]", "rumen555_GL2048171_1 [gene] locus=C28722804_1:848:1165:+[Lack 3'-end]"]
["rumen554_GL1669413_1 [gene] locus=scaffold787818_3:3:290:+[Lack 5'-end]", "rumen3042_GL1858140_1 [gene] locus=scaffold1990046_3:219:506:-[Lack 5'-end]"]
["rumen554_GL1748615_1 [gene] locus=scaffold462637_8:1:444:-[Lack 3'-end]"]
["rumen554_GL1766862_1 [gene] locus=scaffold1837363_1:3:689:-[Lack 3'-end]"]
["rumen554_GL1781225_1 [gene] locus=scaffold702412_4:1738:2037:+[Complete]", "rumen0081_GL0759067_1 [gene] locus=scaffold314097_1:1:300:+[Lack 5'-end]"]
["rumen554_GL1795507_1 [gene] locus=scaffold1884241_1:175:522:+[Lack 3'-end]"]
["rumen554_GL1877580_1 [gene] locus=scaffold319861_1:1:324:-[Lack 3'-end]"]
["rumen554_GL1932074_1 [gene] locus=scaffold664346_1:634:1005:+[Lack 3'-end]"]
["rumen554_GL2069886_1 [gene] locus=C39226807_1:3:389:-[Lack 3'-end]"]
["rumen554_GL2146420_1 [gene] locus=scaffold1274607_1:411:626:-[Lack 5'-end]"]

["rumen554_GL2179928_1 [gene] locus=scaffold981268_6:3:494:-[Lack 3'-end]"]
["rumen554_GL2185713_1 [gene] locus=scaffold1470618_3:2:151:+[Lack 5'-end]"]
["rumen554_GL2277224_1 [gene] locus=scaffold1137894_1:3:356:+[Lack 5'-end]"]
["rumen554_GL2377912_1 [gene] locus=scaffold1992475_3:539:730:-[Lack 5'-end]"]
["rumen554_GL2593257_1 [gene] locus=scaffold140049_2:1499:1711:+[Lack 3'-end]"]
["rumen554_GL2595288_1 [gene] locus=scaffold1257514_3:2:229:-[Lack 3'-end]"]
["rumen554_GL2725600_1 [gene] locus=scaffold2014638_1:3:398:-[Lack 3'-end]", "rumen2009040_GL0113933_1 [gene] locus=scaffold2685079_1:2:397:-[Lack 3'-end]"]
["rumen554_GL2862624_1 [gene] locus=scaffold627097_5:590:901:+[Lack 3'-end]"]
["rumen554_GL2884529_1 [gene] locus=scaffold1669682_1:2:232:+[Lack 5'-end]"]
["rumen554_GL3088331_1 [gene] locus=C39804361_1:2:331:+[Lack 5'-end]"]
["rumen554_GL3091637_1 [gene] locus=scaffold1981977_1:256:666:+[Lack 3'-end]"]
["rumen554_GL3117223_1 [gene] locus=scaffold12496_2:1:405:+[Lack 5'-end]"]
["rumen555_GL0027538_1 [gene] locus=scaffold131276_2:563:1003:+[Lack 3'-end]"]
["rumen555_GL0068504_1 [gene] locus=scaffold1418384_2:3:326:+[Lack 5'-end]"]
["rumen555_GL0072394_1 [gene] locus=C27352657_1:1:282:+[Lack 5'-end]"]
["rumen555_GL0227348_1 [gene] locus=scaffold162383_2:332:655:+[Lack 3'-end]"]
["rumen555_GL0268448_1 [gene] locus=scaffold1543841_1:325:678:-[Lack 5'-end]"]
["rumen555_GL0377058_1 [gene] locus=scaffold1214444_2:2773:3108:+[Lack 3'-end]"]
["rumen555_GL0398033_1 [gene] locus=scaffold1360590_1:3:392:+[Lack 5'-end]"]
["rumen555_GL0517934_1 [gene] locus=C27875116_1:3:314:+[Lack 5'-end]"]
["rumen555_GL0633901_1 [gene] locus=scaffold1502535_1:3:317:+[Lack 5'-end]"]
["rumen555_GL0651556_1 [gene] locus=scaffold308348_2:2:295:-[Lack 3'-end]"]
["rumen555_GL0652635_1 [gene] locus=scaffold1347373_3:532:735:+[Lack 3'-end]"]
["rumen555_GL0670004_1 [gene] locus=scaffold1324758_1:9029:9298:+[Lack 3'-end]"]
["rumen555_GL0922353_1 [gene] locus=scaffold666065_1:773:946:-[Lack 5'-end]"]
["rumen555_GL0956666_1 [gene] locus=scaffold1091563_2:1897:2226:-[Lack 5'-end]"]
["rumen555_GL1184849_1 [gene] locus=scaffold1557299_2:2:274:+[Lack 5'-end]"]
["rumen555_GL1224395_1 [gene] locus=scaffold193196_2:2:154:+[Lack 5'-end]"]
["rumen555_GL1406086_1 [gene] locus=scaffold929941_1:3:311:-[Lack 3'-end]"]
["rumen555_GL1858893_1 [gene] locus=C27598164_1:226:597:+[Lack 3'-end]"]
["rumen555_GL1876032_1 [gene] locus=scaffold7414_1:1:306:+[Lack 5'-end]"]
["rumen555_GL1992655_1 [gene] locus=C28343876_1:1:222:+[Lack 5'-end]"]
["rumen555_GL1995028_1 [gene] locus=scaffold312725_1:111:524:-[Lack 5'-end]"]
["rumen555_GL2118963_1 [gene] locus=scaffold329944_2:277:627:+[Lack 3'-end]"]
["rumen555_GL2180460_1 [gene] locus=scaffold1526821_1:1:393:+[Lack 5'-end]"]
["rumen555_GL2452583_1 [gene] locus=scaffold851016_2:339:710:+[Lack 3'-end]"]
["rumen555_GL2480943_1 [gene] locus=scaffold1347711_1:1117:1287:-[Lack 5'-end]"]
["rumen555_GL2509487_1 [gene] locus=scaffold1350860_1:3:359:+[Lack 5'-end]"]
["rumen583_GL0053729_1 [gene] locus=C5168210_1:2:244:+[Lack 5'-end]"]
["rumen583_GL0053730_1 [gene] locus=C5168210_1:373:603:-[Lack 3'-end]", "rumen2009040_GL0943771_1 [gene] locus=scaffold401680_1:3:233:-[Lack 3'-end]"]
["rumen583_GL0213114_1 [gene] locus=scaffold42773_5:3:260:-[Lack 3'-end]"]

["rumen583_GL0215888_1 [gene] locus=scaffold100224_5:1:312:+[Lack 5'-end]"," "rumen0081_GL0689776_1 [gene] locus=scaffold335362_4:1:312:+[Lack 5'-end]"]
["rumen583_GL0228964_1 [gene] locus=scaffold155921_1:148:429:+[Complete]"]
["rumen583_GL0244099_1 [gene] locus=scaffold26514_7:2:343:-[Lack 3'-end]"]
["rumen583_GL0346722_1 [gene] locus=scaffold212105_4:557:715:-[Lack 5'-end]"]
["rumen583_GL0393253_1 [gene] locus=scaffold92131_1:1:411:-[Lack 3'-end]"]
["rumen583_GL0455644_1 [gene] locus=scaffold143659_1:1:345:+[Lack 5'-end]"]
["rumen583_GL0551175_1 [gene] locus=scaffold225563_1:1055:1315:-[Lack 5'-end]"]
["rumen583_GL0594447_1 [gene] locus=scaffold139170_2:3:140:+[Lack 5'-end]"]
["rumen583_GL0645943_1 [gene] locus=C5419234_1:1:141:+[Lack 5'-end]"]
["rumen7049_GL0001475_1 [gene] locus=C52796474_1:596:940:-[Lack 5'-end]"]
["rumen7049_GL0049077_1 [gene] locus=scaffold1146656_3:2:427:+[Lack 5'-end]"]
["rumen7049_GL0216554_1 [gene] locus=scaffold799511_1:663:833:+[Lack 3'-end]"]
["rumen7049_GL0220356_1 [gene] locus=scaffold2216306_1:426:692:-[Lack 5'-end]"]
["rumen7049_GL0493365_1 [gene] locus=scaffold848548_1:676:1020:+[Lack 3'-end]"]
["rumen7049_GL0534985_1 [gene] locus=scaffold1763776_1:3:347:+[Lack 5'-end]"]
["rumen7049_GL0857407_1 [gene] locus=scaffold1178704_1:482:790:-[Lack 5'-end]"]
["rumen7049_GL0888049_1 [gene] locus=scaffold867490_1:739:1062:-[Lack 5'-end]"]
["rumen7049_GL0989810_1 [gene] locus=scaffold970554_2:355:684:-[Lack 5'-end]"]
["rumen7049_GL1059735_1 [gene] locus=scaffold629855_5:3:305:+[Lack 5'-end]"]
["rumen7049_GL1283114_1 [gene] locus=scaffold1642442_1:421:618:-[Lack 5'-end]"]
["rumen7049_GL1314016_1 [gene] locus=scaffold1326008_1:175:507:+[Lack 3'-end]"]
["rumen7049_GL1367561_1 [gene] locus=scaffold2187250_1:3:527:-[Lack 3'-end]"]
["rumen7049_GL1409444_1 [gene] locus=scaffold844916_3:335:832:+[Lack 3'-end]"]
["rumen7049_GL1438087_1 [gene] locus=scaffold602757_1:3:326:-[Lack 3'-end]"]
["rumen7049_GL1458110_1 [gene] locus=scaffold532368_3:912:1145:-[Lack 5'-end]"]
["rumen7049_GL1544548_1 [gene] locus=C52778990_1:535:930:+[Lack 3'-end]"]
["rumen7049_GL1676226_1 [gene] locus=scaffold942407_1:2:316:-[Lack 3'-end]"]
["rumen7049_GL1899950_1 [gene] locus=scaffold1940712_1:389:604:-[Lack 5'-end]"]
["rumen7049_GL1961835_1 [gene] locus=scaffold1357629_3:2:331:-[Lack 3'-end]"]
["rumen7049_GL2118273_1 [gene] locus=scaffold1193657_2:1395:1556:+[Lack 3'-end]"]
["rumen7049_GL2276028_1 [gene] locus=scaffold185098_2:2033:2350:-[Lack 5'-end]"]
["rumen7049_GL2637773_1 [gene] locus=scaffold1432033_1:598:951:+[Lack 3'-end]"]
["rumen7049_GL2701731_1 [gene] locus=C52742654_1:788:910:-[Lack 5'-end]"]
["rumen7049_GL2729833_1 [gene] locus=C51342306_1:1:225:+[Lack 5'-end]"]
["rumen7049_GL2874857_1 [gene] locus=scaffold2079380_1:950:1180:-[Lack 5'-end]"]



**Table S2**

List of the multi-modular sequences containing a GH130 module, and their location in the meta-nodes.

Sequence ID	Modularity	SSN Cluster
CAZy DB		
ACY49488.1	GH130-GH130	small meta-node (<20 sequences)
AEN74517.1	GH130-GH130	small meta-node (<20 sequences)
AKM78124.1	GH130-GH130	small meta-node (<20 sequences)
AKM83974.1	GH130-GH130	small meta-node (<20 sequences)
CCP27154.1	GH130-GT81	small meta-node (<20 sequences)
AEE92278.1	GH130-GT81	small meta-node (<20 sequences)
Human metagenome		
DOM025_GL0036051	GH130-GH92	Singletons
MH0378_GL0079806	GH92-GH130	C3
MH0369_GL0053907	GH127-GH130_distantly related	small meta-node (<20 sequences)
Rumen metagenome		
0081_GL1521727	GH130-GH78	C3
3042_GL0231557	GH130-GH78	C3
0081_GL0217456	GH130-GH78	C3
7049_GL1068002	GH2-GH130	C3
554_GL2279888	GH92-GH130	C3
7049_GL1012174	GH92-GH130	C3
2009040_GL1278742	GH43-GH130	C3
555_GL0472243	GH130_dist-GH142	UC4
555_GL1429890	GH130_dist-GH142	UC4
0081_GL0027620	GH130_dist-GH142	UC4
0081_GL1803283	GH130_dist-GH142	UC4
2009040_GL1002494	GH130_dist-GH142	UC4
7049_GL0472254	GH130_dist-GH142	UC4
7049_GL0484382	GH130_dist-GH142	UC4
552_GL1270477	GH130_dist-GH142	UC4
554_GL0058843	GH130_dist-GH142	UC4

**Table S3**

Characteristics of the sequences chosen for biochemical characterization.

Meta-node	Sequence ID	Prevalence in the human gut metagenome (% of individuals)	Best Blast hit with a GH130 sequence from the CAZy DB		Best Blast hit with a characterized GH130		Activity
			Query coverage	% Identity	Query coverage	% Identity	
UC1	MH0431_GL0150624	17 %	AVM43672.1		AAO76140.1		β-1,4-mannosyl-glucuronic acid phosphorylase
			95%	59.8%	94%	33.1%	
UC3	MH0373_GL0093988	17 %	APF19181.1		WP_026485574.1		β-1,4-mannooligosaccharide phosphorylase
			95%	43.4%	97%	39.3%	
UC4	MH0011_GL0029022	53 %	AMM53793.1		ACT94389.1		/
			69%	31.1%	57%	30.0%	
UC6	MH0409_GL0096961	4 %	ADO84614.1		VCV21229.1		/
			98%	36.6%	98%	36.6%	
UC7	340101.Vvad_PD3074	12 %	AIQ48603.1		CAZ94304.1		β-1,3-mannosyl-glucose phosphorylase β-1,3-mannooligosaccharide phosphorylase

**Table S4**

Distribution of the predicted phosphorylases and hydrolases in the meta-nodes. The number of sequences includes full-length and truncated sequences.

SSN meta-nodes	C1	C2	C4	C5	C6	UC1	UC2	UC3	UC5	UC6	UC7	UC8	UC9	Total	C3	UC4	Total
Predicted mechanism	GP	GP	GP	GP	GP	GP	GP	GP	GP	GP	GP	GP	GP	GP	GH	GH	GH
<b>CAZy</b>	222	269	290	42	85	31	199	135	61	0	9	26	29	1398	113	0	113
<b>Human mg</b>	347	332	53	51	2	31	0	24	0	20	6	8	0	874	113	31	144
<b>Mouse mg</b>	149	227	18	5	0	1	0	0	0	0	1	2	0	403	26	2	28
<b>Pig mg</b>	235	244	13	13	0	24	0	3	0	1	4	0	0	537	39	5	44
<b>Bovine mg</b>	970	643	19	61	0	118	0	7	0	11	13	0	0	1842	78	53	131
<b>Total</b>	1923	1715	393	172	87	205	199	169	61	32	33	36	29	5054	369	91	460