

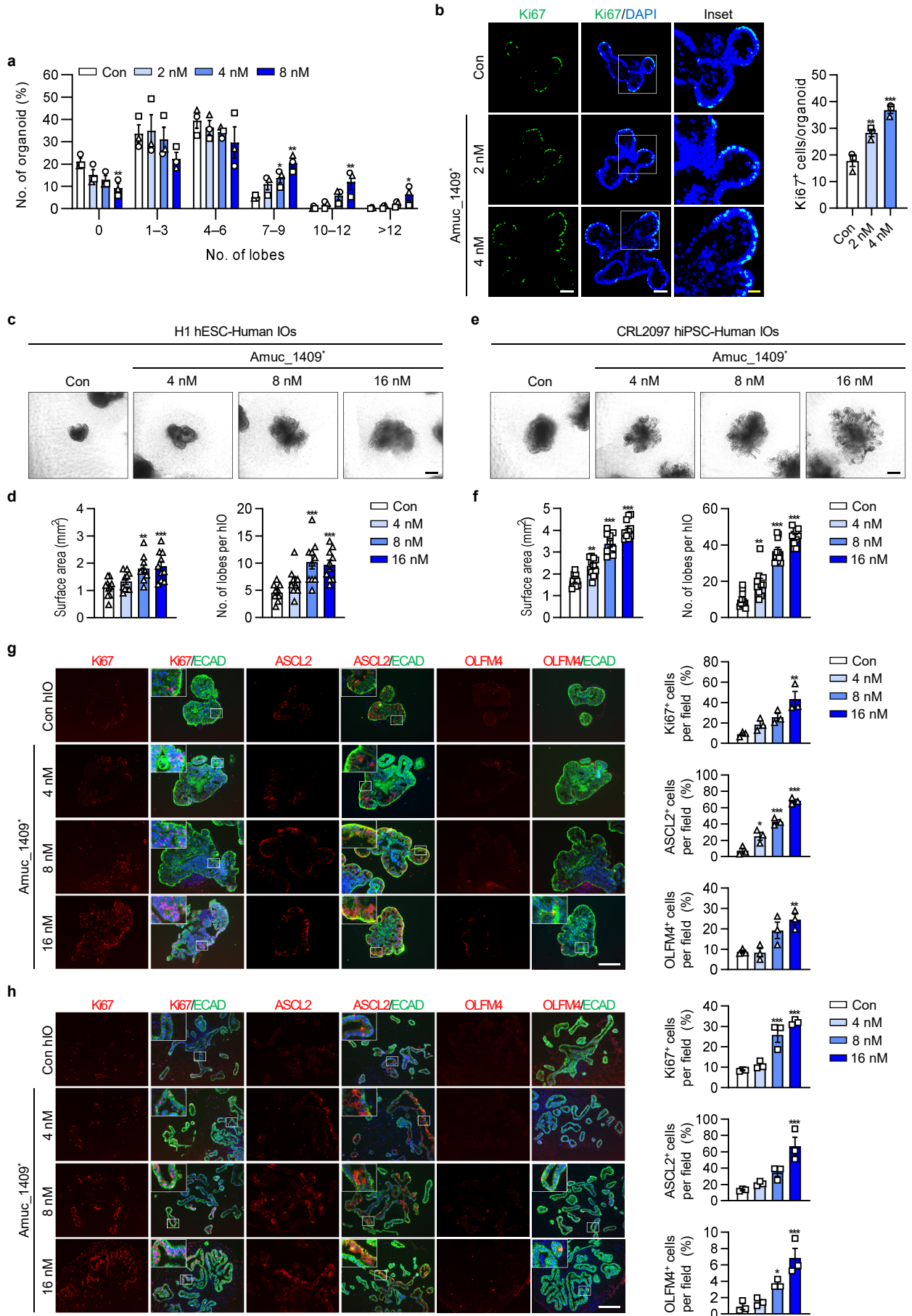
## **Supplementary information**

### **The secreted protein Amuc\_1409 from *Akkermansia muciniphila* improves gut health through intestinal stem cell regulation**

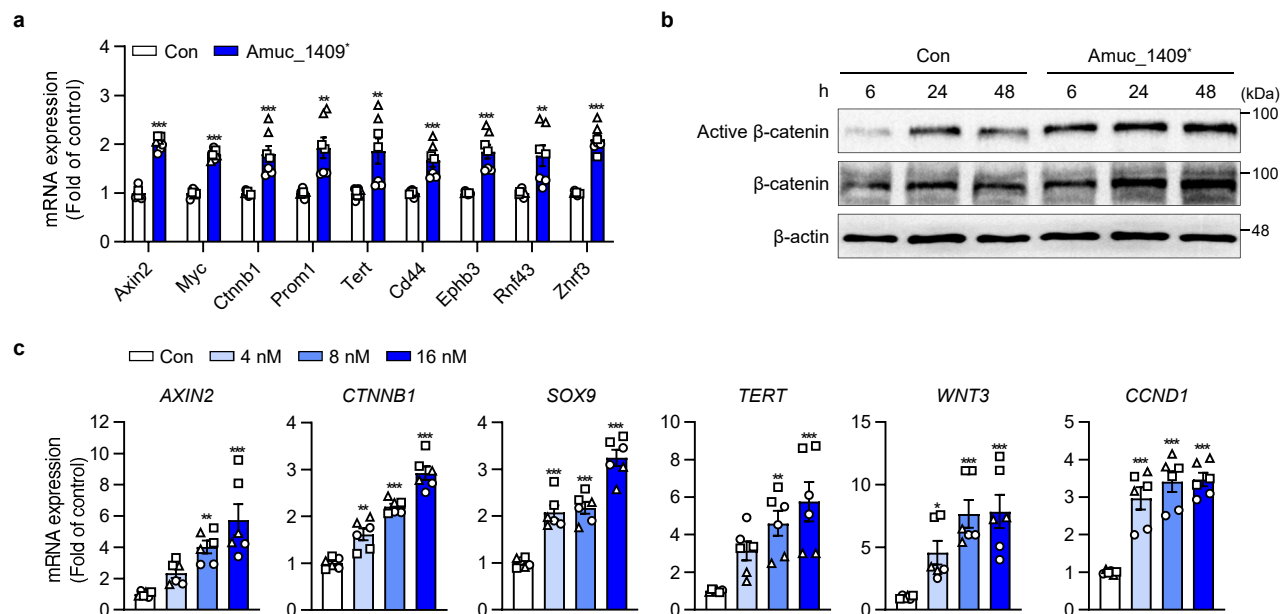
Eun-Jung Kang, Jae-Hoon Kim, Young Eun Kim, Hana Lee, Kwang Bo Jung, Dong-Ho Chang, Youngjin Lee, Shinye Park, Eun-Young Lee, Eun-Ji Lee, Ho Bum Kang, Moon-Young Rhyoo, Seungwoo Seo, Sohee Park, Yubin Huh, Jun Go, Jung Hyeon Choi, Young-Keun Choi, In-Bok Lee, Dong-Hee Choi, Yun Jeong Seo, Jung-Ran Noh, Kyoung-Shim Kim, Jung Hwan Hwang, Ji-Seon Jeong, Ha-Jeong Kwon, Hee Min Yoo, Mi-Young Son, Yeon-Gu Kim, Dae-Hee Lee, Tae-Young Kim, Hyo-Jung Kwon, Myung Hee Kim, Byoung-Chan Kim, Yong-Hoon Kim, Dukjin Kang, and Chul-Ho Lee

**Supplementary Figures 1–16 & Legends**

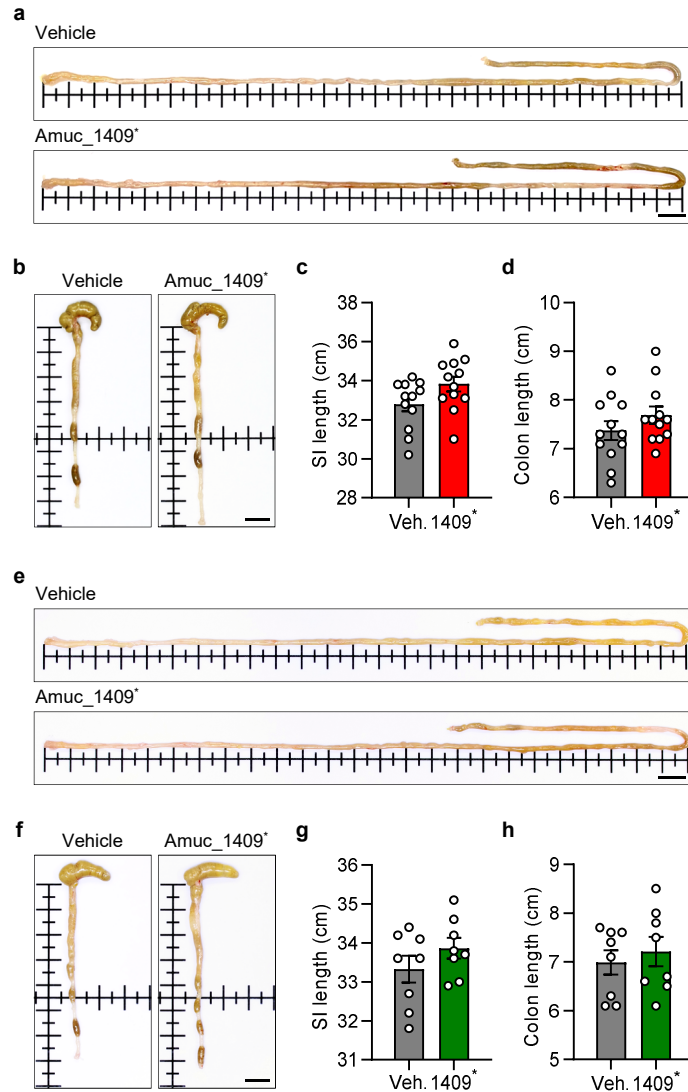
**Supplementary Tables 1–9**



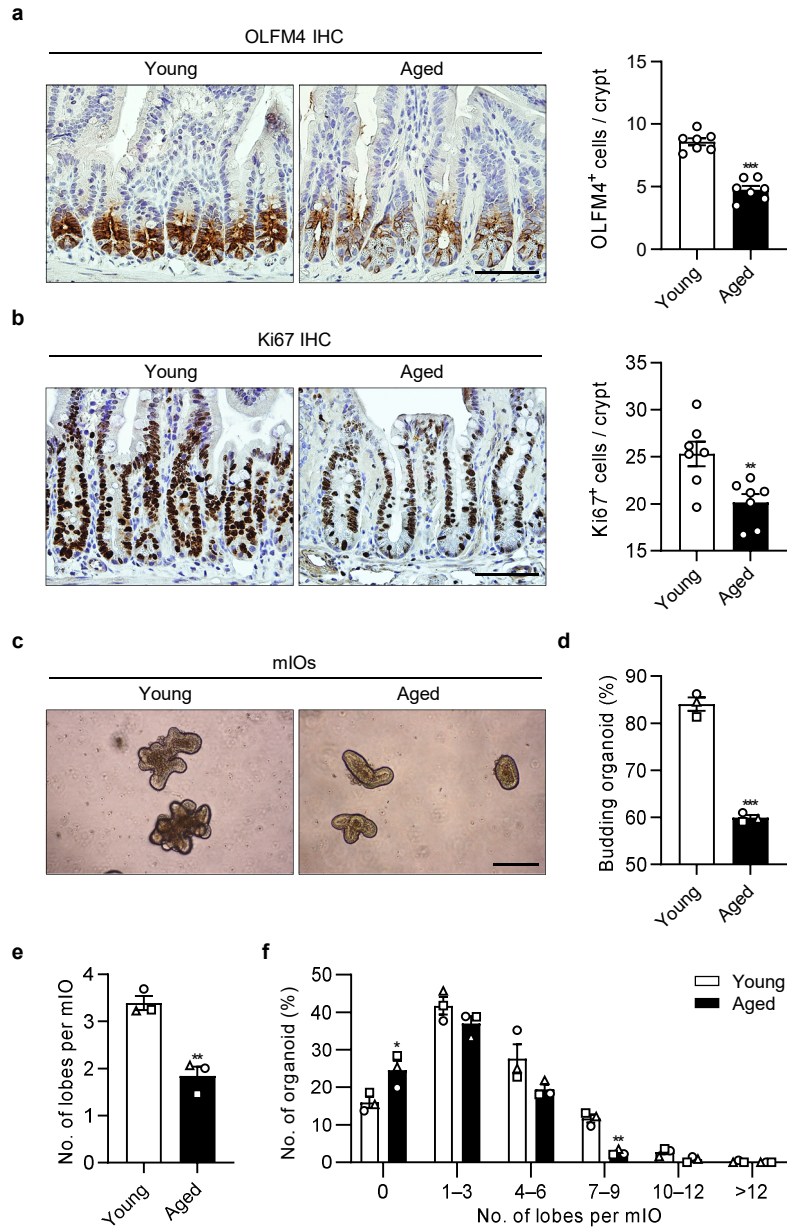
**Supplementary Fig. 1 Amuc\_1409 improves the proliferation and development of intestinal organoids.** **a** The percentage distribution of organoids with the indicated number of lobes per mIO in control and Amuc\_1409\*-treated young mIOs. **b** Representative IF staining images (left panel) for Ki67 (green) and DAPI (nuclei, blue), and quantification of Ki67<sup>+</sup> cells per organoid in control and Amuc\_1409\*-treated young mIOs. White scale bar, 50  $\mu$ m. Yellow scale bar, 20  $\mu$ m. **c, d** Representative brightfield images (**c**), the surface area of hIOs (**d**, left panel), and the number of lobes per hIO (**d**, right panel) in control and Amuc\_1409\*-treated hIOs derived from H1 hESC line.  $n = 10$  organoids per group. Scale bar, 200  $\mu$ m. **e, f** Representative brightfield images (**e**), the surface area of hIOs (**f**, left panel), and the number of lobes per hIO (**f**, right panel) in control and Amuc\_1409\*-treated hIOs derived from CRL2097 hiPSC line.  $n = 10$  organoids per group. Scale bar, 200  $\mu$ m. **g, h** Representative IF staining images (**g, h**, left panel) for the proliferation marker (Ki67), intestinal stem cell marker (ASCL2), and intestinal maturation marker (OLFM4) in control hIOs and Amuc\_1409\*-treated hIOs derived from H1 hESC line (**g**) or CRL2097 hiPSC line (**h**). Quantification of the percentage of positive cells for each marker per field of view is presented (**g, h**, right panel,  $n = 3$  fields per group). Intestinal epithelial cells were identified using E-cadherin (ECAD, green); Ki67, ASCL2, and OLFM4 (red); DAPI (blue). Scale bar, 275  $\mu$ m. All data are presented as the mean  $\pm$  SEM. In **a** and **b**, a different symbol indicates a data point representing each biological replicate from independently established organoid lines derived from distinct mouse litters ( $n = 3$  biologically independent mice). In **b**, Ki67<sup>+</sup> cells were counted in 20 organoids per group from each biological replicate. Statistical analyses were performed via one-way ANOVA with Dunnett's multiple comparisons test (**a, b, d, f, g, h**) (\* $p < 0.05$ , \*\* $p < 0.01$ , and \*\*\* $p < 0.001$  vs control group). Source data, including the exact  $p$ -values, are provided as a Source Data file.



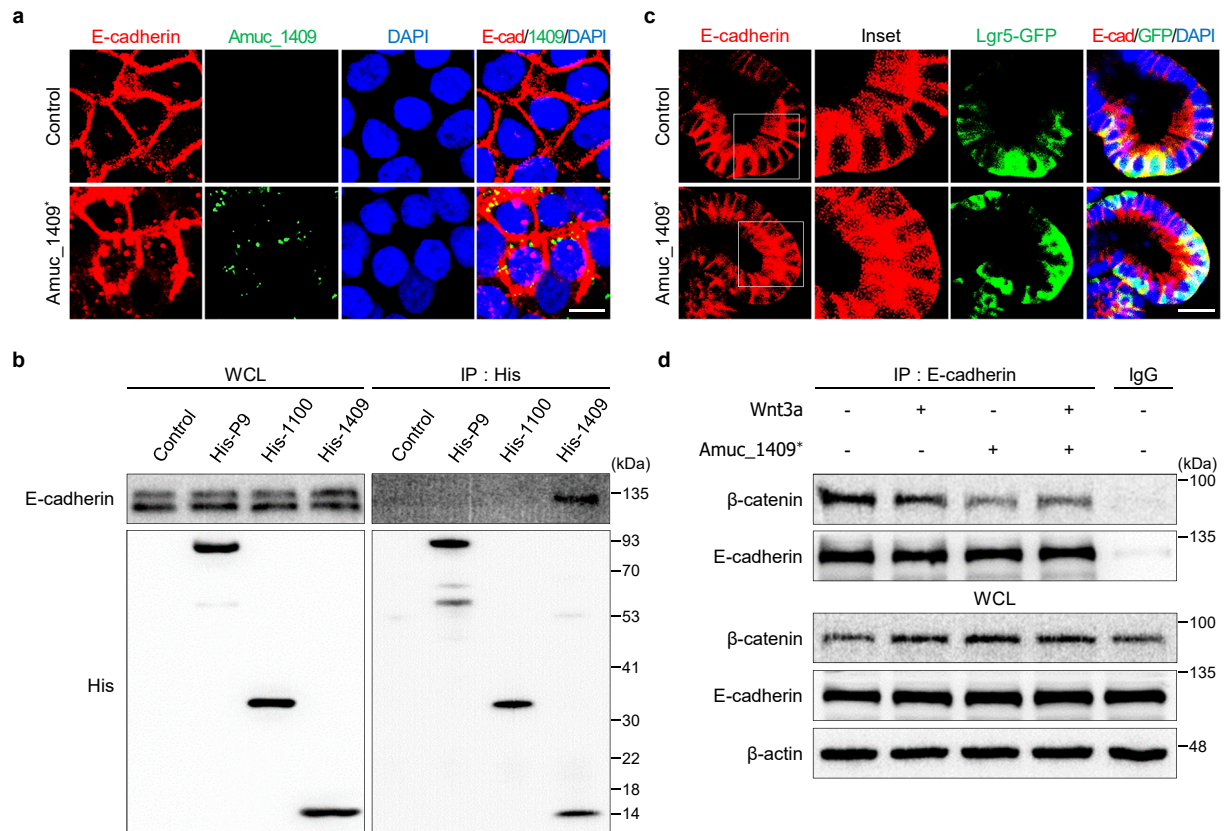
**Supplementary Fig. 2 Amuc\_1409 activates the Wnt/β-catenin signaling pathway in intestinal organoids.** **a** qRT-PCR showing the relative mRNA expression of Wnt/β-catenin target genes in mIOs treated with or without Amuc\_1409\* (8 nM). **b** Western blot results showing the protein levels of active and total β-catenin in mIOs treated with or without Amuc\_1409\* (8 nM) for the indicated times point before harvest. **c** qRT-PCR results showing the relative mRNA expression of Wnt/β-catenin target genes in control hIOs and hIOs treated with the indicated concentration of Amuc\_1409\* (4, 8, and 16 nM). All data are presented as the mean ± SEM. In **a** and **c**, a different symbol indicates a data point representing each biological replicate from independently established organoid lines derived from distinct mouse litters (**a**:  $n = 3$  biologically independent mice) or two hESC/one hiPSC lines (**c**:  $n = 3$  biologically independent organoid lines). Each biological replicate includes two or three technical replicates. In **b**, data shown are representative of two independent biological replicates, each with similar results. Statistical analyses were performed using two-tailed Student's  $t$ -test (**a**) and one-way ANOVA with Dunnett's multiple comparisons test (**c**) ( $*p < 0.05$ ,  $**p < 0.01$ , and  $***p < 0.001$  vs control group). Source data, including the exact  $p$ -values, are provided as a Source Data file. The uncropped western blot images are provided in Supplementary Fig. 13.



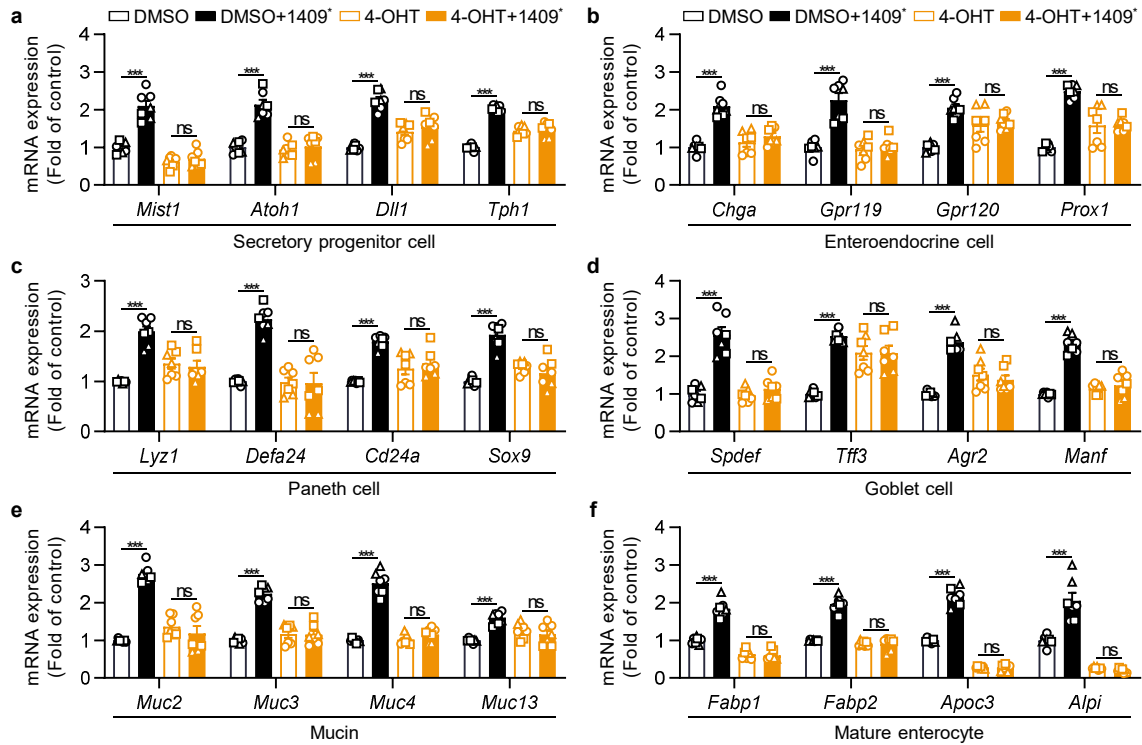
**Supplementary Fig. 3** The effects of Amuc\_1409 administration on changes of intestinal length in irradiated or 5-FU-treated mice. **a–d** Results of gross morphological analyses of the SI and colon from vehicle- or Amuc\_1409\*-treated mice on day 5 after irradiation ( $n = 12$  biological replicate mice per group). Representative macroscopic images of the SI (**a**) and colon (**b**) and quantified length of the SI (**c**) and colon (**d**). Scale bar, 1 cm. **e–h** Results of the gross morphological analyses of the SI and colon from vehicle- or Amuc\_1409\*-treated mice in the 5-FU-induced intestinal damage model ( $n = 8$  biological replicate mice per group). Representative macroscopic images of the SI (**e**) and colon (**f**) and quantified length of the SI (**g**) and colon (**h**). Scale bar, 1 cm. All data are presented as the mean  $\pm$  SEM. Data shown in **a–h** are representative of three independent experiments, each with similar results. Each data point represents a biological replicate, corresponding to one mouse. Statistical analyses were performed using two-tailed Student's *t*-test (**c**, **d**, **g**, **h**). Source data, including the exact *p*-values, are provided as a Source Data file.



**Supplementary Fig. 4 Aging induces a decline in the number and function of ISCs.** **a, b** Comparison of the ISC number and ISC and TA cell proliferation between small intestine (SI) tissue of young (3–4-month-old) and aged (25-month-old) mice via IHC. Representative IHC images for OLFM4 (**a**, left panel) and Ki67 (**b**, left panel), and quantification of OLFM4<sup>+</sup> cells (**a**, right panel) and Ki67<sup>+</sup> cells per crypt (**b**, right panel). Scale bar, 50  $\mu$ m. **c–f**, Comparison of the regenerative capacity of ISC in mIOs formed from SI crypts of young (3–4-month-old) and aged (25-month-old) mice. Representative brightfield images (**c**) and assessment of the percentage of budding organoids (**d**), the number of lobes per mIO (**e**), and the percentage distribution of organoids with indicated number of lobes per mIO (**f**) in the young and aged mIOs on day 4 after the second subculturing passage. Scale bar, 200  $\mu$ m. In **a** and **b**, each data point represents a biological replicate, corresponding to one mouse ( $n = 7$  biological replicate mice per group). In **d–f**, a different symbol indicates a data point representing each biological replicate from independently established organoid lines derived from distinct mouse litters ( $n = 3$  biological replicate mice per group). All data are presented as the mean  $\pm$  SEM. Statistical analyses were performed using two-tailed Student's *t*-test ( $*p < 0.05$ ,  $**p < 0.01$ , and  $***p < 0.001$  vs young group). Source data, including the exact *p*-values, are provided as a Source Data file.

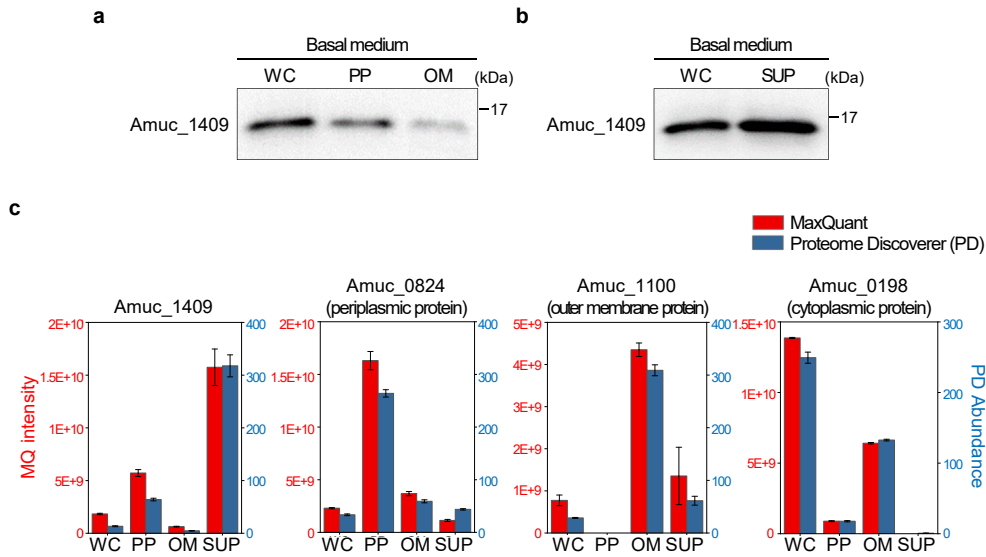


**Supplementary Fig. 5 Amuc<sub>1409</sub> triggers E-cadherin/β-catenin complex dissociation through interaction with E-cadherin.** **a** Representative images of IF staining for E-cadherin and Amuc<sub>1409</sub> in HT-29 cells treated with or without Amuc<sub>1409</sub><sup>\*</sup> for 30 min. E-cadherin (red); Amuc<sub>1409</sub> (green), DAPI (nuclei, blue). Scale bar, 10 μm. **b** Results after WCLs from HT-29 cells incubated with purified His-tagged P9, His-tagged Amuc<sub>1100</sub> or His-tagged Amuc<sub>1409</sub> protein (0.5 μg) for 1 h were subjected to immunoprecipitation using His-antibodies, followed by immunoblotting with the indicated antibodies. His-tagged P9 and His-tagged Amuc<sub>1100</sub> proteins were used as control proteins. **c** Representative images of IF staining for E-cadherin and GFP in vehicle- or Amuc<sub>1409</sub><sup>\*</sup> (16 nM)-treated mIOs derived from *Lgr5-EGFP-IRES-CreERT2* mice. E-cadherin (red); Lgr5-GFP<sup>+</sup> ISC (green), DAPI (nuclei, blue). Scale bar, 20 μm. **d** HT-29 cells were treated with Wnt3a (150 ng/mL), Amuc<sub>1409</sub><sup>\*</sup> (16 nM), or a combination of Wnt3a (150 ng/mL) and Amuc<sub>1409</sub><sup>\*</sup> (16 nM) for 30 min and then, they were harvested. WCLs were prepared to perform immunoprecipitation with E-cadherin, followed by immunoblotting with the indicated antibodies. Data shown in **a–d** are representative of two independent experiments, each with similar results. The uncropped western blot images are provided in Supplementary Fig. 14.

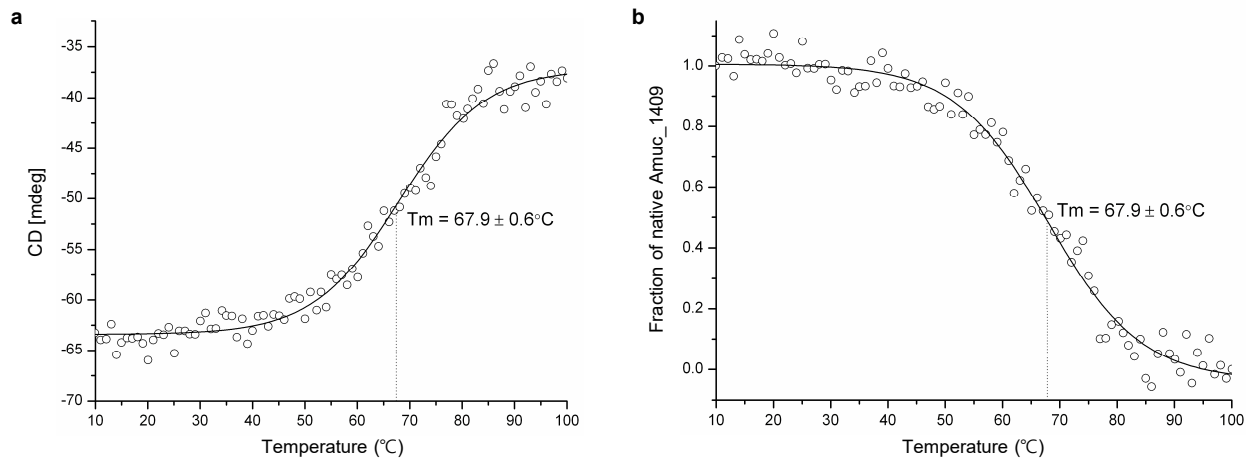


**Supplementary Fig. 6 Amuc<sub>1409</sub> promotes ISC-mediated epithelial differentiation in an E-cadherin-dependent manner.** a–f qRT-PCR results showing the relative mRNA expression of secretory progenitor cell markers (a), enteroendocrine cell markers (b), Paneth cell markers (c), goblet cell markers (d), mucin markers (e), and mature enterocyte markers (f) in mIOs from *Lgr5-CreERT2;Cdh1<sup>fl/fl</sup>* mice treated with or without Amuc<sub>1409</sub>\* (16 nM) at day 5 after either DMSO (vehicle control) or 4-OHT (1  $\mu$ M) addition began. All data are presented as the mean  $\pm$  SEM. A different symbol indicates a data point representing each biological replicate from independently established organoid lines derived from distinct mouse litters ( $n = 3$  biologically independent mice). Each biological replicate includes two or three technical replicates. Statistical analyses were performed using one-way ANOVA with Dunnett’s multiple comparisons test (a–f) (ns, not statistically significant, \*\*\* $p < 0.001$  vs control group). Source data, including the exact  $p$ -values, are provided as a Source Data file.

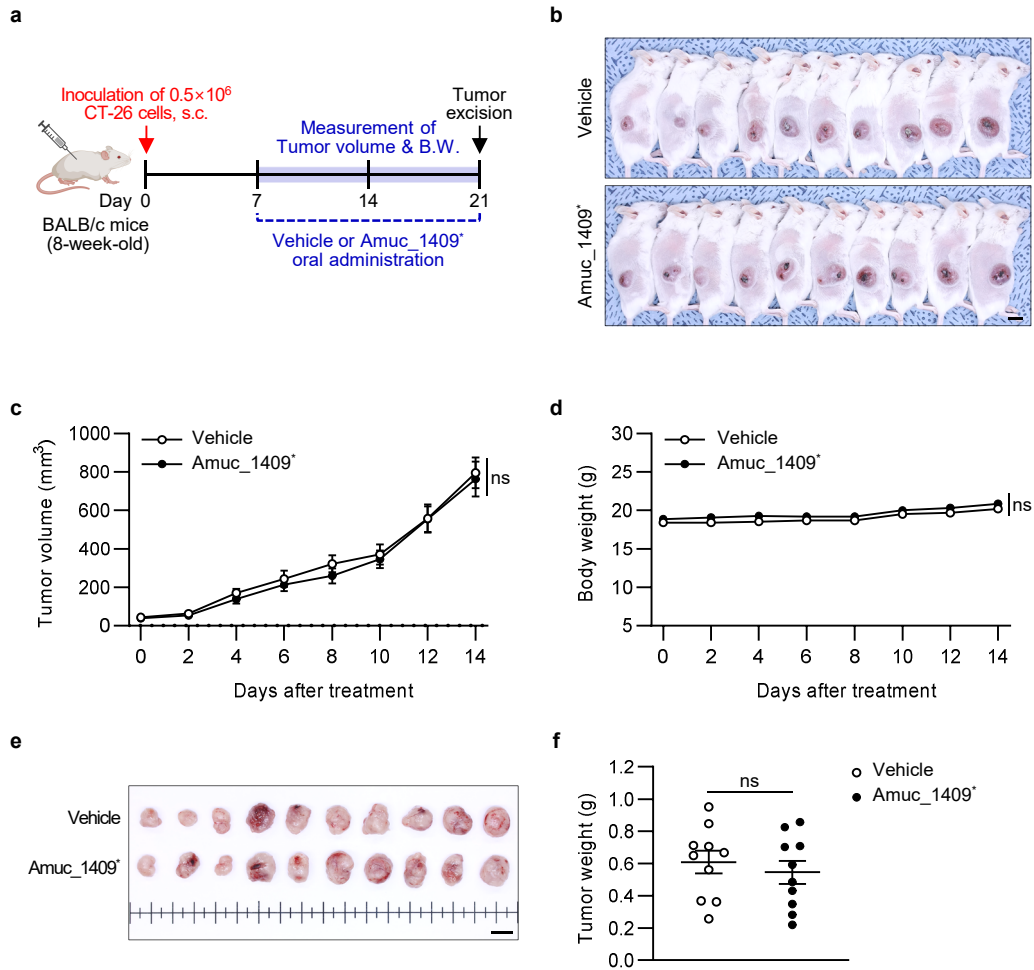




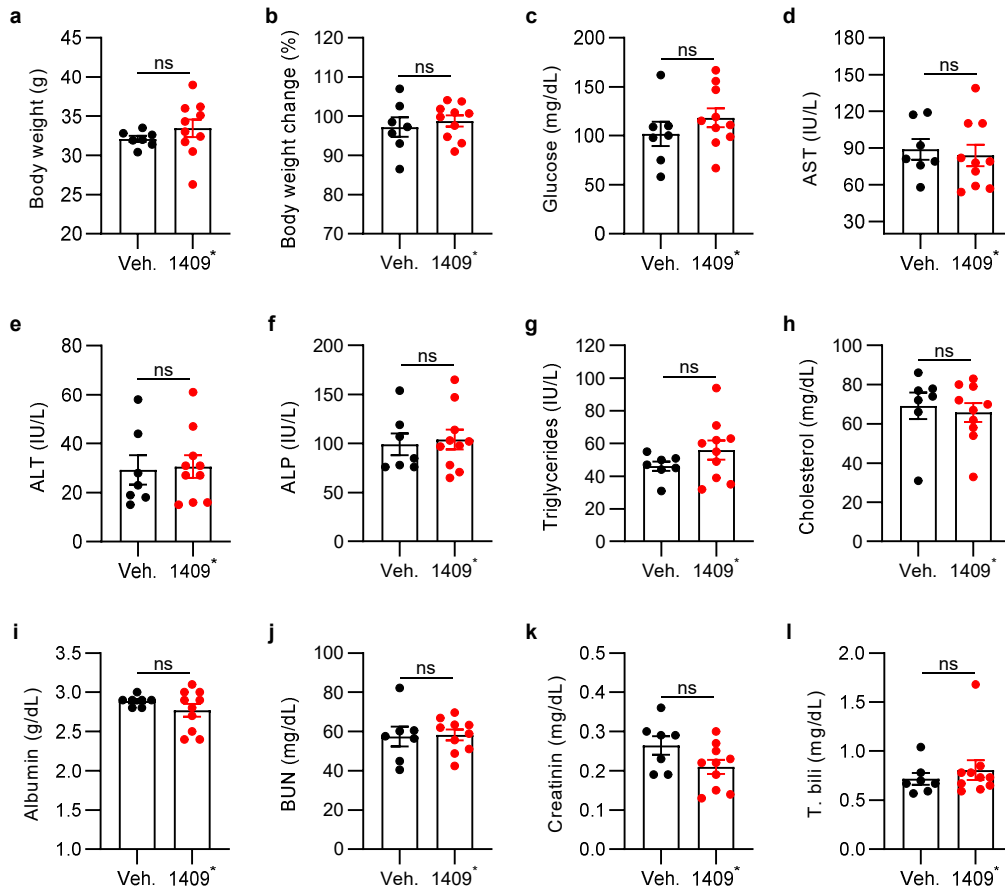
**Supplementary Fig. 7 Subcellular localization of Amuc\_1409 in *A. muciniphila*.** *A. muciniphila* BAA-835<sup>T</sup> was grown in basal medium under anaerobic conditions at 37°C for 48 h and cell pellets and supernatants were collected from this culture. **a** Western blot analysis of Amuc\_1409 in whole cell lysate (WC), periplasmic (PP), and outer membrane (OM) fractions, loaded with 5 µg protein per fraction sample. **b** Western blot analysis of Amuc\_1409 secreted into the cell-free culture supernatant (SUP). **c** Relative quantitative analysis of Amuc\_1409, Amuc\_0824 (PP protein), Amuc\_1100 (OM protein), and Amuc\_0198 (cytoplasmic protein) detected in four samples (WC, PP, OM, and SUP) were carried out via two MS1-based label-free quantitation (LFQ) methods (i. MaxQuant, MQ; ii. Proteome Discoverer Ver 3.0, PD). LFQ-based profiling of four proteins (Amuc\_1409, Amuc\_0824, Amuc\_1100, and Amuc\_0198) was conducted using the MQ (shown in red) and PD with Minora tool (shown in blue) and plotted on a bar chart with two Y-axes (MQ Intensity, left; PD Abundance, right). The relative abundance was calculated as the intensity ratio of each protein to the total protein in each fraction sample. All data are presented as the mean ± SEM. Source data are provided as a Source Data file. The uncropped western blot images are provided in Supplementary Fig. 15.



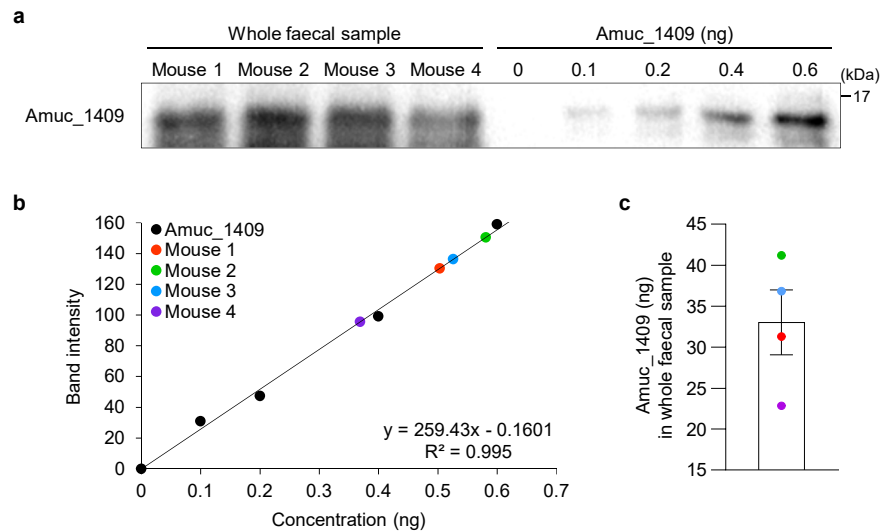
**Supplementary Fig. 8 Thermal unfolding of the Amuc\_1409 protein as monitored with circular dichroism. a, b** Thermal unfolding profile of raw circular dichroism (CD) spectra (a) and a normalized two-state unfolding model (b) of Amuc\_1409 protein by the standard equation: Fraction of native Amuc\_1409 =  $(\theta_t - \theta_{100}) / (\theta_{10} - \theta_{100})$ . The CD spectra were monitored at 216 nm by raising the temperature in 1°C intervals from 10 to 100°C. The melting temperature ( $T_m$ ,  $67.9 \pm 0.6^\circ\text{C}$ ) was calculated by a non-linear curve fit of Boltzmann method using Origin-v8.0 program (Origin Lab Corporation, USA). Source data are provided as a Source Data file.



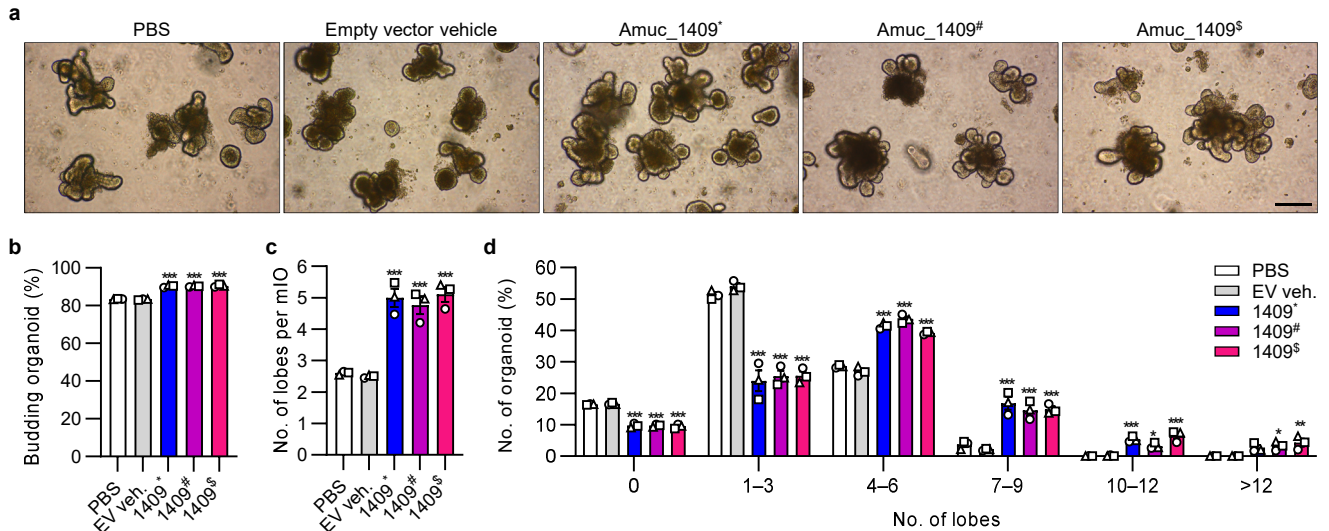
**Supplementary Fig. 9 Amuc\_1409 showed no obvious effect on tumor proliferation in the CT-26 syngeneic mouse model.** **a** Scheme showing the experimental workflow for oral administration of vehicle or Amuc\_1409\* (9  $\mu\text{g}$  per mouse) for 14 days, starting from 7 days after the subcutaneous (s.c.) injection of CT-26 cells in BALB/c mice ( $n = 10$  biological replicate mice per group). Images were created with biorender.com and have been granted a publication license. **b** Gross observation of CT-26 tumor-bearing mice on day 14 after treatment with vehicle or Amuc\_1409\*. Scale bar, 1 cm. **c, d** The changes in the tumor volume (**c**) and body weight (**d**) during the course of treatment. **e, f** Gross observation (**e**) and weight (**f**) of excised tumor from CT-26 tumor-bearing mice sacrificed on day 14 days after treatment with vehicle or Amuc\_1409\*. Scale bar, 1 cm. In **f**, each data point represents a biological replicate, corresponding to one mouse. All data are presented as the mean  $\pm$  SEM. Data shown are representative of three independent experiments, each with similar results. Statistical analyses were performed using two-tailed Student's *t*-test (**c, d, f**) (ns, not statistically significant, vs vehicle-treated group). Source data, including the exact *p*-values, are provided as a Source Data file.



**Supplementary Fig. 10 Long-term administration of Amuc\_1409 has no adverse effects on body weight and blood chemistry values in a natural aging mouse model.** a–l Bar graphs showing the absolute body weight (a), the percentage change in body weight (b), and blood chemistry values (c–l) of each group at 15 weeks after vehicle ( $n = 7$  biological replicate mice) or Amuc\_1409\* ( $n = 10$  biological replicate mice, 4.5  $\mu\text{g}$  per mouse) administration in the natural aging mice (100-week-old) model. AST (aspartate aminotransferase), ALT (alanine aminotransferase), ALP (alkaline phosphatase), BUN (blood urea nitrogen), T. bili (total bilirubin). All data are presented as the mean  $\pm$  SEM. Data shown are representative of three independent experiments, each with similar results. Each data point represents a biological replicate, corresponding to one mouse. Statistical analyses were performed using two-tailed Student's  $t$ -test. (ns, not statistically significant, vs vehicle-treated group). Source data, including the exact  $p$ -values, are provided as a Source Data file.

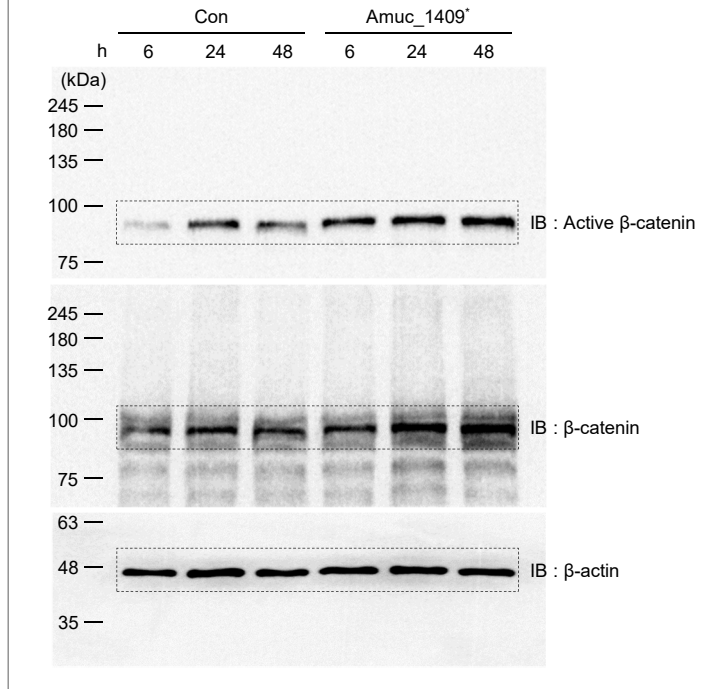


**Supplementary Fig. 11 The quantification of physiological concentration of Amuc\_1409 in whole faecal samples from the mouse gut.** **a** Proteins (100 µg) isolated from whole faecal samples of mouse gut ( $n = 4$  biological replicate mice) were subjected to western blotting in parallel with dilution of purified Amuc\_1409 protein with known concentration and detected using an in-house-made rabbit polyclonal antibody for Amuc\_1409. The signal intensity of each band was measured using ImageJ software. **b** Standard curve for Amuc\_1409 protein was generated using band intensities of different dilutions of purified Amuc\_1409 protein. The physiological concentration of Amuc\_1409 in whole faecal samples was calculated by inserting the sample's band intensity into the standard curve. **c** Bar graphs representing mean values of estimated physiological concentration of Amuc\_1409 in whole faecal samples of mouse gut. All data are presented as the mean  $\pm$  SEM. Source data are provided as a Source Data file. The uncropped western blot image is provided in Supplementary Fig. 16.



**Supplementary Fig. 12 The promotion of organoid growth is specifically attributed to the Amuc\_1409 protein itself, not the His-tag or potential contaminant carryover.** **a–d** Analysis of mIOs treated with PBS, empty vector vehicle, Amuc\_1409\*, Amuc\_1409#, and Amuc\_1409<sup>S</sup> on day 4 after the second subculturing passage. Empty vector vehicle (EV veh.) is the solution obtained from the same purification process of EV-transformed *E. coli*. Amuc\_1409\* is the recombinant His-tagged Amuc\_1409 protein expressed in *E. coli* and purified using NI-NTA affinity chromatography. Amuc\_1409# is the recombinant His-tag cleaved Amuc\_1409 protein by the TEV protease. Amuc\_1409<sup>S</sup> is the recombinant His-tag cleaved Amuc\_1409 protein, which underwent an additional purification step through gel filtration chromatography. Representative brightfield images of the mIOs (**a**), quantitative assessment of the percentage of budding organoids (**b**), the number of lobes per mIO (**c**), and the percentage distribution of organoids with the indicated number of lobes per mIO (**d**) in mIOs. Scale bar, 200  $\mu$ m. All data are presented as the mean  $\pm$  SEM. A different symbol indicates a data point representing each biological replicate from independently established organoid lines derived from distinct mouse litters ( $n = 3$  biologically independent mice). Statistical analyses were performed using one-way ANOVA with Dunnett's multiple comparisons test ( $*p < 0.05$ ,  $**p < 0.01$ , and  $***p < 0.001$  vs PBS-treated group). Source data, including the exact  $p$ -values, are provided as a Source Data file.

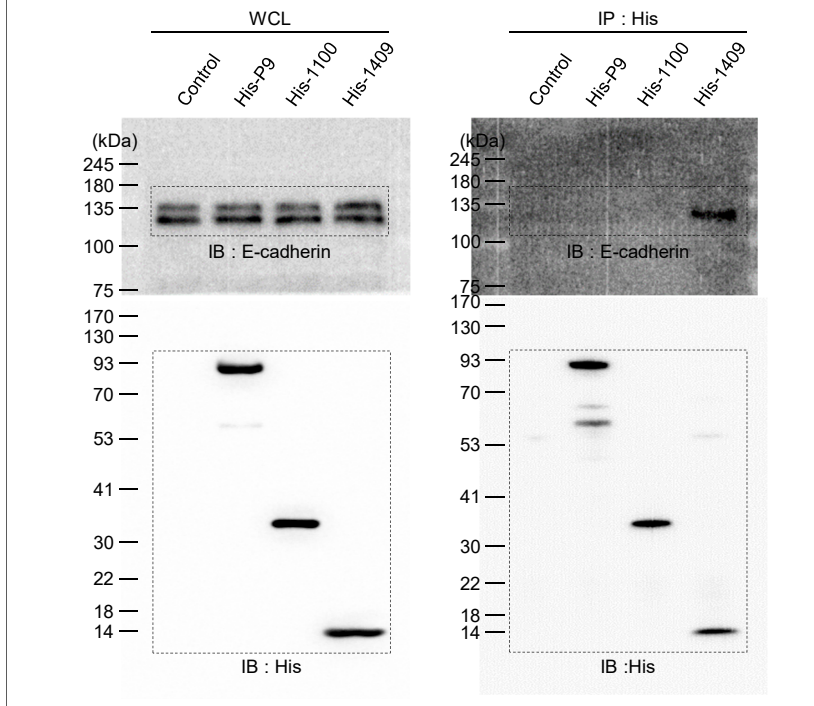
Supplementary Fig. 2b



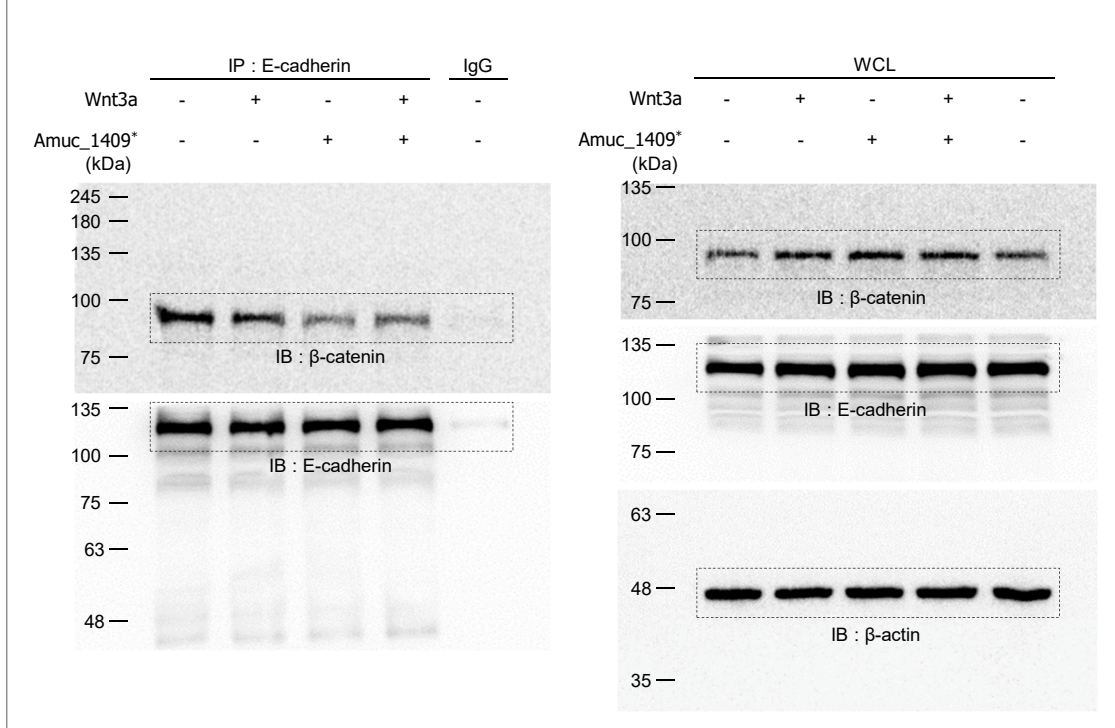
**Supplementary Fig. 13** The uncropped western blot images presented in the indicated figures.

Note: Black dashed lines identify the cropped areas

Supplementary Fig. 5b



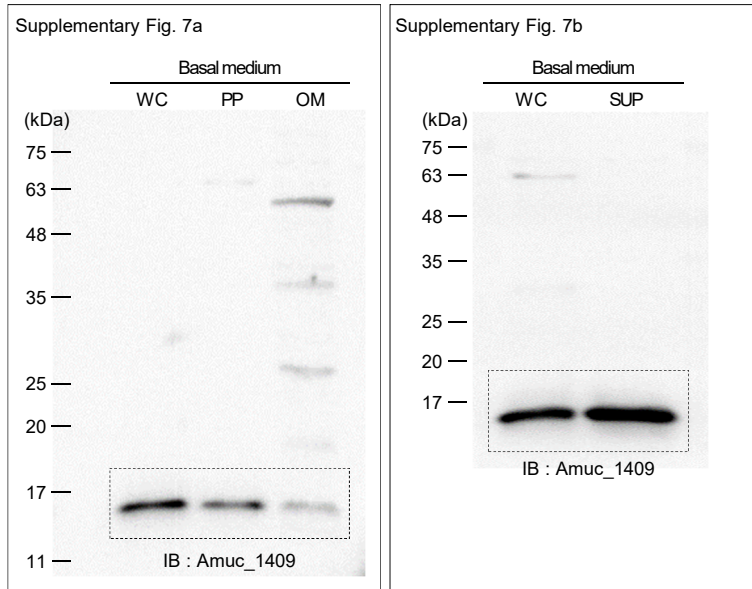
Supplementary Fig. 5d



Supplementary Fig. 14 The uncropped western blot images presented in the indicated figures.

Note: Black dashed lines identify the cropped areas

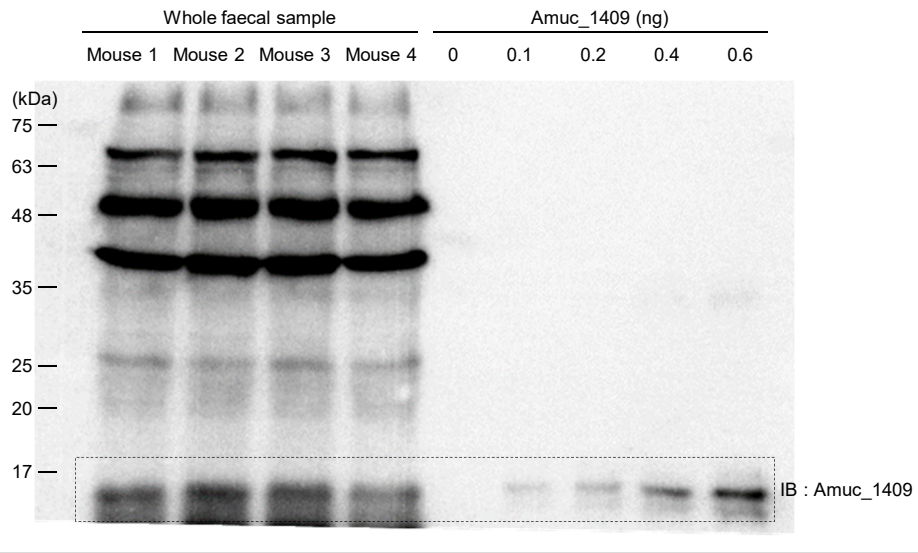




**Supplementary Fig. 15** The uncropped western blot images presented in the indicated figures.

Note: Black dashed lines identify the cropped areas

Supplementary Fig. 11a



**Supplementary Fig. 16** The uncropped western blot images presented in the indicated figures.

Note: Black dashed lines identify the cropped areas

**Supplementary Table 1. List of proteins identified in secretome of *A. muciniphila* cultivated under under basal medium.**

| Majority protein IDs | Fasta headers  | Gene locus | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Sequence lengths | Score  | Intensity | MS/MS count | iBAQ   |
|----------------------|--|------------|----------|-----------------|-----------------------|-------------------|------------------|--------|-----------|-------------|--------|
| B2UKW7               | tr B2UKW7 B2UKW7_AKKM8 Glyceraldehyde-3-phosphate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1417 PE=3 SV=1   | Amuc_1417  | 21       | 21              | 68.00                 | 36.74             | 341              | 323.31 | 5.E+11    | 3106        | 2.E+10 |
| B2UQS2               | sp B2UQS2 ACP_AKKM8 Acyl carrier protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=acpP PE=3 SV=1                               | Amuc_0975  | 3        | 3               | 40.00                 | 8.82              | 80               | 200.16 | 6.E+10    | 1971        | 2.E+10 |
| B2UP94               | tr B2UP94 B2UP94_AKKM8 Rubrerythrin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2055 PE=4 SV=1     | Amuc_2055  | 7        | 5               | 86.00                 | 12.73             | 114              | 264.75 | 1.E+11    | 1261        | 2.E+10 |
| B2UMR7               | tr B2UMR7 B2UMR7_AKKM8 Histone family protein DNA-binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0281 PE=3 SV=1 | Amuc_0281  | 4        | 4               | 50.50                 | 11.25             | 101              | 210.98 | 6.E+10    | 587         | 2.E+10 |
| B2UQP3               | tr B2UQP3 B2UQP3_AKKM8 DJ-1 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0946 PE=4 SV=1                        | Amuc_0946  | 11       | 11              | 67.90                 | 20.11             | 187              | 323.31 | 1.E+11    | 1832        | 1.E+10 |
| B2ULM5               | tr B2ULM5 B2ULM5_AKKM8 Superoxide dismutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1592 PE=3 SV=1                       | Amuc_1592  | 11       | 11              | 56.10                 | 23.92             | 214              | 323.31 | 2.E+11    | 1249        | 1.E+10 |
| B2URC4               | tr B2URC4 B2URC4_AKKM8 Enolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=eno PE=3 SV=1  | Amuc_1184  | 19       | 17              | 67.10                 | 45.68             | 426              | 323.31 | 3.E+11    | 3686        | 1.E+10 |
| B2UPZ3               | tr B2UPZ3 B2UPZ3_AKKM8 Thioredoxin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0691 PE=3 SV=1                                | Amuc_0691  | 5        | 5               | 66.70                 | 11.49             | 105              | 237.29 | 6.E+10    | 502         | 1.E+10 |
| B2URF0               | tr B2URF0 B2URF0_AKKM8 Phosphoenolpyruvate carboxykinase [GTP] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pckG PE=3 SV=1         | Amuc_1210  | 22       | 22              | 48.40                 | 67.52             | 608              | 323.31 | 2.E+11    | 2108        | 8.E+09 |
| B2UN99               | tr B2UN99 B2UN99_AKKM8 Glutamate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0372 PE=3 SV=1                    | Amuc_0372  | 24       | 24              | 65.90                 | 52.46             | 466              | 323.31 | 2.E+11    | 2064        | 7.E+09 |
| B2UKW8               | sp B2UKW8 PGK_AKKM8 Phosphoglycerate kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pgk PE=3 SV=1                             | Amuc_1418  | 24       | 24              | 75.20                 | 42.69             | 403              | 323.31 | 1.E+11    | 2595        | 6.E+09 |
| B2UKV9               | tr B2UKV9 B2UKV9_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1409 PE=4 SV=1       | Amuc_1409  | 8        | 8               | 52.00                 | 16.52             | 150              | 245.16 | 4.E+10    | 538         | 5.E+09 |
| B2UQ05               | tr B2UQ05 B2UQ05_AKKM8 Alanine--glyoxylate transaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0703 PE=3 SV=1           | Amuc_0703  | 20       | 20              | 76.80                 | 39.28             | 357              | 323.31 | 1.E+11    | 2027        | 5.E+09 |
| B2UNK0               | tr B2UNK0 B2UNK0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1902 PE=4 SV=1                    | Amuc_1902  | 13       | 13              | 71.30                 | 24.93             | 230              | 323.31 | 5.E+10    | 917         | 4.E+09 |
| B2UN29               | tr B2UN29 B2UN29_AKKM8 Glucosamine-6-phosphate deaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=nagB PE=3 SV=1               | Amuc_1822  | 10       | 10              | 46.90                 | 32.84             | 303              | 323.31 | 6.E+10    | 535         | 4.E+09 |
| B2UNL9               | tr B2UNL9 B2UNL9_AKKM8 Putative ferredoxin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1922 PE=4 SV=1                        | Amuc_1922  | 2        | 2               | 24.70                 | 8.40              | 77               | 134.67 | 2.E+10    | 78          | 3.E+09 |

|        |   |           |    |    |       |       |     |        |        |      |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|------|--------|
| B2UNS8 | tr B2UNS8 B2UNS8_AKKM8 Methylmalonyl-CoA mutase, large subunit OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1983 PE=4 SV=1       | Amuc_1983 | 25 | 25 | 46.50 | 78.41 | 714 | 323.31 | 1.E+11 | 1974 | 3.E+09 |
| B2UL96 | sp B2UL96 GLSA_AKKM8 Glutaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glSA PE=3 SV=1  | Amuc_0038 | 7  | 7  | 31.00 | 33.13 | 313 | 186.41 | 3.E+10 | 391  | 3.E+09 |
| B2UPF0 | tr B2UPF0 B2UPF0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0590 PE=4 SV=1                       | Amuc_0590 | 22 | 22 | 51.50 | 50.45 | 460 | 323.31 | 6.E+10 | 1665 | 3.E+09 |
| B2ULM2 | tr B2ULM2 B2ULM2_AKKM8 Aminotransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1589 PE=3 SV=1                              | Amuc_1589 | 14 | 14 | 52.80 | 42.44 | 388 | 323.31 | 4.E+10 | 986  | 3.E+09 |
| B2UNH3 | tr B2UNH3 B2UNH3_AKKM8 Glycine cleavage system H protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gcvH PE=3 SV=1                  | Amuc_0447 | 3  | 3  | 40.50 | 13.72 | 126 | 120.45 | 5.E+09 | 111  | 3.E+09 |
| B2UKY5 | sp B2UKY5 MDH_AKKM8 Malate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=mdh PE=3 SV=1                                   | Amuc_1436 | 13 | 13 | 47.10 | 35.10 | 329 | 323.31 | 4.E+10 | 548  | 2.E+09 |
| B2URG7 | sp B2URG7 Y1227_AKKM8 Nucleoid-associated protein Amuc_1227 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1227 PE=3 SV=1          | Amuc_1227 | 1  | 1  | 13.50 | 10.91 | 104 | 2.56   | 8.E+09 | 36   | 2.E+09 |
| B2UQP5 | tr B2UQP5 B2UQP5_AKKM8 N-acetylglucosamine-6-phosphate deacetylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0948 PE=3 SV=1   | Amuc_0948 | 12 | 12 | 45.30 | 40.83 | 382 | 323.31 | 4.E+10 | 614  | 2.E+09 |
| B2UNS2 | tr B2UNS2 B2UNS2_AKKM8 Glucose-6-phosphate isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pgi PE=3 SV=1                       | Amuc_1975 | 25 | 25 | 58.30 | 55.47 | 515 | 323.31 | 6.E+10 | 1407 | 2.E+09 |
| B2UP29 | tr B2UP29 B2UP29_AKKM8 Triosephosphate isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tpiA PE=3 SV=1                          | Amuc_0562 | 10 | 10 | 61.40 | 26.99 | 254 | 323.31 | 2.E+10 | 517  | 2.E+09 |
| B2UL55 | tr B2UL55 B2UL55_AKKM8 Malonyl CoA-acyl carrier protein transacylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1507 PE=3 SV=1 | Amuc_1507 | 9  | 9  | 41.90 | 32.57 | 308 | 323.31 | 3.E+10 | 444  | 2.E+09 |
| B2URK9 | tr B2URK9 B2URK9_AKKM8 Thioredoxin reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1269 PE=3 SV=1                         | Amuc_1269 | 8  | 8  | 31.70 | 33.21 | 309 | 248.71 | 2.E+10 | 506  | 2.E+09 |
| B2UPR8 | tr B2UPR8 B2UPR8_AKKM8 Nitroreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2137 PE=3 SV=1                                | Amuc_2137 | 11 | 11 | 49.30 | 24.41 | 215 | 275.58 | 2.E+10 | 767  | 2.E+09 |
| B2ULH2 | tr B2ULH2 B2ULH2_AKKM8 OsmC family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1538 PE=4 SV=1                           | Amuc_1538 | 4  | 4  | 49.30 | 14.99 | 136 | 173.93 | 9.E+09 | 241  | 1.E+09 |
| B2UR48 | tr B2UR48 B2UR48_AKKM8 ATP phosphoribosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=hisG PE=3 SV=1                      | Amuc_1107 | 11 | 11 | 52.20 | 32.70 | 291 | 323.31 | 2.E+10 | 397  | 1.E+09 |
| B2UP53 | tr B2UP53 B2UP53_AKKM8 Cysteine synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2014 PE=3 SV=1                             | Amuc_2014 | 15 | 15 | 86.40 | 32.53 | 309 | 323.31 | 2.E+10 | 867  | 1.E+09 |
| B2UPE1 | tr B2UPE1 B2UPE1_AKKM8 Meso-diaminopimelate D-dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0581 PE=3 SV=1          | Amuc_0581 | 17 | 17 | 72.40 | 31.31 | 293 | 323.31 | 2.E+10 | 1032 | 1.E+09 |
| B2URE7 | sp B2URE7 PDXJ_AKKM8 Pyridoxine 5-phosphate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pxdJ PE=3 SV=1                      | Amuc_1207 | 7  | 7  | 49.60 | 27.11 | 246 | 323.31 | 1.E+10 | 1276 | 1.E+09 |

|        |   |           |    |    |       |       |     |        |        |      |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|------|--------|
| B2UL89 | tr B2UL89 B2UL89_AKKM8 NTP_transferase domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0031 PE=4 SV=1                       | Amuc_0031 | 10 | 10 | 46.70 | 32.12 | 291 | 164.51 | 2.E+10 | 381  | 1.E+09 |
| B2UMF1 | sp B2UMF1 DAPB_AKKM8 4-hydroxy-tetrahydrodipicolinate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dapB PE=3 SV=1                             | Amuc_0257 | 8  | 8  | 50.00 | 26.31 | 246 | 289.43 | 2.E+10 | 443  | 1.E+09 |
| B2UMG7 | tr B2UMG7 B2UMG7_AKKM8 Endoribonuclease L-PSP OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1705 PE=4 SV=1  | Amuc_1705 | 6  | 6  | 67.90 | 16.64 | 156 | 323.31 | 8.E+09 | 590  | 1.E+09 |
| B2UNK1 | tr B2UNK1 B2UNK1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1903 PE=4 SV=1   | Amuc_1903 | 10 | 10 | 40.30 | 35.41 | 335 | 323.31 | 2.E+10 | 554  | 1.E+09 |
| B2UM96 | tr B2UM96 B2UM96_AKKM8 Carboxyl transferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0201 PE=4 SV=1  | Amuc_0201 | 11 | 11 | 33.60 | 56.01 | 521 | 323.31 | 2.E+10 | 506  | 1.E+09 |
| B2ULV5 | tr B2ULV5 B2ULV5_AKKM8 Phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain I OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0155 PE=3 SV=1 | Amuc_0155 | 20 | 20 | 42.70 | 71.24 | 651 | 323.31 | 3.E+10 | 1126 | 1.E+09 |
| B2UP27 | tr B2UP27 B2UP27_AKKM8 Argininosuccinate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=argG PE=3 SV=1   | Amuc_0559 | 14 | 14 | 44.70 | 47.87 | 430 | 308.42 | 2.E+10 | 1173 | 1.E+09 |
| B2UQY9 | sp B2UQY9 EFTU_AKKM8 Elongation factor Tu OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tuf PE=3 SV=1  | Amuc_1048 | 10 | 10 | 34.30 | 43.43 | 394 | 323.31 | 2.E+10 | 628  | 1.E+09 |
| B2UMA1 | tr B2UMA1 B2UMA1_AKKM8 Succinate CoA transferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0206 PE=3 SV=1                                       | Amuc_0206 | 23 | 23 | 61.00 | 54.05 | 498 | 323.31 | 2.E+10 | 859  | 9.E+08 |
| B2UKM8 | tr B2UKM8 B2UKM8_AKKM8 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1327 PE=3 SV=1                     | Amuc_1327 | 8  | 8  | 34.70 | 43.82 | 415 | 251.36 | 1.E+10 | 885  | 9.E+08 |
| B2UMF2 | tr B2UMF2 B2UMF2_AKKM8 4-hydroxy-tetrahydrodipicolinate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dapA PE=3 SV=1                            | Amuc_0258 | 7  | 7  | 34.10 | 31.25 | 293 | 205.55 | 2.E+10 | 458  | 9.E+08 |
| B2UNS9 | tr B2UNS9 B2UNS9_AKKM8 Methylmalonyl-CoA mutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1984 PE=4 SV=1  | Amuc_1984 | 26 | 26 | 50.60 | 74.10 | 684 | 323.31 | 3.E+10 | 1054 | 9.E+08 |
| B2UP95 | tr B2UP95 B2UP95_AKKM8 Rubrerythrin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2056 PE=4 SV=1                          | Amuc_2056 | 3  | 1  | 36.60 | 13.69 | 123 | 78.43  | 6.E+09 | 123  | 8.E+08 |
| B2UPB0 | tr B2UPB0 B2UPB0_AKKM8 Rubrerythrin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2072 PE=4 SV=1  | Amuc_2072 | 3  | 3  | 19.90 | 21.34 | 191 | 177.17 | 6.E+09 | 143  | 8.E+08 |
| B2UQW7 | tr B2UQW7 B2UQW7_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1026 PE=3 SV=1                             | Amuc_1026 | 5  | 5  | 47.90 | 17.92 | 167 | 260.88 | 6.E+09 | 192  | 8.E+08 |
| B2UQ07 | tr B2UQ07 B2UQ07_AKKM8 2-oxoglutarate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0705 PE=3 SV=1  | Amuc_0705 | 14 | 14 | 37.90 | 56.68 | 523 | 323.31 | 2.E+10 | 561  | 8.E+08 |
| B2UMX5 | tr B2UMX5 B2UMX5_AKKM8 OsmC family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0342 PE=4 SV=1   | Amuc_0342 | 7  | 7  | 65.20 | 14.48 | 135 | 113.32 | 5.E+09 | 262  | 8.E+08 |

|        |  |           |    |    |       |        |     |        |        |      |        |
|--------|--|-----------|----|----|-------|--------|-----|--------|--------|------|--------|
| B2UNP8 | tr B2UNP8 B2UNP8_AKKM8 NADH:flavin oxidoreductase/NADH oxidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1951 PE=4 SV=1              | Amuc_1951 | 16 | 16 | 49.90 | 40.82  | 367 | 323.31 | 1.E+10 | 578  | 7.E+08 |
| B2UPU6 | tr B2UPU6 B2UPU6_AKKM8 Oligopeptidase A OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2167 PE=3 SV=1                                     | Amuc_2167 | 18 | 18 | 38.40 | 79.32  | 700 | 323.31 | 3.E+10 | 871  | 7.E+08 |
| B2URP8 | tr B2URP8 B2URP8_AKKM8 Aldose 1-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1309 PE=3 SV=1                                   | Amuc_1309 | 11 | 11 | 49.20 | 34.50  | 319 | 287.90 | 1.E+10 | 405  | 7.E+08 |
| B2UL16 | tr B2UL16 B2UL16_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1467 PE=4 SV=1                              | Amuc_1467 | 4  | 4  | 16.50 | 22.00  | 194 | 98.66  | 6.E+09 | 160  | 7.E+08 |
| B2UN39 | tr B2UN39 B2UN39_AKKM8 L-fucose isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1832 PE=3 SV=1                                   | Amuc_1832 | 20 | 20 | 39.20 | 64.70  | 592 | 323.31 | 2.E+10 | 765  | 7.E+08 |
| B2UML6 | sp B2UML6 OTC_AKKM8 Ornithine carbamoyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=arcB PE=3 SV=1                               | Amuc_1630 | 11 | 11 | 47.90 | 34.14  | 305 | 323.31 | 1.E+10 | 527  | 7.E+08 |
| B2UMU5 | sp B2UMU5 GPMI_AKKM8 2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gpmI PE=3 SV=1 | Amuc_0309 | 14 | 14 | 37.70 | 56.14  | 514 | 323.31 | 2.E+10 | 554  | 7.E+08 |
| B2UPJ1 | tr B2UPJ1 B2UPJ1_AKKM8 FAD-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0631 PE=4 SV=1                           | Amuc_0631 | 13 | 13 | 53.50 | 41.44  | 376 | 323.31 | 1.E+10 | 521  | 7.E+08 |
| B2UNK9 | tr B2UNK9 B2UNK9_AKKM8 Iron-containing alcohol dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1911 PE=4 SV=1                | Amuc_1911 | 9  | 9  | 37.60 | 41.35  | 386 | 175.54 | 9.E+09 | 482  | 7.E+08 |
| B2UMC9 | tr B2UMC9 B2UMC9_AKKM8 Alpha-glucan phosphorylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0235 PE=3 SV=1                           | Amuc_0235 | 22 | 22 | 49.50 | 63.41  | 554 | 323.31 | 2.E+10 | 936  | 6.E+08 |
| B2UPE0 | tr B2UPE0 B2UPE0_AKKM8 Entericidin EcnAB OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0580 PE=4 SV=1                                    | Amuc_0580 | 1  | 1  | 29.80 | 4.74   | 47  | 40.49  | 1.E+09 | 24   | 6.E+08 |
| B2UPQ6 | tr B2UPQ6 B2UPQ6_AKKM8 Adenylosuccinate synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=purA PE=3 SV=1                               | Amuc_2125 | 10 | 10 | 28.80 | 46.05  | 423 | 219.74 | 1.E+10 | 788  | 6.E+08 |
| B2UL87 | tr B2UL87 B2UL87_AKKM8 NAD-dependent epimerase/dehydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0029 PE=4 SV=1                  | Amuc_0029 | 10 | 10 | 39.30 | 33.59  | 308 | 165.07 | 1.E+10 | 440  | 6.E+08 |
| B2UP16 | tr B2UP16 B2UP16_AKKM8 MotA/TolQ/ExbB proton channel OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0548 PE=3 SV=1                        | Amuc_0548 | 2  | 2  | 11.80 | 28.34  | 263 | 12.58  | 3.E+09 | 44   | 6.E+08 |
| B2UNS1 | tr B2UNS1 B2UNS1_AKKM8 Pyruvate, phosphate dikinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1974 PE=3 SV=1                         | Amuc_1974 | 22 | 22 | 30.60 | 100.12 | 914 | 323.31 | 3.E+10 | 1239 | 6.E+08 |
| B2UKY9 | tr B2UKY9 B2UKY9_AKKM8 Nitroreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1440 PE=3 SV=1                                       | Amuc_1440 | 7  | 7  | 31.60 | 24.93  | 215 | 58.67  | 5.E+09 | 169  | 6.E+08 |
| B2UQR6 | tr B2UQR6 B2UQR6_AKKM8 Galactokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0969 PE=3 SV=1  | Amuc_0969 | 9  | 9  | 29.30 | 42.15  | 392 | 223.84 | 1.E+10 | 418  | 5.E+08 |

|        |  |           |    |    |       |       |     |        |        |      |        |
|--------|--|-----------|----|----|-------|-------|-----|--------|--------|------|--------|
| B2UN63 | tr B2UN63 B2UN63_AKKM8 Formate--tetrahydrofolate ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fhs PE=3 SV=1                                 | Amuc_1860 | 17 | 17 | 40.90 | 59.80 | 557 | 323.31 | 2.E+10 | 898  | 5.E+08 |
| B2UMC7 | tr B2UMC7 B2UMC7_AKKM8 L-threonine 3-dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tdh PE=3 SV=1                                      | Amuc_0233 | 7  | 7  | 31.00 | 37.54 | 345 | 250.40 | 7.E+09 | 294  | 5.E+08 |
| B2UM06 | tr B2UM06 B2UM06_AKKM8 Serine hydroxymethyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glyA PE=3 SV=1                                 | Amuc_1630 | 22 | 22 | 50.40 | 61.10 | 566 | 323.31 | 2.E+10 | 849  | 5.E+08 |
| B2UP04 | tr B2UP04 B2UP04_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0536 PE=4 SV=1                                    | Amuc_0536 | 6  | 6  | 34.00 | 28.70 | 259 | 195.84 | 6.E+09 | 190  | 5.E+08 |
| B2UMA5 | tr B2UMA5 B2UMA5_AKKM8 6-phosphofructokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0210 PE=4 SV=1                                      | Amuc_0210 | 7  | 7  | 25.00 | 35.31 | 320 | 144.82 | 6.E+09 | 251  | 5.E+08 |
| B2UQW6 | tr B2UQW6 B2UQW6_AKKM8 Disulfide bond chaperones of the HSP33 family-like protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1025 PE=4 SV=1 | Amuc_1025 | 10 | 10 | 47.10 | 30.09 | 257 | 310.77 | 7.E+09 | 575  | 5.E+08 |
| B2UNP3 | tr B2UNP3 B2UNP3_AKKM8 Dihydrodipicolinate synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1946 PE=3 SV=1                             | Amuc_1946 | 6  | 6  | 25.60 | 33.03 | 305 | 119.27 | 8.E+09 | 463  | 5.E+08 |
| B2UPS4 | tr B2UPS4 B2UPS4_AKKM8 Fumarate hydratase class I OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2144 PE=3 SV=1                                 | Amuc_2144 | 21 | 21 | 53.80 | 60.10 | 548 | 323.31 | 2.E+10 | 611  | 5.E+08 |
| B2UN19 | tr B2UN19 B2UN19_AKKM8 Alpha amylase catalytic region OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1812 PE=3 SV=1                             | Amuc_1812 | 12 | 12 | 37.00 | 56.72 | 492 | 162.51 | 1.E+10 | 509  | 4.E+08 |
| B2UQK1 | tr B2UQK1 B2UQK1_AKKM8 Aconitate hydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0904 PE=3 SV=1  | Amuc_0904 | 23 | 23 | 38.40 | 99.01 | 917 | 323.31 | 2.E+10 | 1077 | 4.E+08 |
| B2URI9 | tr B2URI9 B2URI9_AKKM8 GDP-mannose 4,6-dehydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gmd PE=3 SV=1                                      | Amuc_1249 | 14 | 14 | 51.00 | 40.86 | 355 | 219.04 | 9.E+09 | 591  | 4.E+08 |
| B2UQE5 | tr B2UQE5 B2UQE5_AKKM8 Metal dependent phosphohydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0847 PE=4 SV=1                           | Amuc_0847 | 9  | 9  | 33.90 | 39.25 | 354 | 58.34  | 7.E+09 | 76   | 4.E+08 |
| B2UMK3 | tr B2UMK3 B2UMK3_AKKM8 UTP--glucose-1-phosphate uridylyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1741 PE=3 SV=1               | Amuc_1741 | 15 | 15 | 42.50 | 50.44 | 461 | 291.62 | 9.E+09 | 394  | 4.E+08 |
| B2UN83 | tr B2UN83 B2UN83_AKKM8 Isocitrate dehydrogenase [NADP] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1880 PE=4 SV=1                            | Amuc_1880 | 18 | 18 | 50.10 | 45.31 | 415 | 166.12 | 9.E+09 | 552  | 4.E+08 |
| B2UQ06 | tr B2UQ06 B2UQ06_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0704 PE=4 SV=1                                    | Amuc_0704 | 9  | 9  | 26.40 | 47.48 | 417 | 313.47 | 8.E+09 | 349  | 4.E+08 |
| B2UMM1 | tr B2UMM1 B2UMM1_AKKM8 Peptidase M20 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1759 PE=4 SV=1  | Amuc_1759 | 11 | 11 | 24.30 | 50.33 | 465 | 139.33 | 7.E+09 | 496  | 3.E+08 |
| B2UR66 | tr B2UR66 B2UR66_AKKM8 UDP-glucose 4-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1125 PE=3 SV=1                                    | Amuc_1125 | 7  | 7  | 31.30 | 36.07 | 329 | 100.94 | 5.E+09 | 310  | 3.E+08 |

|        |   |           |    |    |       |       |     |        |        |     |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|-----|--------|
| B2UKM2 | tr B2UKM2 B2UKM2_AKKM8 Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1321 PE=3 SV=1 | Amuc_1321 | 5  | 5  | 36.20 | 22.83 | 207 | 126.45 | 3.E+09 | 170 | 3.E+08 |
| B2UN36 | tr B2UN36 B2UN36_AKKM8 Class II aldolase/adducin family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1829 PE=4 SV=1                                | Amuc_1829 | 7  | 7  | 39.90 | 29.81 | 271 | 200.78 | 4.E+09 | 313 | 3.E+08 |
| B2UKP3 | tr B2UKP3 B2UKP3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1342 PE=4 SV=1   | Amuc_1342 | 4  | 4  | 17.30 | 34.98 | 312 | 90.38  | 5.E+09 | 235 | 3.E+08 |
| B2UMG1 | tr B2UMG1 B2UMG1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0267 PE=4 SV=1   | Amuc_0267 | 5  | 5  | 30.10 | 18.11 | 163 | 118.25 | 3.E+09 | 255 | 3.E+08 |
| B2UR47 | tr B2UR47 B2UR47_AKKM8 Peptidase M24 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1106 PE=4 SV=1   | Amuc_1106 | 11 | 11 | 26.00 | 48.19 | 427 | 134.55 | 6.E+09 | 465 | 3.E+08 |
| B2ULA2 | tr B2ULA2 B2ULA2_AKKM8 Diaminopimelate epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dapF PE=3 SV=1  | Amuc_0044 | 6  | 6  | 28.50 | 29.30 | 274 | 140.20 | 4.E+09 | 193 | 3.E+08 |
| B2UL47 | tr B2UL47 B2UL47_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1498 PE=3 SV=1   | Amuc_1498 | 8  | 8  | 43.20 | 25.20 | 229 | 106.89 | 3.E+09 | 238 | 3.E+08 |
| B2UPF7 | tr B2UPF7 B2UPF7_AKKM8 Flavin_Reduct domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0597 PE=4 SV=1                                 | Amuc_0597 | 4  | 4  | 30.40 | 19.05 | 168 | 60.60  | 2.E+09 | 220 | 3.E+08 |
| B2UQT1 | tr B2UQT1 B2UQT1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0987 PE=4 SV=1   | Amuc_0987 | 5  | 5  | 67.80 | 9.56  | 90  | 65.07  | 2.E+09 | 167 | 3.E+08 |
| B2URF8 | tr B2URF8 B2URF8_AKKM8 3-dehydroquinase synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=aroB PE=3 SV=1  | Amuc_1218 | 11 | 11 | 44.10 | 39.26 | 370 | 178.11 | 6.E+09 | 214 | 3.E+08 |
| B2UR44 | tr B2UR44 B2UR44_AKKM8 Glutamyl aminopeptidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1103 PE=3 SV=1   | Amuc_1103 | 8  | 8  | 29.50 | 38.13 | 359 | 70.29  | 5.E+09 | 169 | 3.E+08 |
| B2UQ25 | tr B2UQ25 B2UQ25_AKKM8 Branched-chain-amino-acid aminotransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ilvE PE=3 SV=1                                   | Amuc_0723 | 6  | 6  | 31.90 | 31.84 | 288 | 120.56 | 5.E+09 | 154 | 3.E+08 |
| B2UKZ6 | sp B2UKZ6 ARGC_AKKM8 N-acetyl-gamma-glutamyl-phosphate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=argC PE=3 SV=1                                    | Amuc_1447 | 7  | 7  | 34.60 | 37.59 | 347 | 137.05 | 4.E+09 | 246 | 3.E+08 |
| B2UPN7 | tr B2UPN7 B2UPN7_AKKM8 Malate dehydrogenase (Oxaloacetate-decarboxylating) (NADP(+)) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2106 PE=3 SV=1           | Amuc_2106 | 12 | 12 | 45.00 | 47.52 | 436 | 166.38 | 6.E+09 | 271 | 3.E+08 |
| B2UMD1 | tr B2UMD1 B2UMD1_AKKM8 Arsenate reductase and related OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0237 PE=3 SV=1  | Amuc_0237 | 5  | 5  | 46.20 | 13.52 | 119 | 55.32  | 2.E+09 | 110 | 3.E+08 |
| B2URB8 | sp B2URB8 ILVC_AKKM8 Ketol-acid reductoisomerase (NADP(+)) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ilvC PE=3 SV=1  | Amuc_1178 | 10 | 10 | 44.80 | 35.14 | 326 | 175.89 | 4.E+09 | 297 | 3.E+08 |
| B2UMZ5 | tr B2UMZ5 B2UMZ5_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0362 PE=4 SV=1   | Amuc_0362 | 2  | 2  | 19.30 | 15.36 | 140 | 49.49  | 2.E+09 | 70  | 2.E+08 |



|        |  |           |    |    |       |        |      |        |        |     |        |
|--------|--|-----------|----|----|-------|--------|------|--------|--------|-----|--------|
| B2UMM9 | tr B2UMM9 B2UMM9_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1767 PE=4 SV=1                                      | Amuc_1767 | 11 | 11 | 47.60 | 32.22  | 296  | 317.01 | 4.E+09 | 236 | 2.E+08 |
| B2UP96 | tr B2UP96 B2UP96_AKKM8 Thioredoxin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2057 PE=4 SV=1                        | Amuc_2057 | 4  | 4  | 29.30 | 18.12  | 167  | 48.08  | 2.E+09 | 144 | 2.E+08 |
| B2ULL3 | tr B2ULL3 B2ULL3_AKKM8 Nucleoside-diphosphate kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1580 PE=3 SV=1                                | Amuc_1580 | 6  | 6  | 41.70 | 16.91  | 151  | 72.83  | 3.E+09 | 130 | 2.E+08 |
| B2ULU7 | tr B2ULU7 B2ULU7_AKKM8 Thioredoxin domain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0147 PE=4 SV=1   | Amuc_0147 | 9  | 9  | 29.60 | 34.97  | 321  | 86.17  | 4.E+09 | 274 | 2.E+08 |
| B2UP90 | tr B2UP90 B2UP90_AKKM8 Glutamate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2051 PE=3 SV=1                                      | Amuc_2051 | 14 | 14 | 41.70 | 49.57  | 451  | 226.25 | 7.E+09 | 417 | 2.E+08 |
| B2UQH2 | tr B2UQH2 B2UQH2_AKKM8 Elongation factor P OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=efp PE=3 SV=1  | Amuc_0874 | 4  | 4  | 23.40 | 20.91  | 188  | 93.81  | 2.E+09 | 50  | 2.E+08 |
| B2UPN4 | tr B2UPN4 B2UPN4_AKKM8 Methionine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2103 PE=3 SV=1                                      | Amuc_2103 | 9  | 9  | 19.30 | 62.13  | 550  | 235.75 | 5.E+09 | 320 | 2.E+08 |
| B2UPY9 | tr B2UPY9 B2UPY9_AKKM8 Outer membrane autotransporter barrel domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0687 PE=4 SV=1         | Amuc_0687 | 13 | 13 | 27.30 | 107.54 | 1044 | 323.31 | 8.E+09 | 284 | 2.E+08 |
| B2UQ32 | tr B2UQ32 B2UQ32_AKKM8 ATP-grasp domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0730 PE=4 SV=1                          | Amuc_0730 | 9  | 9  | 33.70 | 38.30  | 341  | 127.29 | 4.E+09 | 366 | 2.E+08 |
| B2UQB4 | tr B2UQB4 B2UQB4_AKKM8 Beta sliding clamp OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0816 PE=3 SV=1   | Amuc_0816 | 11 | 11 | 42.30 | 40.54  | 366  | 168.71 | 5.E+09 | 246 | 2.E+08 |
| B2UQ98 | tr B2UQ98 B2UQ98_AKKM8 Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0799 PE=3 SV=1 | Amuc_0799 | 22 | 22 | 27.50 | 129.66 | 1192 | 323.31 | 1.E+10 | 737 | 2.E+08 |
| B2ULC0 | tr B2ULC0 B2ULC0_AKKM8 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0064 PE=4 SV=1           | Amuc_0064 | 7  | 7  | 36.00 | 31.33  | 292  | 130.07 | 3.E+09 | 226 | 2.E+08 |
| B2UN16 | tr B2UN16 B2UN16_AKKM8 NAD(P)H dehydrogenase (Quinone) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1809 PE=4 SV=1                              | Amuc_1809 | 5  | 5  | 26.50 | 20.95  | 185  | 48.54  | 2.E+09 | 122 | 2.E+08 |
| B2UQ84 | tr B2UQ84 B2UQ84_AKKM8 3-isopropylmalate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=leuB PE=3 SV=1                                   | Amuc_0785 | 10 | 10 | 29.00 | 39.80  | 369  | 148.93 | 4.E+09 | 271 | 2.E+08 |
| B2UNN8 | tr B2UNN8 B2UNN8_AKKM8 Adenylosuccinate lyase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1941 PE=3 SV=1                                       | Amuc_1941 | 12 | 12 | 33.50 | 52.42  | 474  | 272.31 | 5.E+09 | 378 | 2.E+08 |
| B2UNE7 | tr B2UNE7 B2UNE7_AKKM8 Glutamine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glnS PE=3 SV=1  | Amuc_0421 | 13 | 13 | 32.20 | 64.11  | 559  | 251.66 | 6.E+09 | 305 | 2.E+08 |
| B2UMG2 | tr B2UMG2 B2UMG2_AKKM8 Histidine triad (HIT) protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0268 PE=4 SV=1                                | Amuc_0268 | 2  | 2  | 21.90 | 12.49  | 114  | 22.34  | 1.E+09 | 82  | 2.E+08 |

|        |   |           |    |    |       |       |     |        |        |     |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|-----|--------|
| B2UM17 | sp B2UM17 FOLD_AKKM8 Bifunctional protein FoID OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=foID PE=3 SV=1                          | Amuc_1641 | 10 | 10 | 51.20 | 30.85 | 291 | 136.95 | 3.E+09 | 230 | 2.E+08 |
| B2UPP6 | sp B2UPP6 SYS_AKKM8 Serine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=serS PE=3 SV=1                                 | Amuc_2115 | 7  | 7  | 21.60 | 47.90 | 426 | 128.81 | 3.E+09 | 208 | 2.E+08 |
| B2UPN2 | tr B2UPN2 B2UPN2_AKKM8 D-ribose pyranase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2101 PE=4 SV=1                           | Amuc_2101 | 4  | 4  | 36.70 | 15.08 | 139 | 39.18  | 8.E+08 | 69  | 2.E+08 |
| B2UQ02 | tr B2UQ02 B2UQ02_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0700 PE=4 SV=1                     | Amuc_0700 | 2  | 2  | 13.70 | 15.12 | 139 | 51.76  | 5.E+08 | 26  | 2.E+08 |
| B2UNE0 | sp B2UNE0 GMHA_AKKM8 Phosphoheptose isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gmhA PE=3 SV=1                           | Amuc_0414 | 3  | 3  | 20.60 | 20.11 | 189 | 73.52  | 1.E+09 | 132 | 2.E+08 |
| B2UQT2 | tr B2UQT2 B2UQT2_AKKM8 TatD-related deoxyribonuclease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0988 PE=4 SV=1              | Amuc_0988 | 6  | 6  | 32.50 | 30.79 | 271 | 102.11 | 3.E+09 | 192 | 2.E+08 |
| B2UMM5 | tr B2UMM5 B2UMM5_AKKM8 Pyridoxal phosphate homeostasis protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1763 PE=3 SV=1     | Amuc_1763 | 5  | 5  | 27.70 | 25.63 | 231 | 63.66  | 2.E+09 | 246 | 1.E+08 |
| B2UN34 | tr B2UN34 B2UN34_AKKM8 Pirin domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1827 PE=3 SV=1                        | Amuc_1827 | 4  | 4  | 12.10 | 26.34 | 232 | 15.68  | 2.E+09 | 105 | 1.E+08 |
| B2UNI4 | tr B2UNI4 B2UNI4_AKKM8 Glutamine amidotransferase class-II OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0458 PE=4 SV=1         | Amuc_0458 | 18 | 18 | 33.30 | 72.22 | 639 | 236.68 | 4.E+09 | 410 | 1.E+08 |
| B2UM77 | tr B2UM77 B2UM77_AKKM8 Ferritin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1703 PE=3 SV=1                                    | Amuc_1703 | 3  | 3  | 17.10 | 18.97 | 164 | 16.60  | 1.E+09 | 84  | 1.E+08 |
| B2ULR5 | tr B2ULR5 B2ULR5_AKKM8 N5-carboxyaminoimidazole ribonucleotide mutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=purE PE=3 SV=1   | Amuc_0114 | 4  | 4  | 40.40 | 14.14 | 136 | 30.20  | 8.E+08 | 69  | 1.E+08 |
| B2ULP8 | tr B2ULP8 B2ULP8_AKKM8 ROK family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0097 PE=4 SV=1                          | Amuc_0097 | 5  | 5  | 22.60 | 33.91 | 319 | 76.81  | 2.E+09 | 164 | 1.E+08 |
| B2UME9 | tr B2UME9 B2UME9_AKKM8 3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=panB PE=3 SV=1 | Amuc_0255 | 6  | 6  | 30.50 | 27.64 | 262 | 65.83  | 1.E+09 | 180 | 1.E+08 |
| B2UR09 | sp B2UR09 METK_AKKM8 S-adenosylmethionine synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=metK PE=3 SV=1                      | Amuc_1068 | 9  | 9  | 29.20 | 43.52 | 394 | 58.07  | 3.E+09 | 145 | 1.E+08 |
| B2UQ68 | tr B2UQ68 B2UQ68_AKKM8 Ferripyochelin binding protein (Fbp) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0768 PE=4 SV=1        | Amuc_0768 | 2  | 2  | 14.00 | 19.07 | 178 | 8.97   | 5.E+08 | 108 | 1.E+08 |
| B2UPW8 | sp B2UPW8 LEUC_AKKM8 3-isopropylmalate dehydratase large subunit OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=leuC PE=3 SV=1        | Amuc_0666 | 9  | 9  | 27.00 | 50.53 | 470 | 94.34  | 3.E+09 | 166 | 1.E+08 |
| B2UPA8 | tr B2UPA8 B2UPA8_AKKM8 Catalase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2070 PE=3 SV=1                                    | Amuc_2070 | 17 | 17 | 29.60 | 84.03 | 751 | 146.98 | 4.E+09 | 296 | 1.E+08 |
| B2UR10 | tr B2UR10 B2UR10_AKKM8 Adenosylhomocysteinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ahcY PE=3 SV=1                           | Amuc_1069 | 7  | 7  | 23.10 | 52.07 | 471 | 123.87 | 3.E+09 | 214 | 1.E+08 |

|        |   |           |    |    |       |        |     |        |        |     |        |
|--------|---|-----------|----|----|-------|--------|-----|--------|--------|-----|--------|
| B2UPH1 | tr B2UPH1 B2UPH1_AKKM8 Phosphoribosyl-AMP cyclohydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=hisI PE=3 SV=1                | Amuc_0611 | 3  | 3  | 23.30 | 17.86  | 163 | 9.66   | 8.E+08 | 52  | 1.E+08 |
| B2UN13 | tr B2UN13 B2UN13_AKKM8 Carboxymuconolactone decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1806 PE=4 SV=1          | Amuc_1806 | 6  | 6  | 29.40 | 28.21  | 255 | 94.40  | 2.E+09 | 161 | 1.E+08 |
| B2ULU8 | tr B2ULU8 B2ULU8_AKKM8 Saccharopine dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0148 PE=4 SV=1                  | Amuc_0148 | 7  | 7  | 28.10 | 45.82  | 409 | 119.97 | 2.E+09 | 185 | 1.E+08 |
| B2UKV6 | sp B2UKV6 DNAK_AKKM8 Chaperone protein DnaK OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dnaK PE=3 SV=1                             | Amuc_1406 | 13 | 13 | 29.30 | 68.85  | 642 | 196.07 | 3.E+09 | 365 | 1.E+08 |
| B2UR52 | sp B2UR52 ILVD_AKKM8 Dihydroxy-acid dehydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ilvD PE=3 SV=1                         | Amuc_1111 | 9  | 9  | 24.60 | 59.48  | 558 | 87.53  | 2.E+09 | 96  | 1.E+08 |
| B2UPP1 | tr B2UPP1 B2UPP1_AKKM8 Orotate phosphoribosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pyrE PE=3 SV=1                | Amuc_2110 | 4  | 4  | 33.90 | 20.13  | 189 | 46.38  | 9.E+08 | 30  | 1.E+08 |
| B2UQ23 | tr B2UQ23 B2UQ23_AKKM8 Fructose-bisphosphate aldolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0721 PE=3 SV=1              | Amuc_0721 | 7  | 7  | 33.20 | 36.92  | 343 | 133.49 | 2.E+09 | 164 | 1.E+08 |
| B2UPS6 | tr B2UPS6 B2UPS6_AKKM8 6-carboxy-5,6,7,8-tetrahydropterin synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2146 PE=3 SV=1 | Amuc_2146 | 4  | 4  | 32.70 | 17.24  | 150 | 29.24  | 9.E+08 | 74  | 1.E+08 |
| B2UNH4 | sp B2UNH4 GCSP_AKKM8 Glycine dehydrogenase (decarboxylating) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gcvP PE=3 SV=1            | Amuc_0448 | 12 | 12 | 15.80 | 102.65 | 948 | 167.26 | 4.E+09 | 140 | 1.E+08 |
| B2UM95 | tr B2UM95 B2UM95_AKKM8 Methylmalonyl-CoA epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0200 PE=3 SV=1                 | Amuc_0200 | 2  | 2  | 19.30 | 15.05  | 140 | 16.76  | 8.E+08 | 49  | 1.E+08 |
| B2UL88 | tr B2UL88 B2UL88_AKKM8 APH domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0030 PE=4 SV=1               | Amuc_0030 | 10 | 10 | 31.60 | 41.66  | 364 | 98.24  | 3.E+09 | 286 | 1.E+08 |
| B2UQP6 | tr B2UQP6 B2UQP6_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0949 PE=3 SV=1         | Amuc_0949 | 2  | 2  | 12.70 | 20.97  | 197 | 47.03  | 6.E+08 | 127 | 1.E+08 |
| B2UM88 | tr B2UM88 B2UM88_AKKM8 Cysteine desulfurase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0193 PE=3 SV=1                        | Amuc_0193 | 10 | 10 | 37.30 | 44.14  | 408 | 88.82  | 2.E+09 | 151 | 1.E+08 |
| B2UL59 | tr B2UL59 B2UL59_AKKM8 NUDIX hydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0001 PE=4 SV=1                             | Amuc_0001 | 3  | 3  | 27.40 | 20.60  | 186 | 60.00  | 7.E+08 | 60  | 9.E+07 |
| B2UNG5 | sp B2UNG5 RS13_AKKM8 30S ribosomal protein S13 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsM PE=3 SV=1                          | Amuc_0439 | 3  | 3  | 31.20 | 14.21  | 125 | 31.36  | 6.E+08 | 29  | 9.E+07 |
| B2UMU1 | sp B2UMU1 RS10_AKKM8 30S ribosomal protein S10 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsJ PE=3 SV=1                          | Amuc_0305 | 2  | 2  | 21.60 | 11.71  | 102 | 13.75  | 4.E+08 | 35  | 9.E+07 |
| B2UN72 | tr B2UN72 B2UN72_AKKM8 Glycosyl transferase group 1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1869 PE=4 SV=1                | Amuc_1869 | 12 | 12 | 30.10 | 47.87  | 432 | 120.81 | 2.E+09 | 139 | 9.E+07 |

|        |   |           |    |    |       |       |     |        |        |     |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|-----|--------|
| B2UM63 | tr B2UM63 B2UM63_AKKM8 Dihydrolypoyl dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1689 PE=3 SV=1                             | Amuc_1689 | 9  | 9  | 25.30 | 48.95 | 462 | 92.78  | 2.E+09 | 159 | 9.E+07 |
| B2ULD3 | tr B2ULD3 B2ULD3_AKKM8 2-amino-3-ketobutyrate coenzyme A ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=kbl PE=3 SV=1                      | Amuc_0077 | 8  | 8  | 27.60 | 43.36 | 399 | 102.03 | 2.E+09 | 156 | 9.E+07 |
| B2UQY3 | sp B2UQY3 JRL7_AKKM8 50S ribosomal protein L7/L12 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpL PE=3 SV=1                                    | Amuc_1042 | 3  | 3  | 27.40 | 12.64 | 124 | 57.71  | 6.E+08 | 60  | 9.E+07 |
| B2UP74 | tr B2UP74 B2UP74_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2035 PE=4 SV=1                                 | Amuc_2035 | 4  | 4  | 22.30 | 27.43 | 251 | 116.43 | 1.E+09 | 59  | 9.E+07 |
| B2UNZ8 | tr B2UNZ8 B2UNZ8_AKKM8 Transketolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0530 PE=3 SV=1   | Amuc_0530 | 17 | 17 | 33.50 | 72.86 | 677 | 157.84 | 3.E+09 | 296 | 8.E+07 |
| B2UP35 | tr B2UP35 B2UP35_AKKM8 Tryptophanase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1995 PE=3 SV=1   | Amuc_1995 | 7  | 7  | 17.90 | 54.00 | 487 | 107.46 | 2.E+09 | 195 | 8.E+07 |
| B2UP77 | tr B2UP77 B2UP77_AKKM8 PUR-alpha/beta/gamma DNA/RNA-binding OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2038 PE=4 SV=1                    | Amuc_2038 | 4  | 4  | 52.90 | 8.11  | 70  | 11.84  | 2.E+08 | 51  | 8.E+07 |
| B2URK3 | tr B2URK3 B2URK3_AKKM8 Quinolinate phosphoribosyltransferase [decarboxylating] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1263 PE=3 SV=1 | Amuc_1263 | 3  | 3  | 13.90 | 30.91 | 287 | 48.31  | 8.E+08 | 108 | 8.E+07 |
| B2UPP7 | tr B2UPP7 B2UPP7_AKKM8 Alcohol dehydrogenase zinc-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2116 PE=3 SV=1       | Amuc_2116 | 7  | 7  | 26.80 | 40.38 | 373 | 64.36  | 1.E+09 | 184 | 8.E+07 |
| B2UKV8 | sp B2UKV8 CH60_AKKM8 60 kDa chaperonin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=grgL PE=3 SV=1  | Amuc_1408 | 11 | 11 | 29.10 | 58.44 | 550 | 157.91 | 3.E+09 | 247 | 7.E+07 |
| B2UM62 | tr B2UM62 B2UM62_AKKM8 Amidohydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1688 PE=4 SV=1  | Amuc_1688 | 4  | 4  | 15.20 | 47.60 | 440 | 55.44  | 1.E+09 | 55  | 7.E+07 |
| B2UPW3 | tr B2UPW3 B2UPW3_AKKM8 D-alanine--D-alanine ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ddl PE=3 SV=1                                   | Amuc_0661 | 3  | 3  | 10.30 | 33.30 | 311 | 23.44  | 1.E+09 | 89  | 7.E+07 |
| B2UNP4 | tr B2UNP4 B2UNP4_AKKM8 N-acylglucosamine 2-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1947 PE=4 SV=1                           | Amuc_1947 | 6  | 6  | 20.60 | 45.60 | 393 | 31.79  | 1.E+09 | 124 | 6.E+07 |
| B2URK6 | tr B2URK6 B2URK6_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1266 PE=4 SV=1                                 | Amuc_1266 | 1  | 1  | 7.70  | 22.40 | 220 | 5.69   | 1.E+08 | 7   | 6.E+07 |
| B2URQ1 | tr B2URQ1 B2URQ1_AKKM8 Peptidase M16 domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1312 PE=4 SV=1                            | Amuc_1312 | 9  | 9  | 14.90 | 93.01 | 840 | 150.12 | 2.E+09 | 211 | 6.E+07 |
| B2UQL1 | tr B2UQL1 B2UQL1_AKKM8 Cupin 2 conserved barrel domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0914 PE=4 SV=1                 | Amuc_0914 | 2  | 2  | 18.80 | 12.31 | 112 | 11.16  | 3.E+08 | 34  | 6.E+07 |
| B2UNJ7 | tr B2UNJ7 B2UNJ7_AKKM8 Flavodoxin/nitric oxide synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1899 PE=4 SV=1                        | Amuc_1899 | 2  | 2  | 14.60 | 15.84 | 144 | 16.15  | 3.E+08 | 31  | 6.E+07 |
| B2UN86 | tr B2UN86 B2UN86_AKKM8 Beta-lactamase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1883 PE=4 SV=1                           | Amuc_1883 | 7  | 7  | 20.20 | 50.21 | 456 | 38.43  | 1.E+09 | 90  | 6.E+07 |

|        |   |           |    |    |       |        |      |        |        |     |        |
|--------|---|-----------|----|----|-------|--------|------|--------|--------|-----|--------|
| B2UPT0 | tr B2UPT0 B2UPT0_AKKM8 Quinolinate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2150 PE=4 SV=1                          | Amuc_2150 | 3  | 3  | 15.80 | 34.45  | 311  | 47.91  | 1.E+09 | 59  | 6.E+07 |
| B2UKP4 | tr B2UKP4 B2UKP4_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1343 PE=4 SV=1                       | Amuc_1343 | 2  | 2  | 13.30 | 20.32  | 188  | 12.68  | 4.E+08 | 41  | 5.E+07 |
| B2UNX2 | tr B2UNX2 B2UNX2_AKKM8 DUF5069 domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0504 PE=4 SV=1             | Amuc_0504 | 2  | 2  | 14.40 | 21.45  | 187  | 13.69  | 5.E+08 | 100 | 5.E+07 |
| B2UMI8 | tr B2UMI8 B2UMI8_AKKM8 UDP-glucuronate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1726 PE=3 SV=1                 | Amuc_1726 | 6  | 6  | 20.60 | 35.03  | 310  | 47.48  | 8.E+08 | 163 | 5.E+07 |
| B2UPX3 | tr B2UPX3 B2UPX3_AKKM8 3-dehydroquinone synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0671 PE=4 SV=1                     | Amuc_0671 | 4  | 4  | 13.20 | 42.15  | 387  | 47.64  | 1.E+09 | 121 | 5.E+07 |
| B2URI5 | tr B2URI5 B2URI5_AKKM8 Mannose-6-phosphate isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1245 PE=3 SV=1                 | Amuc_1245 | 8  | 8  | 32.70 | 34.83  | 306  | 39.99  | 7.E+08 | 60  | 5.E+07 |
| B2UNZ3 | tr B2UNZ3 B2UNZ3_AKKM8 Cycloartenol synthase-like protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0525 PE=4 SV=1            | Amuc_0525 | 8  | 8  | 30.40 | 43.36  | 392  | 42.09  | 1.E+09 | 69  | 5.E+07 |
| B2UM18 | tr B2UM18 B2UM18_AKKM8 Enoyl-[acyl-carrier-protein] reductase [NADH] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1642 PE=3 SV=1 | Amuc_1642 | 5  | 5  | 19.60 | 27.88  | 260  | 26.48  | 8.E+08 | 75  | 5.E+07 |
| B2UKX4 | tr B2UKX4 B2UKX4_AKKM8 Kelch repeat-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1425 PE=4 SV=1               | Amuc_1425 | 2  | 2  | 9.20  | 35.13  | 327  | 29.39  | 7.E+08 | 56  | 5.E+07 |
| B2UQX4 | tr B2UQX4 B2UQX4_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1033 PE=3 SV=1                                     | Amuc_1033 | 9  | 9  | 18.20 | 67.00  | 581  | 42.47  | 2.E+09 | 103 | 5.E+07 |
| B2ULX5 | tr B2ULX5 B2ULX5_AKKM8 PDZ/DHR/GLGF domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0175 PE=4 SV=1                   | Amuc_0175 | 1  | 1  | 4.40  | 42.68  | 390  | 27.86  | 8.E+08 | 20  | 5.E+07 |
| B2UM28 | tr B2UM28 B2UM28_AKKM8 Ribulose-phosphate 3-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpe PE=3 SV=1                      | Amuc_1653 | 3  | 3  | 12.40 | 23.63  | 217  | 15.85  | 2.E+08 | 12  | 5.E+07 |
| B2UPD6 | tr B2UPD6 B2UPD6_AKKM8 Peptidase M16 domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0576 PE=3 SV=1                  | Amuc_0576 | 22 | 22 | 16.90 | 160.48 | 1442 | 199.61 | 4.E+09 | 264 | 5.E+07 |
| B2UQ36 | tr B2UQ36 B2UQ36_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0735 PE=4 SV=1                             | Amuc_0735 | 23 | 23 | 19.20 | 212.82 | 1938 | 161.17 | 4.E+09 | 172 | 4.E+07 |
| B2UQY5 | tr B2UQY5 B2UQY5_AKKM8 50S ribosomal protein L1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rplA PE=3 SV=1                           | Amuc_1044 | 4  | 4  | 26.60 | 24.67  | 233  | 41.16  | 5.E+08 | 34  | 4.E+07 |
| B2UQJ3 | tr B2UQJ3 B2UQJ3_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0895 PE=4 SV=1          | Amuc_0895 | 3  | 3  | 24.30 | 16.87  | 152  | 8.63   | 3.E+08 | 24  | 4.E+07 |
| B2UMU3 | sp B2UMU3 RS7_AKKM8 30S ribosomal protein S7 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsG PE=3 SV=1                              | Amuc_0307 | 2  | 2  | 25.50 | 17.94  | 157  | 28.58  | 3.E+08 | 42  | 4.E+07 |
| B2UL08 | tr B2UL08 B2UL08_AKKM8 Protein GrpE OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=grpE PE=3 SV=1                                       | Amuc_1459 | 2  | 2  | 17.90 | 20.67  | 184  | 32.19  | 2.E+08 | 16  | 4.E+07 |

|               |  |           |    |    |       |        |         |        |        |     |        |
|---------------|--|-----------|----|----|-------|--------|---------|--------|--------|-----|--------|
| B2UP30        | tr B2UP30 B2UP30_AKKM8 Pyrroline-5-carboxylate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=proc PE=3 SV=1   | Amuc_1990 | 3  | 3  | 15.70 | 27.92  | 268     | 30.52  | 5.E+08 | 43  | 4.E+07 |
| B2URK5        | tr B2URK5 B2URK5_AKKM8 Aspartate-semialdehyde dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=asd PE=3 SV=1   | Amuc_1265 | 4  | 4  | 16.70 | 36.06  | 336     | 98.04  | 7.E+08 | 38  | 4.E+07 |
| B2UKZ7        | tr B2UKZ7 B2UKZ7_AKKM8 Arginine biosynthesis bifunctional protein ArgJ OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=argJ PE=3 SV=1   | Amuc_1448 | 6  | 6  | 19.70 | 44.44  | 417     | 35.58  | 9.E+08 | 51  | 4.E+07 |
| B2UQ11        | tr B2UQ11 B2UQ11_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0883 PE=4 SV=1  | Amuc_0883 | 2  | 2  | 21.00 | 6.74   | 62      | 29.80  | 8.E+07 | 4   | 4.E+07 |
| B2UN37        | tr B2UN37 B2UN37_AKKM8 L-fuculokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fuck PE=3 SV=1  | Amuc_1830 | 6  | 6  | 20.50 | 51.25  | 474     | 46.09  | 7.E+08 | 85  | 4.E+07 |
| B2UP85        | tr B2UP85 B2UP85_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2046 PE=4 SV=1  | Amuc_2046 | 4  | 4  | 27.70 | 22.81  | 206     | 27.75  | 5.E+08 | 93  | 4.E+07 |
| B2UNN9        | tr B2UNN9 B2UNN9_AKKM8 Peptidase T OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pepT PE=3 SV=1   | Amuc_1942 | 5  | 5  | 17.70 | 45.12  | 417     | 37.50  | 6.E+08 | 48  | 4.E+07 |
| B2URI3        | sp B2URI3 ISPF_AKKM8 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ispF PE=3 SV=1                                     | Amuc_1243 | 3  | 3  | 21.30 | 17.69  | 169     | 15.18  | 3.E+08 | 15  | 4.E+07 |
| B2UL30        | tr B2UL30 B2UL30_AKKM8 ATP-dependent 6-phosphofructokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pfkA PE=3 SV=1   | Amuc_1481 | 5  | 5  | 15.90 | 37.95  | 359     | 14.12  | 7.E+08 | 53  | 4.E+07 |
| B2UMH5        | sp B2UMH5 SUCC_AKKM8 Succinate--CoA ligase [ADP-forming] subunit beta OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=sucC PE=3 SV=1  | Amuc_1713 | 6  | 6  | 20.40 | 42.34  | 393     | 102.02 | 1.E+09 | 77  | 4.E+07 |
| B2UMH4        | tr B2UMH4 B2UMH4_AKKM8 Succinate--CoA ligase [ADP-forming] subunit alpha OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=sucD PE=3 SV=1                                       | Amuc_1712 | 4  | 4  | 18.60 | 30.57  | 295     | 20.75  | 5.E+08 | 39  | 4.E+07 |
| B2UP52        | tr B2UP52 B2UP52_AKKM8 O-acetylhomoserine/O-acetyls erine sulfhydrylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2013 PE=3 SV=1                                   | Amuc_2013 | 3  | 3  | 8.40  | 46.41  | 428     | 32.68  | 7.E+08 | 51  | 4.E+07 |
| B2UQI4        | tr B2UQI4 B2UQI4_AKKM8 Transketolase central region OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0886 PE=4 SV=1   | Amuc_0886 | 7  | 7  | 30.90 | 35.59  | 324     | 53.97  | 6.E+08 | 81  | 4.E+07 |
| B2UQG5        | tr B2UQG5 B2UQG5_AKKM8 Peptidase M42 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0867 PE=3 SV=1   | Amuc_0867 | 5  | 5  | 19.10 | 41.20  | 382     | 37.51  | 7.E+08 | 38  | 3.E+07 |
| B2UNI3        | tr B2UNI3 B2UNI3_AKKM8 AIR synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0457 PE=3 SV=1   | Amuc_0457 | 5  | 5  | 20.10 | 36.49  | 333     | 66.15  | 6.E+08 | 55  | 3.E+07 |
| B2UN30;B2UQW1 | tr B2UN30 B2UN30_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1823 PE=4 SV=1;tr B2UQW1 B2UQW1_AKKM8 Uncharacterized protein OS=Akkerman | Amuc_1823 | 6  | 6  | 15.40 | 61.69  | 545;546 | 132.90 | 9.E+08 | 75  | 3.E+07 |
| B2UMD4        | tr B2UMD4 B2UMD4_AKKM8 Sec-independent protein translocase protein TatA OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tatA PE=3 SV=1  | Amuc_0240 | 1  | 1  | 19.20 | 10.90  | 99      | 2.87   | 1.E+08 | 8   | 3.E+07 |
| B2UQC2        | tr B2UQC2 B2UQC2_AKKM8 Lactase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0824 PE=3 SV=1  | Amuc_0824 | 20 | 20 | 18.00 | 142.05 | 1264    | 124.73 | 2.E+09 | 273 | 3.E+07 |

|        |   |           |    |    |       |        |      |        |        |     |        |
|--------|---|-----------|----|----|-------|--------|------|--------|--------|-----|--------|
| B2UNT6 | tr B2UNT6 B2UNT6_AKKM8 Transcriptional regulator, DeoR family OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0468 PE=4 SV=1            | Amuc_0468 | 3  | 3  | 14.10 | 27.12  | 249  | 15.20  | 4.E+08 | 30  | 3.E+07 |
| B2UQG3 | tr B2UQG3 B2UQG3_AKKM8 Rubrerythrin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0865 PE=4 SV=1                                      | Amuc_0865 | 4  | 4  | 29.70 | 19.53  | 182  | 35.11  | 3.E+08 | 31  | 3.E+07 |
| B2URJ1 | tr B2URJ1 B2URJ1_AKKM8 Carbamoyl-phosphate synthase large chain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=carB PE=3 SV=1               | Amuc_1251 | 16 | 16 | 21.00 | 117.47 | 1067 | 120.87 | 2.E+09 | 230 | 3.E+07 |
| B2UQE2 | tr B2UQE2 B2UQE2_AKKM8 Enolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=eno PE=3 SV=1   | Amuc_0844 | 6  | 4  | 19.30 | 45.97  | 429  | 25.17  | 5.E+08 | 26  | 3.E+07 |
| B2UP25 | sp B2UP25 RS14_AKKM8 30S ribosomal protein S14 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsN PE=3 SV=1                                | Amuc_0557 | 2  | 2  | 25.80 | 10.28  | 89   | 7.50   | 6.E+07 | 15  | 3.E+07 |
| B2UL21 | sp B2UL21 RL25_AKKM8 50S ribosomal protein L25 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rplY PE=3 SV=1                                | Amuc_1472 | 2  | 2  | 15.40 | 21.01  | 201  | 14.15  | 2.E+08 | 31  | 3.E+07 |
| B2UME2 | tr B2UME2 B2UME2_AKKM8 Nitroreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0248 PE=4 SV=1                                    | Amuc_0248 | 1  | 1  | 7.30  | 20.92  | 193  | 35.31  | 2.E+08 | 30  | 3.E+07 |
| B2UN14 | tr B2UN14 B2UN14_AKKM8 Aldo/keto reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1807 PE=4 SV=1                               | Amuc_1807 | 7  | 7  | 33.40 | 34.57  | 314  | 25.97  | 5.E+08 | 86  | 3.E+07 |
| B2UQC0 | tr B2UQC0 B2UQC0_AKKM8 TatD-related deoxyribonuclease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0822 PE=4 SV=1                    | Amuc_0822 | 4  | 4  | 19.20 | 30.49  | 271  | 25.97  | 5.E+08 | 44  | 3.E+07 |
| B2UQQ6 | tr B2UQQ6 B2UQQ6_AKKM8 dITP/XTP pyrophosphatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0959 PE=3 SV=1                          | Amuc_0959 | 3  | 3  | 21.00 | 23.54  | 214  | 12.43  | 2.E+08 | 34  | 3.E+07 |
| B2UNA9 | sp B2UNA9 PNP_AKKM8 Polyribonucleotide nucleotidyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pnp PE=3 SV=1                  | Amuc_0382 | 8  | 8  | 15.80 | 77.48  | 714  | 35.83  | 9.E+08 | 84  | 3.E+07 |
| B2URG3 | tr B2URG3 B2URG3_AKKM8 Orotidine-5-phosphate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1223 PE=4 SV=1               | Amuc_1223 | 4  | 4  | 22.70 | 28.31  | 264  | 47.74  | 4.E+08 | 49  | 3.E+07 |
| B2UN11 | tr B2UN11 B2UN11_AKKM8 Flavodoxin-like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1804 PE=4 SV=1         | Amuc_1804 | 2  | 2  | 14.00 | 19.22  | 178  | 8.61   | 3.E+08 | 16  | 3.E+07 |
| B2URD0 | tr B2URD0 B2URD0_AKKM8 Alcohol dehydrogenase zinc-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1190 PE=4 SV=1 | Amuc_1190 | 6  | 6  | 25.50 | 36.08  | 333  | 43.43  | 5.E+08 | 62  | 3.E+07 |
| B2UMF9 | sp B2UMF9 PLSX_AKKM8 Phosphate acyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=plsX PE=3 SV=1                                | Amuc_0265 | 1  | 1  | 4.30  | 37.05  | 349  | 5.05   | 5.E+08 | 27  | 3.E+07 |
| B2ULH7 | tr B2ULH7 B2ULH7_AKKM8 Formate C-acetyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1543 PE=3 SV=1                       | Amuc_1543 | 11 | 11 | 20.70 | 85.23  | 755  | 80.99  | 1.E+09 | 158 | 2.E+07 |
| B2ULM1 | tr B2ULM1 B2ULM1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1588 PE=4 SV=1                           | Amuc_1588 | 4  | 4  | 27.80 | 18.54  | 169  | 21.44  | 2.E+08 | 29  | 2.E+07 |
| B2UQI5 | tr B2UQI5 B2UQI5_AKKM8 Dehydrogenase E1 component OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0887 PE=4 SV=1                        | Amuc_0887 | 7  | 7  | 23.70 | 33.92  | 312  | 28.90  | 4.E+08 | 50  | 2.E+07 |

|        |  |           |    |    |       |        |      |        |        |     |        |
|--------|--|-----------|----|----|-------|--------|------|--------|--------|-----|--------|
| B2ULE0 | tr B2ULE0 B2ULE0_AKKM8 PA14 domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0084 PE=4 SV=1                                   | Amuc_0084 | 3  | 3  | 9.90  | 61.62  | 547  | 47.40  | 7.E+08 | 49  | 2.E+07 |
| B2URI2 | tr B2URI2 B2URI2_AKKM8 Inositol-1-monophosphatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1242 PE=3 SV=1                                       | Amuc_1242 | 3  | 3  | 14.20 | 28.52  | 254  | 11.42  | 2.E+08 | 27  | 2.E+07 |
| B2ULB4 | tr B2ULB4 B2ULB4_AKKM8 UvrB/UvrC protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0057 PE=4 SV=1  | Amuc_0057 | 1  | 1  | 7.30  | 19.74  | 178  | 8.37   | 1.E+08 | 15  | 2.E+07 |
| B2UKU8 | tr B2UKU8 B2UKU8_AKKM8 Histidine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1397 PE=3 SV=1   | Amuc_1397 | 7  | 7  | 20.50 | 47.05  | 424  | 40.52  | 5.E+08 | 66  | 2.E+07 |
| B2UN97 | sp B2UN97 AROA_AKKM8 3-phosphoshikimate 1-carboxyvinyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=aroA PE=3 SV=1                            | Amuc_1894 | 3  | 3  | 11.50 | 46.11  | 435  | 19.31  | 3.E+08 | 17  | 2.E+07 |
| B2UL94 | tr B2UL94 B2UL94_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0036 PE=4 SV=1  | Amuc_0036 | 26 | 26 | 19.70 | 214.69 | 1957 | 147.05 | 2.E+09 | 211 | 2.E+07 |
| B2UR15 | tr B2UR15 B2UR15_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1074 PE=3 SV=1  | Amuc_1074 | 5  | 5  | 10.10 | 62.82  | 552  | 18.05  | 5.E+08 | 74  | 2.E+07 |
| B2UQ75 | tr B2UQ75 B2UQ75_AKKM8 Thioesterase superfamily protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0775 PE=3 SV=1                                 | Amuc_0775 | 1  | 1  | 9.70  | 16.96  | 155  | 35.42  | 1.E+08 | 28  | 2.E+07 |
| B2URJ2 | tr B2URJ2 B2URJ2_AKKM8 Glutamine synthetase catalytic region OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1252 PE=3 SV=1                            | Amuc_1252 | 1  | 1  | 1.80  | 78.73  | 711  | 2.27   | 6.E+08 | 1   | 2.E+07 |
| B2UN71 | tr B2UN71 B2UN71_AKKM8 Glycoside hydrolase family 57 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1868 PE=4 SV=1                                    | Amuc_1868 | 5  | 5  | 15.70 | 45.10  | 395  | 13.43  | 3.E+08 | 14  | 2.E+07 |
| B2UPB5 | tr B2UPB5 B2UPB5_AKKM8 Polysaccharide export protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2077 PE=4 SV=1                                    | Amuc_2077 | 4  | 4  | 20.40 | 28.03  | 260  | 35.78  | 3.E+08 | 35  | 2.E+07 |
| B2UM84 | tr B2UM84 B2UM84_AKKM8 Isoleucine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ileS PE=3 SV=1   | Amuc_0189 | 12 | 12 | 16.80 | 102.39 | 909  | 47.91  | 9.E+08 | 189 | 2.E+07 |
| B2UMZ3 | tr B2UMZ3 B2UMZ3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0360 PE=4 SV=1  | Amuc_0360 | 1  | 1  | 11.40 | 19.02  | 184  | 5.77   | 5.E+07 | 6   | 2.E+07 |
| B2UNL2 | tr B2UNL2 B2UNL2_AKKM8 Site-specific DNA-methyltransferase (adenine-specific) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1915 PE=3 SV=1           | Amuc_1915 | 12 | 12 | 15.00 | 95.77  | 853  | 40.70  | 8.E+08 | 86  | 2.E+07 |
| B2ULS7 | tr B2ULS7 B2ULS7_AKKM8 Transposase IS3/IS911 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0127 PE=4 SV=1                             | Amuc_0127 | 3  | 3  | 31.70 | 13.95  | 126  | 16.53  | 1.E+08 | 9   | 2.E+07 |
| B2URJ0 | sp B2URJ0 CARA_AKKM8 Carbamoyl-phosphate synthase small chain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=carA PE=3 SV=1                                | Amuc_1250 | 4  | 4  | 17.70 | 40.19  | 372  | 13.16  | 2.E+08 | 34  | 2.E+07 |
| B2UPP9 | tr B2UPP9 B2UPP9_AKKM8 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2118 PE=4 SV=1 | Amuc_2118 | 3  | 3  | 11.90 | 32.04  | 285  | 14.89  | 2.E+08 | 23  | 2.E+07 |



|               |  |           |    |    |       |        |           |       |        |     |        |
|---------------|--|-----------|----|----|-------|--------|-----------|-------|--------|-----|--------|
| B2UPD0        | tr B2UPD0 B2UPD0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0570 PE=4 SV=1  | Amuc_0570 | 1  | 1  | 17.00 | 12.10  | 100       | 9.16  | 1.E+08 | 8   | 2.E+07 |
| B2UL26        | tr B2UL26 B2UL26_AKKM8 4-hydroxythreonine-4-phosphate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1477 PE=4 SV=1                                       | Amuc_1477 | 3  | 3  | 17.30 | 31.16  | 289       | 16.71 | 2.E+08 | 27  | 2.E+07 |
| B2UPT2;B2UQS7 | tr B2UPT2 B2UPT2_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2152 PE=4 SV=1;tr B2UQS7 B2UQS7_AKKM8 YD repeat protein OS=Akkermansia muciniph | Amuc_2152 | 19 | 19 | 14.20 | 208.44 | 1912;1929 | 76.75 | 1.E+09 | 112 | 2.E+07 |
| B2UPC8        | tr B2UPC8 B2UPC8_AKKM8 Thioesterase superfamily protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0568 PE=3 SV=1   | Amuc_0568 | 2  | 2  | 18.90 | 16.61  | 143       | 14.15 | 1.E+08 | 6   | 1.E+07 |
| B2URL1        | tr B2URL1 B2URL1_AKKM8 GCN5-related N-acetyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1271 PE=4 SV=1   | Amuc_1271 | 1  | 1  | 7.70  | 21.25  | 181       | 13.28 | 1.E+08 | 13  | 1.E+07 |
| B2UM07        | tr B2UM07 B2UM07_AKKM8 Carboxyl-terminal protease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1631 PE=3 SV=1   | Amuc_1631 | 8  | 8  | 13.60 | 83.86  | 748       | 47.61 | 4.E+08 | 31  | 1.E+07 |
| B2UP66        | tr B2UP66 B2UP66_AKKM8 Dihydroorotase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pyrC PE=3 SV=1  | Amuc_2027 | 5  | 5  | 16.80 | 36.40  | 333       | 11.33 | 2.E+08 | 14  | 1.E+07 |
| B2UN04        | tr B2UN04 B2UN04_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1797 PE=4 SV=1  | Amuc_1797 | 2  | 2  | 9.70  | 33.10  | 290       | 6.38  | 2.E+08 | 33  | 1.E+07 |
| B2UR35        | tr B2UR35 B2UR35_AKKM8 ROK family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1094 PE=4 SV=1   | Amuc_1094 | 2  | 2  | 8.70  | 35.76  | 332       | 12.46 | 2.E+08 | 34  | 1.E+07 |
| B2UMD2        | tr B2UMD2 B2UMD2_AKKM8 Beta-lactamase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0238 PE=4 SV=1  | Amuc_0238 | 5  | 5  | 13.00 | 52.42  | 468       | 14.04 | 3.E+08 | 43  | 1.E+07 |
| B2UL38        | tr B2UL38 B2UL38_AKKM8 GMP kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1489 PE=3 SV=1   | Amuc_1489 | 1  | 1  | 5.50  | 22.19  | 200       | 6.92  | 1.E+08 | 30  | 1.E+07 |
| B2ULD1        | tr B2ULD1 B2ULD1_AKKM8 PfkB domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0075 PE=4 SV=1  | Amuc_0075 | 3  | 3  | 11.80 | 39.38  | 355       | 15.84 | 2.E+08 | 7   | 1.E+07 |
| B2UQN1        | tr B2UQN1 B2UQN1_AKKM8 Adenylate kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=adk PE=3 SV=1   | Amuc_0934 | 2  | 2  | 12.00 | 24.69  | 216       | 8.73  | 1.E+08 | 22  | 1.E+07 |
| B2UQM3        | tr B2UQM3 B2UQM3_AKKM8 50S ribosomal protein L5 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpIE PE=3 SV=1  | Amuc_0926 | 1  | 1  | 6.20  | 21.72  | 193       | 5.58  | 1.E+08 | 9   | 1.E+07 |
| B2URF3        | tr B2URF3 B2URF3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1213 PE=4 SV=1  | Amuc_1213 | 2  | 2  | 19.70 | 16.13  | 147       | 5.45  | 7.E+07 | 2   | 9.E+06 |
| B2UL75        | sp B2UL75 G1091_AKKM8 Glycosyl hydrolase family 109 protein 1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0017 PE=3 SV=1   | Amuc_0017 | 4  | 4  | 11.40 | 53.80  | 481       | 43.96 | 2.E+08 | 14  | 9.E+06 |
| B2UNI6        | tr B2UNI6 B2UNI6_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0460 PE=4 SV=1  | Amuc_0460 | 1  | 1  | 14.50 | 19.71  | 173       | 2.24  | 7.E+07 | 5   | 9.E+06 |
| B2UQ57        | tr B2UQ57 B2UQ57_AKKM8 ADP-L-glycero-D-manno-heptose-6-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=hldD PE=3 SV=1   | Amuc_0756 | 4  | 4  | 16.20 | 36.86  | 328       | 14.77 | 2.E+08 | 13  | 9.E+06 |

|        |  |           |   |   |       |       |     |       |        |    |        |
|--------|--|-----------|---|---|-------|-------|-----|-------|--------|----|--------|
| B2UNI9 | tr B2UNI9 B2UNI9_AKKM8 Phosphopantothencysteine decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0463 PE=4 SV=1                 | Amuc_0463 | 2 | 2 | 14.00 | 19.18 | 179 | 7.73  | 6.E+07 | 13 | 9.E+06 |
| B2UNU4 | tr B2UNU4 B2UNU4_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0476 PE=4 SV=1                                | Amuc_0476 | 1 | 1 | 4.60  | 33.64 | 304 | 13.98 | 2.E+08 | 7  | 9.E+06 |
| B2ULS2 | tr B2ULS2 B2ULS2_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0121 PE=3 SV=1  | Amuc_0121 | 6 | 6 | 16.20 | 57.46 | 526 | 22.83 | 3.E+08 | 36 | 9.E+06 |
| B2UN08 | tr B2UN08 B2UN08_AKKM8 Peptidase S15 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1801 PE=4 SV=1  | Amuc_1801 | 5 | 5 | 20.10 | 39.75 | 359 | 23.41 | 2.E+08 | 18 | 9.E+06 |
| B2UN18 | tr B2UN18 B2UN18_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1811 PE=4 SV=1                                | Amuc_1811 | 3 | 3 | 22.00 | 17.22 | 150 | 9.25  | 8.E+07 | 15 | 9.E+06 |
| B2UKV7 | tr B2UKV7 B2UKV7_AKKM8 10 kDa chaperonin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1407 PE=3 SV=1                                      | Amuc_1407 | 2 | 2 | 29.20 | 10.31 | 96  | 7.25  | 4.E+07 | 3  | 8.E+06 |
| B2UQZ5 | tr B2UQZ5 B2UQZ5_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1054 PE=4 SV=1                                | Amuc_1054 | 1 | 1 | 6.40  | 27.80 | 249 | 13.01 | 9.E+07 | 13 | 8.E+06 |
| B2UQQ5 | tr B2UQQ5 B2UQQ5_AKKM8 Exodeoxyribonuclease III OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0958 PE=3 SV=1                               | Amuc_0958 | 2 | 2 | 7.10  | 28.58 | 253 | 6.92  | 1.E+08 | 18 | 8.E+06 |
| B2UL25 | sp B2UL25 RS6_AKKM8 30S ribosomal protein S6 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsF PE=3 SV=1                                       | Amuc_1476 | 1 | 1 | 19.10 | 10.64 | 94  | 2.72  | 4.E+07 | 5  | 8.E+06 |
| B2UKW1 | tr B2UKW1 B2UKW1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1411 PE=4 SV=1                                | Amuc_1411 | 2 | 2 | 16.10 | 21.91 | 224 | 5.25  | 4.E+07 | 2  | 7.E+06 |
| B2UMT3 | sp B2UMT3 RS3_AKKM8 30S ribosomal protein S3 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsC PE=3 SV=1                                       | Amuc_0297 | 3 | 3 | 18.80 | 25.87 | 229 | 19.13 | 1.E+08 | 29 | 7.E+06 |
| B2UQJ8 | tr B2UQJ8 B2UQJ8_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0900 PE=4 SV=1                                | Amuc_0900 | 1 | 1 | 9.80  | 16.58 | 143 | 3.61  | 4.E+07 | 14 | 7.E+06 |
| B2UN24 | tr B2UN24 B2UN24_AKKM8 dTDP-4-dehydrohamnose reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1817 PE=3 SV=1                        | Amuc_1817 | 1 | 1 | 6.60  | 33.39 | 301 | 2.95  | 9.E+07 | 4  | 6.E+06 |
| B2UNL1 | tr B2UNL1 B2UNL1_AKKM8 Restriction modification system DNA specificity domain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1914 PE=4 SV=1 | Amuc_1914 | 2 | 2 | 9.80  | 43.90 | 386 | 11.72 | 1.E+08 | 12 | 6.E+06 |
| B2UNC1 | tr B2UNC1 B2UNC1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0394 PE=4 SV=1                                | Amuc_0394 | 1 | 1 | 6.70  | 27.22 | 252 | 3.45  | 6.E+07 | 12 | 6.E+06 |
| B2URC9 | sp B2URC9 RL28_AKKM8 50S ribosomal protein L28 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpmB PE=3 SV=1                                     | Amuc_1189 | 2 | 2 | 23.00 | 9.85  | 87  | 4.41  | 2.E+07 | 3  | 6.E+06 |
| B2UKX6 | tr B2UKX6 B2UKX6_AKKM8 Histidinol-phosphatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1427 PE=3 SV=1                                 | Amuc_1427 | 2 | 2 | 6.30  | 30.87 | 269 | 2.45  | 7.E+07 | 2  | 5.E+06 |
| B2UQK6 | tr B2UQK6 B2UQK6_AKKM8 3-phosphate/5-hydroxy nucleic acid ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0909 PE=3 SV=1              | Amuc_0909 | 4 | 4 | 13.70 | 41.25 | 371 | 8.23  | 1.E+08 | 10 | 5.E+06 |

|        |   |           |   |   |       |        |      |       |        |    |        |
|--------|---|-----------|---|---|-------|--------|------|-------|--------|----|--------|
| B2UNM5 | tr B2UNM5 B2UNM5_AKKM8 Periplasmic binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1928 PE=4 SV=1                               | Amuc_1928 | 3 | 3 | 14.00 | 32.90  | 307  | 6.88  | 1.E+08 | 22 | 5.E+06 |
| B2URM0 | tr B2URM0 B2URM0_AKKM8 Aminopeptidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1280 PE=4 SV=1  | Amuc_1280 | 2 | 2 | 8.40  | 40.49  | 369  | 7.98  | 9.E+07 | 5  | 5.E+06 |
| B2UPU2 | tr B2UPU2 B2UPU2_AKKM8 Sel1 domain protein repeat-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2163 PE=4 SV=1             | Amuc_2163 | 1 | 1 | 1.60  | 101.34 | 920  | 13.11 | 3.E+08 | 11 | 5.E+06 |
| B2UQ85 | tr B2UQ85 B2UQ85_AKKM8 FAD dependent oxidoreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0786 PE=4 SV=1                              | Amuc_0786 | 2 | 2 | 10.10 | 38.46  | 346  | 6.14  | 9.E+07 | 17 | 5.E+06 |
| B2UPK9 | tr B2UPK9 B2UPK9_AKKM8 Transcriptional regulator MraZ OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=mraZ PE=3 SV=1                                 | Amuc_0649 | 3 | 3 | 24.50 | 17.05  | 151  | 5.24  | 5.E+07 | 9  | 5.E+06 |
| B2UPI5 | tr B2UPI5 B2UPI5_AKKM8 Exo-alpha-sialidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0625 PE=4 SV=1                                       | Amuc_0625 | 2 | 2 | 5.70  | 45.59  | 419  | 3.33  | 1.E+08 | 6  | 5.E+06 |
| B2UQH0 | tr B2UQH0 B2UQH0_AKKM8 Acetylornithine and succinylornithine aminotransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0872 PE=3 SV=1    | Amuc_0872 | 4 | 4 | 12.20 | 45.36  | 418  | 12.23 | 1.E+08 | 23 | 5.E+06 |
| B2URI8 | tr B2URI8 B2URI8_AKKM8 GDP-L-fucose synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fcd PE=3 SV=1   | Amuc_1248 | 3 | 3 | 13.50 | 40.65  | 362  | 10.52 | 7.E+07 | 12 | 4.E+06 |
| B2UL95 | tr B2UL95 B2UL95_AKKM8 Amino acid permease-associated region OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0037 PE=4 SV=1                     | Amuc_0037 | 1 | 1 | 3.40  | 54.19  | 494  | 4.05  | 3.E+07 | 4  | 4.E+06 |
| B2URJ3 | tr B2URJ3 B2URJ3_AKKM8 Glutamate synthase (Ferredoxin) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1253 PE=3 SV=1                           | Amuc_1253 | 6 | 6 | 5.70  | 161.75 | 1479 | 44.35 | 2.E+08 | 17 | 4.E+06 |
| B2URK4 | tr B2URK4 B2URK4_AKKM8 Polyprenyl synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1264 PE=3 SV=1                                     | Amuc_1264 | 1 | 1 | 3.70  | 32.11  | 297  | 4.53  | 3.E+07 | 3  | 3.E+06 |
| B2URE6 | tr B2URE6 B2URE6_AKKM8 Bifunctional purine biosynthesis protein PurH OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=purH PE=3 SV=1                  | Amuc_1206 | 2 | 2 | 4.50  | 56.36  | 515  | 5.65  | 1.E+08 | 16 | 3.E+06 |
| B2UL15 | tr B2UL15 B2UL15_AKKM8 FAD linked oxidase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1466 PE=4 SV=1                         | Amuc_1466 | 4 | 4 | 12.90 | 48.88  | 458  | 8.03  | 8.E+07 | 10 | 3.E+06 |
| B2UMH6 | tr B2UMH6 B2UMH6_AKKM8 Histidinol dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1714 PE=3 SV=1                                  | Amuc_1714 | 2 | 2 | 5.30  | 46.29  | 432  | 8.97  | 6.E+07 | 7  | 3.E+06 |
| B2UKT9 | sp B2UKT9 SPG_AKKM8 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ispG PE=3 SV=1 | Amuc_1388 | 5 | 5 | 13.20 | 64.49  | 585  | 15.11 | 1.E+08 | 26 | 3.E+06 |
| B2ULH3 | tr B2ULH3 B2ULH3_AKKM8 Homoserine O-acetyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=metXA PE=3 SV=1                                | Amuc_1539 | 2 | 2 | 7.50  | 42.86  | 387  | 13.92 | 6.E+07 | 21 | 3.E+06 |
| B2UNN7 | tr B2UNN7 B2UNN7_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1940 PE=4 SV=1                                   | Amuc_1940 | 1 | 1 | 7.30  | 17.21  | 151  | 2.86  | 2.E+07 | 2  | 3.E+06 |

|        |   |           |   |   |       |        |      |       |        |    |        |
|--------|---|-----------|---|---|-------|--------|------|-------|--------|----|--------|
| B2UQU9 | tr B2UQU9 B2UQU9_AKKM8 Glycoside hydrolase family 31 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1008 PE=3 SV=1   | Amuc_1008 | 4 | 4 | 5.30  | 146.26 | 1311 | 11.39 | 2.E+08 | 15 | 3.E+06 |
| B2UND5 | tr B2UND5 B2UND5_AKKM8 Putative substrate-binding protein of aliphatic sulfonate ABC transporter OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0409 PE=4 SV=1 | Amuc_0409 | 2 | 2 | 8.30  | 38.40  | 348  | 3.16  | 5.E+07 | 13 | 3.E+06 |
| B2UNJ4 | tr B2UNJ4 B2UNJ4_AKKM8 Histone family protein DNA-binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1896 PE=3 SV=1                                | Amuc_1896 | 1 | 1 | 11.20 | 9.46   | 89   | 2.66  | 1.E+07 | 5  | 3.E+06 |
| B2UQE7 | sp B2UQE7 MIAB_AKKM8 tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=miaB PE=3 SV=1                           | Amuc_0849 | 2 | 2 | 6.80  | 51.96  | 458  | 6.71  | 7.E+07 | 16 | 3.E+06 |
| B2URA2 | tr B2URA2 B2URA2_AKKM8 Threonine aldolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1162 PE=4 SV=1  | Amuc_1162 | 1 | 1 | 4.60  | 38.74  | 345  | 3.75  | 5.E+07 | 0  | 2.E+06 |
| B2ULC6 | tr B2ULC6 B2ULC6_AKKM8 Tryptophan--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=trpS PE=3 SV=1  | Amuc_0070 | 2 | 2 | 10.00 | 35.86  | 321  | 6.09  | 4.E+07 | 3  | 2.E+06 |
| B2UNV4 | tr B2UNV4 B2UNV4_AKKM8 Ferric uptake regulator, Fur family OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0486 PE=4 SV=1                                       | Amuc_0486 | 1 | 1 | 7.50  | 16.55  | 146  | 6.05  | 2.E+07 | 3  | 2.E+06 |
| B2UQX2 | tr B2UQX2 B2UQX2_AKKM8 Cysteine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=cysS PE=3 SV=1  | Amuc_1031 | 3 | 3 | 7.00  | 53.02  | 471  | 8.35  | 5.E+07 | 16 | 2.E+06 |
| B2UQI0 | tr B2UQI0 B2UQI0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0882 PE=4 SV=1   | Amuc_0882 | 1 | 1 | 11.90 | 11.35  | 109  | 2.99  | 6.E+06 | 2  | 2.E+06 |
| B2UMT7 | sp B2UMT7 RL2_AKKM8 50S ribosomal protein L2 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpIB PE=3 SV=1  | Amuc_0301 | 1 | 1 | 5.40  | 30.66  | 278  | 3.19  | 2.E+07 | 4  | 2.E+06 |
| B2UN50 | tr B2UN50 B2UN50_AKKM8 PDZ/DHR/GLGF domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1844 PE=4 SV=1   | Amuc_1844 | 2 | 2 | 10.00 | 34.08  | 319  | 5.79  | 2.E+07 | 3  | 1.E+06 |
| B2ULN0 | tr B2ULN0 B2ULN0_AKKM8 Polyprenyl synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1597 PE=3 SV=1   | Amuc_1597 | 2 | 2 | 5.70  | 37.33  | 336  | 2.80  | 2.E+07 | 10 | 1.E+06 |
| B2ULK3 | tr B2ULK3 B2ULK3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1569 PE=4 SV=1   | Amuc_1569 | 1 | 1 | 7.50  | 18.51  | 173  | 5.63  | 1.E+07 | 1  | 1.E+06 |
| B2UM66 | tr B2UM66 B2UM66_AKKM8 2-oxoglutarate dehydrogenase complex component E2 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1692 PE=3 SV=1                         | Amuc_1692 | 1 | 1 | 5.20  | 39.16  | 363  | 3.09  | 2.E+07 | 4  | 1.E+06 |
| B2UQQ8 | tr B2UQQ8 B2UQQ8_AKKM8 DUF362 domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0961 PE=4 SV=1  | Amuc_0961 | 1 | 1 | 5.30  | 30.33  | 282  | 5.62  | 1.E+07 | 4  | 9.E+05 |
| B2UQJ6 | tr B2UQJ6 B2UQJ6_AKKM8 DNA topoisomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0898 PE=3 SV=1   | Amuc_0898 | 4 | 4 | 4.90  | 97.19  | 869  | 7.12  | 5.E+07 | 8  | 9.E+05 |
| B2ULZ9 | sp B2ULZ9 RIMO_AKKM8 Ribosomal protein S12 methyltransferase RimO OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rmo PE=3 SV=1                                      | Amuc_1623 | 4 | 4 | 10.00 | 50.86  | 452  | 5.59  | 2.E+07 | 5  | 9.E+05 |

|        |  |           |   |   |       |        |      |      |        |   |        |
|--------|--|-----------|---|---|-------|--------|------|------|--------|---|--------|
| B2UQE3 | sp B2UQE3 END4_AKKM8 Probable endonuclease 4 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=info PE=3 SV=1                           | Amuc_0845 | 3 | 3 | 14.10 | 30.78  | 277  | 4.26 | 1.E+07 | 1 | 8.E+05 |
| B2UMT6 | sp B2UMT6 RS19_AKKM8 30S ribosomal protein S19 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsS PE=3 SV=1                         | Amuc_0300 | 1 | 1 | 16.90 | 9.80   | 89   | 3.40 | 5.E+06 | 1 | 8.E+05 |
| B2UN91 | sp B2UN91 SYE_AKKM8 Glutamate--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gltx PE=3 SV=1                             | Amuc_1888 | 2 | 2 | 7.60  | 48.61  | 433  | 6.33 | 2.E+07 | 7 | 8.E+05 |
| B2UNY2 | tr B2UNY2 B2UNY2_AKKM8 Peptidoglycan glycosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0514 PE=4 SV=1          | Amuc_0514 | 2 | 2 | 4.10  | 89.28  | 822  | 7.04 | 3.E+07 | 3 | 7.E+05 |
| B2UR84 | tr B2UR84 B2UR84_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1143 PE=4 SV=1                          | Amuc_1143 | 3 | 3 | 2.40  | 217.62 | 1991 | 2.39 | 6.E+07 | 4 | 7.E+05 |
| B2ULH4 | tr B2ULH4 B2ULH4_AKKM8 50S ribosomal protein L36 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpmJ PE=3 SV=1                       | Amuc_1540 | 1 | 1 | 6.20  | 16.69  | 144  | 3.70 | 7.E+06 | 1 | 7.E+05 |
| B2UNB9 | tr B2UNB9 B2UNB9_AKKM8 Coagulation factor 5/8 type domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0392 PE=4 SV=1 | Amuc_0392 | 1 | 1 | 1.10  | 78.57  | 709  | 2.49 | 3.E+07 | 8 | 6.E+05 |
| B2UQ76 | tr B2UQ76 B2UQ76_AKKM8 Short-chain dehydrogenase/reductase SDR OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0777 PE=4 SV=1    | Amuc_0777 | 1 | 1 | 4.30  | 32.30  | 299  | 5.96 | 9.E+06 | 2 | 5.E+05 |
| B2UKU3 | tr B2UKU3 B2UKU3_AKKM8 Beta-ketoacyl synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1392 PE=3 SV=1                     | Amuc_1392 | 2 | 2 | 6.40  | 40.31  | 390  | 2.93 | 4.E+06 | 1 | 2.E+05 |
| B2URL5 | tr B2URL5 B2URL5_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1275 PE=4 SV=1                    | Amuc_1275 | 2 | 2 | 6.60  | 38.86  | 348  | 3.84 | 2.E+06 | 2 | 1.E+05 |
| B2UPQ8 | tr B2UPQ8 B2UPQ8_AKKM8 Carbohydrate-selective porin OprB OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2127 PE=3 SV=1          | Amuc_2127 | 1 | 1 | 3.00  | 53.33  | 494  | 2.50 | 0.E+00 | 2 | 0.E+00 |
| B2UL46 | tr B2UL46 B2UL46_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1497 PE=4 SV=1                    | Amuc_1497 | 2 | 2 | 6.60  | 38.92  | 349  | 2.63 | 0.E+00 | 2 | 0.E+00 |

**Supplementary Table 2. List of proteins with at least two unique peptides identified in secretome of *A. muciniphila* cultivated under basal medium.**

| Majority protein IDs | Fasta headers  | Gene locus | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Sequence lengths | Score  | Intensity | MS/MS count | iBAQ   |
|----------------------|--|------------|----------|-----------------|-----------------------|-------------------|------------------|--------|-----------|-------------|--------|
| B2UKW7               | tr B2UKW7 B2UKW7_AKKM8 Glyceraldehyde-3-phosphate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1417 PE=3 SV=1   | Amuc_1417  | 21       | 21              | 68.00                 | 36.74             | 341              | 323.31 | 5.E+11    | 3106        | 2.E+10 |
| B2UQS2               | sp B2UQS2 ACP_AKKM8 Acyl carrier protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=acpP PE=3 SV=1                               | Amuc_0975  | 3        | 3               | 40.00                 | 8.82              | 80               | 200.16 | 6.E+10    | 1971        | 2.E+10 |
| B2UP94               | tr B2UP94 B2UP94_AKKM8 Rubrerythrin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2055 PE=4 SV=1     | Amuc_2055  | 7        | 5               | 86.00                 | 12.73             | 114              | 264.75 | 1.E+11    | 1261        | 2.E+10 |
| B2UMR7               | tr B2UMR7 B2UMR7_AKKM8 Histone family protein DNA-binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0281 PE=3 SV=1 | Amuc_0281  | 4        | 4               | 50.50                 | 11.25             | 101              | 210.98 | 6.E+10    | 587         | 2.E+10 |
| B2UQP3               | tr B2UQP3 B2UQP3_AKKM8 DJ-1 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0946 PE=4 SV=1                        | Amuc_0946  | 11       | 11              | 67.90                 | 20.11             | 187              | 323.31 | 1.E+11    | 1832        | 1.E+10 |
| B2ULM5               | tr B2ULM5 B2ULM5_AKKM8 Superoxide dismutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1592 PE=3 SV=1                       | Amuc_1592  | 11       | 11              | 56.10                 | 23.92             | 214              | 323.31 | 2.E+11    | 1249        | 1.E+10 |
| B2URC4               | tr B2URC4 B2URC4_AKKM8 Enolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=eno PE=3 SV=1  | Amuc_1184  | 19       | 17              | 67.10                 | 45.68             | 426              | 323.31 | 3.E+11    | 3686        | 1.E+10 |
| B2UPZ3               | tr B2UPZ3 B2UPZ3_AKKM8 Thioredoxin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0691 PE=3 SV=1                                | Amuc_0691  | 5        | 5               | 66.70                 | 11.49             | 105              | 237.29 | 6.E+10    | 502         | 1.E+10 |
| B2URF0               | tr B2URF0 B2URF0_AKKM8 Phosphoenolpyruvate carboxykinase [GTP] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pckG PE=3 SV=1         | Amuc_1210  | 22       | 22              | 48.40                 | 67.52             | 608              | 323.31 | 2.E+11    | 2108        | 8.E+09 |
| B2UN99               | tr B2UN99 B2UN99_AKKM8 Glutamate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0372 PE=3 SV=1                    | Amuc_0372  | 24       | 24              | 65.90                 | 52.46             | 466              | 323.31 | 2.E+11    | 2064        | 7.E+09 |
| B2UKW8               | sp B2UKW8 PGK_AKKM8 Phosphoglycerate kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pgk PE=3 SV=1                             | Amuc_1418  | 24       | 24              | 75.20                 | 42.69             | 403              | 323.31 | 1.E+11    | 2595        | 6.E+09 |
| B2UKV9               | tr B2UKV9 B2UKV9_AKKM8 PepSY-like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1409 PE=4 SV=1       | Amuc_1409  | 8        | 8               | 52.00                 | 16.52             | 150              | 245.16 | 4.E+10    | 538         | 5.E+09 |
| B2UQ05               | tr B2UQ05 B2UQ05_AKKM8 Alanine--glyoxylate transaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0703 PE=3 SV=1           | Amuc_0703  | 20       | 20              | 76.80                 | 39.28             | 357              | 323.31 | 1.E+11    | 2027        | 5.E+09 |
| B2UNK0               | tr B2UNK0 B2UNK0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1902 PE=4 SV=1                    | Amuc_1902  | 13       | 13              | 71.30                 | 24.93             | 230              | 323.31 | 5.E+10    | 917         | 4.E+09 |
| B2UN29               | tr B2UN29 B2UN29_AKKM8 Glucosamine-6-phosphate deaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=nagB PE=3 SV=1               | Amuc_1822  | 10       | 10              | 46.90                 | 32.84             | 303              | 323.31 | 6.E+10    | 535         | 4.E+09 |
| B2UNL9               | tr B2UNL9 B2UNL9_AKKM8 Putative ferredoxin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1922 PE=4 SV=1                        | Amuc_1922  | 2        | 2               | 24.70                 | 8.40              | 77               | 134.67 | 2.E+10    | 78          | 3.E+09 |

|        |   |           |    |    |       |       |     |        |        |      |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|------|--------|
| B2UNS8 | trjB2UNS8 B2UNS8_AKKM8 Methylmalonyl-CoA mutase, large subunit OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1983 PE=4 SV=1       | Amuc_1983 | 25 | 25 | 46.50 | 78.41 | 714 | 323.31 | 1.E+11 | 1974 | 3.E+09 |
| B2UL96 | spjB2UL96 GLSA_AKKM8 Glutaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glSA PE=3 SV=1  | Amuc_0038 | 7  | 7  | 31.00 | 33.13 | 313 | 186.41 | 3.E+10 | 391  | 3.E+09 |
| B2UPF0 | trjB2UPF0 B2UPF0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0590 PE=4 SV=1                       | Amuc_0590 | 22 | 22 | 51.50 | 50.45 | 460 | 323.31 | 6.E+10 | 1665 | 3.E+09 |
| B2ULM2 | trjB2ULM2 B2ULM2_AKKM8 Aminotransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1589 PE=3 SV=1                              | Amuc_1589 | 14 | 14 | 52.80 | 42.44 | 388 | 323.31 | 4.E+10 | 986  | 3.E+09 |
| B2UNH3 | trjB2UNH3 B2UNH3_AKKM8 Glycine cleavage system H protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gcvH PE=3 SV=1                  | Amuc_0447 | 3  | 3  | 40.50 | 13.72 | 126 | 120.45 | 5.E+09 | 111  | 3.E+09 |
| B2UKY5 | spjB2UKY5 MDH_AKKM8 Malate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=mdh PE=3 SV=1                                   | Amuc_1436 | 13 | 13 | 47.10 | 35.10 | 329 | 323.31 | 4.E+10 | 548  | 2.E+09 |
| B2UQP5 | trjB2UQP5 B2UQP5_AKKM8 N-acetylglucosamine-6-phosphate deacetylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0948 PE=3 SV=1   | Amuc_0948 | 12 | 12 | 45.30 | 40.83 | 382 | 323.31 | 4.E+10 | 614  | 2.E+09 |
| B2UNS2 | trjB2UNS2 B2UNS2_AKKM8 Glucose-6-phosphate isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pgi PE=3 SV=1                       | Amuc_1975 | 25 | 25 | 58.30 | 55.47 | 515 | 323.31 | 6.E+10 | 1407 | 2.E+09 |
| B2UP29 | trjB2UP29 B2UP29_AKKM8 Triosephosphate isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tpiA PE=3 SV=1                          | Amuc_0562 | 10 | 10 | 61.40 | 26.99 | 254 | 323.31 | 2.E+10 | 517  | 2.E+09 |
| B2UL55 | trjB2UL55 B2UL55_AKKM8 Malonyl CoA-acyl carrier protein transacylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1507 PE=3 SV=1 | Amuc_1507 | 9  | 9  | 41.90 | 32.57 | 308 | 323.31 | 3.E+10 | 444  | 2.E+09 |
| B2URK9 | trjB2URK9 B2URK9_AKKM8 Thioredoxin reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1269 PE=3 SV=1                         | Amuc_1269 | 8  | 8  | 31.70 | 33.21 | 309 | 248.71 | 2.E+10 | 506  | 2.E+09 |
| B2UPR8 | trjB2UPR8 B2UPR8_AKKM8 Nitroreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2137 PE=3 SV=1                                | Amuc_2137 | 11 | 11 | 49.30 | 24.41 | 215 | 275.58 | 2.E+10 | 767  | 2.E+09 |
| B2ULH2 | trjB2ULH2 B2ULH2_AKKM8 OsmC family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1538 PE=4 SV=1                           | Amuc_1538 | 4  | 4  | 49.30 | 14.99 | 136 | 173.93 | 9.E+09 | 241  | 1.E+09 |
| B2UR48 | trjB2UR48 B2UR48_AKKM8 ATP phosphoribosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=hisG PE=3 SV=1                      | Amuc_1107 | 11 | 11 | 52.20 | 32.70 | 291 | 323.31 | 2.E+10 | 397  | 1.E+09 |
| B2UP53 | trjB2UP53 B2UP53_AKKM8 Cysteine synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2014 PE=3 SV=1                             | Amuc_2014 | 15 | 15 | 86.40 | 32.53 | 309 | 323.31 | 2.E+10 | 867  | 1.E+09 |
| B2UPE1 | trjB2UPE1 B2UPE1_AKKM8 Meso-diaminopimelate D-dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0581 PE=3 SV=1          | Amuc_0581 | 17 | 17 | 72.40 | 31.31 | 293 | 323.31 | 2.E+10 | 1032 | 1.E+09 |
| B2URE7 | spjB2URE7 PDXJ_AKKM8 Pyridoxine 5-phosphate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pxdJ PE=3 SV=1                      | Amuc_1207 | 7  | 7  | 49.60 | 27.11 | 246 | 323.31 | 1.E+10 | 1276 | 1.E+09 |

|        |   |           |    |    |       |       |     |        |        |      |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|------|--------|
| B2UL89 | trjB2UL89 B2UL89_AKKM8 NTP_transferase domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0031 PE=4 SV=1                       | Amuc_0031 | 10 | 10 | 46.70 | 32.12 | 291 | 164.51 | 2.E+10 | 381  | 1.E+09 |
| B2UMF1 | sp B2UMF1 DAPB_AKKM8 4-hydroxy-tetrahydrodipicolinate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dapB PE=3 SV=1                             | Amuc_0257 | 8  | 8  | 50.00 | 26.31 | 246 | 289.43 | 2.E+10 | 443  | 1.E+09 |
| B2UMG7 | trjB2UMG7 B2UMG7_AKKM8 Endoribonuclease L-PSP OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1705 PE=4 SV=1  | Amuc_1705 | 6  | 6  | 67.90 | 16.64 | 156 | 323.31 | 8.E+09 | 590  | 1.E+09 |
| B2UNK1 | trjB2UNK1 B2UNK1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1903 PE=4 SV=1   | Amuc_1903 | 10 | 10 | 40.30 | 35.41 | 335 | 323.31 | 2.E+10 | 554  | 1.E+09 |
| B2UM96 | trjB2UM96 B2UM96_AKKM8 Carboxyl transferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0201 PE=4 SV=1  | Amuc_0201 | 11 | 11 | 33.60 | 56.01 | 521 | 323.31 | 2.E+10 | 506  | 1.E+09 |
| B2ULV5 | trjB2ULV5 B2ULV5_AKKM8 Phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain I OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0155 PE=3 SV=1 | Amuc_0155 | 20 | 20 | 42.70 | 71.24 | 651 | 323.31 | 3.E+10 | 1126 | 1.E+09 |
| B2UP27 | trjB2UP27 B2UP27_AKKM8 Argininosuccinate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=argJ PE=3 SV=1   | Amuc_0559 | 14 | 14 | 44.70 | 47.87 | 430 | 308.42 | 2.E+10 | 1173 | 1.E+09 |
| B2UQY9 | sp B2UQY9 EFTU_AKKM8 Elongation factor Tu OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tuf PE=3 SV=1  | Amuc_1048 | 10 | 10 | 34.30 | 43.43 | 394 | 323.31 | 2.E+10 | 628  | 1.E+09 |
| B2UMA1 | trjB2UMA1 B2UMA1_AKKM8 Succinate CoA transferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0206 PE=3 SV=1                                       | Amuc_0206 | 23 | 23 | 61.00 | 54.05 | 498 | 323.31 | 2.E+10 | 859  | 9.E+08 |
| B2UKM8 | trjB2UKM8 B2UKM8_AKKM8 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1327 PE=3 SV=1                     | Amuc_1327 | 8  | 8  | 34.70 | 43.82 | 415 | 251.36 | 1.E+10 | 885  | 9.E+08 |
| B2UMF2 | trjB2UMF2 B2UMF2_AKKM8 4-hydroxy-tetrahydrodipicolinate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dapA PE=3 SV=1                            | Amuc_0258 | 7  | 7  | 34.10 | 31.25 | 293 | 205.55 | 2.E+10 | 458  | 9.E+08 |
| B2UNS9 | trjB2UNS9 B2UNS9_AKKM8 Methylmalonyl-CoA mutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1984 PE=4 SV=1  | Amuc_1984 | 26 | 26 | 50.60 | 74.10 | 684 | 323.31 | 3.E+10 | 1054 | 9.E+08 |
| B2UPB0 | trjB2UPB0 B2UPB0_AKKM8 Rubrerythrin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2072 PE=4 SV=1  | Amuc_2072 | 3  | 3  | 19.90 | 21.34 | 191 | 177.17 | 6.E+09 | 143  | 8.E+08 |
| B2UQW7 | trjB2UQW7 B2UQW7_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1026 PE=3 SV=1                             | Amuc_1026 | 5  | 5  | 47.90 | 17.92 | 167 | 260.88 | 6.E+09 | 192  | 8.E+08 |
| B2UQ07 | trjB2UQ07 B2UQ07_AKKM8 2-oxoglutarate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0705 PE=3 SV=1  | Amuc_0705 | 14 | 14 | 37.90 | 56.68 | 523 | 323.31 | 2.E+10 | 561  | 8.E+08 |
| B2UMX5 | trjB2UMX5 B2UMX5_AKKM8 OsmC family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0342 PE=4 SV=1   | Amuc_0342 | 7  | 7  | 65.20 | 14.48 | 135 | 113.32 | 5.E+09 | 262  | 8.E+08 |
| B2UNP8 | trjB2UNP8 B2UNP8_AKKM8 NADH:flavin oxidoreductase/NADH oxidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1951 PE=4 SV=1                         | Amuc_1951 | 16 | 16 | 49.90 | 40.82 | 367 | 323.31 | 1.E+10 | 578  | 7.E+08 |



|        |  |           |    |    |       |        |     |        |        |      |        |
|--------|--|-----------|----|----|-------|--------|-----|--------|--------|------|--------|
| B2UPU6 | tr B2UPU6 B2UPU6_AKKM8 Oligopeptidase A OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2167 PE=3 SV=1                                     | Amuc_2167 | 18 | 18 | 38.40 | 79.32  | 700 | 323.31 | 3.E+10 | 871  | 7.E+08 |
| B2URP8 | tr B2URP8 B2URP8_AKKM8 Aldose 1-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1309 PE=3 SV=1                                   | Amuc_1309 | 11 | 11 | 49.20 | 34.50  | 319 | 287.90 | 1.E+10 | 405  | 7.E+08 |
| B2UL16 | tr B2UL16 B2UL16_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1467 PE=4 SV=1                              | Amuc_1467 | 4  | 4  | 16.50 | 22.00  | 194 | 98.66  | 6.E+09 | 160  | 7.E+08 |
| B2UN39 | tr B2UN39 B2UN39_AKKM8 L-fucose isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fucl PE=3 SV=1  | Amuc_1832 | 20 | 20 | 39.20 | 64.70  | 592 | 323.31 | 2.E+10 | 765  | 7.E+08 |
| B2UML6 | sp B2UML6 OTC_AKKM8 Ornithine carbamoyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=arcB PE=3 SV=1                               | Amuc_1630 | 11 | 11 | 47.90 | 34.14  | 305 | 323.31 | 1.E+10 | 527  | 7.E+08 |
| B2UMU5 | sp B2UMU5 GPMI_AKKM8 2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gpmI PE=3 SV=1 | Amuc_0309 | 14 | 14 | 37.70 | 56.14  | 514 | 323.31 | 2.E+10 | 554  | 7.E+08 |
| B2UPJ1 | tr B2UPJ1 B2UPJ1_AKKM8 FAD-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0631 PE=4 SV=1                           | Amuc_0631 | 13 | 13 | 53.50 | 41.44  | 376 | 323.31 | 1.E+10 | 521  | 7.E+08 |
| B2UNK9 | tr B2UNK9 B2UNK9_AKKM8 Iron-containing alcohol dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1911 PE=4 SV=1                | Amuc_1911 | 9  | 9  | 37.60 | 41.35  | 386 | 175.54 | 9.E+09 | 482  | 7.E+08 |
| B2UMC9 | tr B2UMC9 B2UMC9_AKKM8 Alpha-glucan phosphorylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0235 PE=3 SV=1                           | Amuc_0235 | 22 | 22 | 49.50 | 63.41  | 554 | 323.31 | 2.E+10 | 936  | 6.E+08 |
| B2UPQ6 | tr B2UPQ6 B2UPQ6_AKKM8 Adenylosuccinate synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=purA PE=3 SV=1                               | Amuc_2125 | 10 | 10 | 28.80 | 46.05  | 423 | 219.74 | 1.E+10 | 788  | 6.E+08 |
| B2UL87 | tr B2UL87 B2UL87_AKKM8 NAD-dependent epimerase/dehydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0029 PE=4 SV=1                  | Amuc_0029 | 10 | 10 | 39.30 | 33.59  | 308 | 165.07 | 1.E+10 | 440  | 6.E+08 |
| B2UP16 | tr B2UP16 B2UP16_AKKM8 MotA/TolQ/ExbB proton channel OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0548 PE=3 SV=1                        | Amuc_0548 | 2  | 2  | 11.80 | 28.34  | 263 | 12.58  | 3.E+09 | 44   | 6.E+08 |
| B2UNS1 | tr B2UNS1 B2UNS1_AKKM8 Pyruvate, phosphate dikinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1974 PE=3 SV=1                         | Amuc_1974 | 22 | 22 | 30.60 | 100.12 | 914 | 323.31 | 3.E+10 | 1239 | 6.E+08 |
| B2UKY9 | tr B2UKY9 B2UKY9_AKKM8 Nitroreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1440 PE=3 SV=1                                       | Amuc_1440 | 7  | 7  | 31.60 | 24.93  | 215 | 58.67  | 5.E+09 | 169  | 6.E+08 |
| B2UQR6 | tr B2UQR6 B2UQR6_AKKM8 Galactokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0969 PE=3 SV=1  | Amuc_0969 | 9  | 9  | 29.30 | 42.15  | 392 | 223.84 | 1.E+10 | 418  | 5.E+08 |
| B2UN63 | tr B2UN63 B2UN63_AKKM8 Formate--tetrahydrofolate ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fhs PE=3 SV=1                           | Amuc_1860 | 17 | 17 | 40.90 | 59.80  | 557 | 323.31 | 2.E+10 | 898  | 5.E+08 |
| B2UMC7 | tr B2UMC7 B2UMC7_AKKM8 L-threonine 3-dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=tdh PE=3 SV=1                                | Amuc_0233 | 7  | 7  | 31.00 | 37.54  | 345 | 250.40 | 7.E+09 | 294  | 5.E+08 |

|        |   |           |    |    |       |       |     |        |        |      |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|------|--------|
| B2UM06 | tr B2UM06 B2UM06_AKKM8 Serine hydroxymethyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glyA PE=3 SV=1  | Amuc_1630 | 22 | 22 | 50.40 | 61.10 | 566 | 323.31 | 2.E+10 | 849  | 5.E+08 |
| B2UP04 | tr B2UP04 B2UP04_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0536 PE=4 SV=1   | Amuc_0536 | 6  | 6  | 34.00 | 28.70 | 259 | 195.84 | 6.E+09 | 190  | 5.E+08 |
| B2UMA5 | tr B2UMA5 B2UMA5_AKKM8 6-phosphofructokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0210 PE=4 SV=1   | Amuc_0210 | 7  | 7  | 25.00 | 35.31 | 320 | 144.82 | 6.E+09 | 251  | 5.E+08 |
| B2UQW6 | tr B2UQW6 B2UQW6_AKKM8 Disulfide bond chaperones of the HSP33 family-like protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1025 PE=4 SV=1              | Amuc_1025 | 10 | 10 | 47.10 | 30.09 | 257 | 310.77 | 7.E+09 | 575  | 5.E+08 |
| B2UNP3 | tr B2UNP3 B2UNP3_AKKM8 Dihydropicolinate synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1946 PE=3 SV=1  | Amuc_1946 | 6  | 6  | 25.60 | 33.03 | 305 | 119.27 | 8.E+09 | 463  | 5.E+08 |
| B2UPS4 | tr B2UPS4 B2UPS4_AKKM8 Fumarate hydratase class I OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2144 PE=3 SV=1  | Amuc_2144 | 21 | 21 | 53.80 | 60.10 | 548 | 323.31 | 2.E+10 | 611  | 5.E+08 |
| B2UN19 | tr B2UN19 B2UN19_AKKM8 Alpha amylase catalytic region OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1812 PE=3 SV=1  | Amuc_1812 | 12 | 12 | 37.00 | 56.72 | 492 | 162.51 | 1.E+10 | 509  | 4.E+08 |
| B2UQK1 | tr B2UQK1 B2UQK1_AKKM8 Aconitate hydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0904 PE=3 SV=1   | Amuc_0904 | 23 | 23 | 38.40 | 99.01 | 917 | 323.31 | 2.E+10 | 1077 | 4.E+08 |
| B2URI9 | tr B2URI9 B2URI9_AKKM8 GDP-mannose 4,6-dehydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gmd PE=3 SV=1   | Amuc_1249 | 14 | 14 | 51.00 | 40.86 | 355 | 219.04 | 9.E+09 | 591  | 4.E+08 |
| B2UQE5 | tr B2UQE5 B2UQE5_AKKM8 Metal dependent phosphohydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0847 PE=4 SV=1  | Amuc_0847 | 9  | 9  | 33.90 | 39.25 | 354 | 58.34  | 7.E+09 | 76   | 4.E+08 |
| B2UMK3 | tr B2UMK3 B2UMK3_AKKM8 UTP--glucose-1-phosphate uridylyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1741 PE=3 SV=1                            | Amuc_1741 | 15 | 15 | 42.50 | 50.44 | 461 | 291.62 | 9.E+09 | 394  | 4.E+08 |
| B2UN83 | tr B2UN83 B2UN83_AKKM8 Isocitrate dehydrogenase [NADP] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1880 PE=4 SV=1   | Amuc_1880 | 18 | 18 | 50.10 | 45.31 | 415 | 166.12 | 9.E+09 | 552  | 4.E+08 |
| B2UQ06 | tr B2UQ06 B2UQ06_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0704 PE=4 SV=1   | Amuc_0704 | 9  | 9  | 26.40 | 47.48 | 417 | 313.47 | 8.E+09 | 349  | 4.E+08 |
| B2UMM1 | tr B2UMM1 B2UMM1_AKKM8 Peptidase M20 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1759 PE=4 SV=1   | Amuc_1759 | 11 | 11 | 24.30 | 50.33 | 465 | 139.33 | 7.E+09 | 496  | 3.E+08 |
| B2UR66 | tr B2UR66 B2UR66_AKKM8 UDP-glucose 4-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1125 PE=3 SV=1   | Amuc_1125 | 7  | 7  | 31.30 | 36.07 | 329 | 100.94 | 5.E+09 | 310  | 3.E+08 |
| B2UKM2 | tr B2UKM2 B2UKM2_AKKM8 Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1321 PE=3 SV=1 | Amuc_1321 | 5  | 5  | 36.20 | 22.83 | 207 | 126.45 | 3.E+09 | 170  | 3.E+08 |
| B2UN36 | tr B2UN36 B2UN36_AKKM8 Class II aldolase/adducin family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1829 PE=4 SV=1                                | Amuc_1829 | 7  | 7  | 39.90 | 29.81 | 271 | 200.78 | 4.E+09 | 313  | 3.E+08 |

|        |   |           |    |    |       |       |     |        |        |     |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|-----|--------|
| B2UKP3 | tr B2UKP3 B2UKP3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1342 PE=4 SV=1                                       | Amuc_1342 | 4  | 4  | 17.30 | 34.98 | 312 | 90.38  | 5.E+09 | 235 | 3.E+08 |
| B2UMG1 | tr B2UMG1 B2UMG1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0267 PE=4 SV=1                                       | Amuc_0267 | 5  | 5  | 30.10 | 18.11 | 163 | 118.25 | 3.E+09 | 255 | 3.E+08 |
| B2UR47 | tr B2UR47 B2UR47_AKKM8 Peptidase M24 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1106 PE=4 SV=1   | Amuc_1106 | 11 | 11 | 26.00 | 48.19 | 427 | 134.55 | 6.E+09 | 465 | 3.E+08 |
| B2ULA2 | tr B2ULA2 B2ULA2_AKKM8 Diaminopimelate epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dapF PE=3 SV=1  | Amuc_0044 | 6  | 6  | 28.50 | 29.30 | 274 | 140.20 | 4.E+09 | 193 | 3.E+08 |
| B2UL47 | tr B2UL47 B2UL47_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1498 PE=3 SV=1                                       | Amuc_1498 | 8  | 8  | 43.20 | 25.20 | 229 | 106.89 | 3.E+09 | 238 | 3.E+08 |
| B2UPF7 | tr B2UPF7 B2UPF7_AKKM8 Flavin Reduct domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0597 PE=4 SV=1                       | Amuc_0597 | 4  | 4  | 30.40 | 19.05 | 168 | 60.60  | 2.E+09 | 220 | 3.E+08 |
| B2UQT1 | tr B2UQT1 B2UQT1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0987 PE=4 SV=1                                       | Amuc_0987 | 5  | 5  | 67.80 | 9.56  | 90  | 65.07  | 2.E+09 | 167 | 3.E+08 |
| B2URF8 | tr B2URF8 B2URF8_AKKM8 3-dehydroquinate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=aroB PE=3 SV=1  | Amuc_1218 | 11 | 11 | 44.10 | 39.26 | 370 | 178.11 | 6.E+09 | 214 | 3.E+08 |
| B2UR44 | tr B2UR44 B2UR44_AKKM8 Glutamyl aminopeptidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1103 PE=3 SV=1                                       | Amuc_1103 | 8  | 8  | 29.50 | 38.13 | 359 | 70.29  | 5.E+09 | 169 | 3.E+08 |
| B2UQ25 | tr B2UQ25 B2UQ25_AKKM8 Branched-chain-amino-acid aminotransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ilvE PE=3 SV=1                         | Amuc_0723 | 6  | 6  | 31.90 | 31.84 | 288 | 120.56 | 5.E+09 | 154 | 3.E+08 |
| B2UKZ6 | sp B2UKZ6 ARGC_AKKM8 N-acetyl-gamma-glutamyl-phosphate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=argC PE=3 SV=1                          | Amuc_1447 | 7  | 7  | 34.60 | 37.59 | 347 | 137.05 | 4.E+09 | 246 | 3.E+08 |
| B2UPN7 | tr B2UPN7 B2UPN7_AKKM8 Malate dehydrogenase (Oxaloacetate-decarboxylating) (NADP(+)) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2106 PE=3 SV=1 | Amuc_2106 | 12 | 12 | 45.00 | 47.52 | 436 | 166.38 | 6.E+09 | 271 | 3.E+08 |
| B2UMD1 | tr B2UMD1 B2UMD1_AKKM8 Arsenate reductase and related OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0237 PE=3 SV=1                                | Amuc_0237 | 5  | 5  | 46.20 | 13.52 | 119 | 55.32  | 2.E+09 | 110 | 3.E+08 |
| B2URB8 | sp B2URB8 ILVC_AKKM8 Ketol-acid reductoisomerase (NADP(+)) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ilvC PE=3 SV=1                                | Amuc_1178 | 10 | 10 | 44.80 | 35.14 | 326 | 175.89 | 4.E+09 | 297 | 3.E+08 |
| B2UMZ5 | tr B2UMZ5 B2UMZ5_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0362 PE=4 SV=1                                       | Amuc_0362 | 2  | 2  | 19.30 | 15.36 | 140 | 49.49  | 2.E+09 | 70  | 2.E+08 |
| B2UMM9 | tr B2UMM9 B2UMM9_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1767 PE=4 SV=1                                       | Amuc_1767 | 11 | 11 | 47.60 | 32.22 | 296 | 317.01 | 4.E+09 | 236 | 2.E+08 |
| B2UP96 | tr B2UP96 B2UP96_AKKM8 Thioredoxin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2057 PE=4 SV=1                         | Amuc_2057 | 4  | 4  | 29.30 | 18.12 | 167 | 48.08  | 2.E+09 | 144 | 2.E+08 |

|        |  |           |    |    |       |        |      |        |        |     |        |
|--------|--|-----------|----|----|-------|--------|------|--------|--------|-----|--------|
| B2ULL3 | trjB2ULL3 B2ULL3_AKKM8 Nucleoside-diphosphate kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1580 PE=3 SV=1                                | Amuc_1580 | 6  | 6  | 41.70 | 16.91  | 151  | 72.83  | 3.E+09 | 130 | 2.E+08 |
| B2ULU7 | trjB2ULU7 B2ULU7_AKKM8 Thioredoxin domain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0147 PE=4 SV=1   | Amuc_0147 | 9  | 9  | 29.60 | 34.97  | 321  | 86.17  | 4.E+09 | 274 | 2.E+08 |
| B2UP90 | trjB2UP90 B2UP90_AKKM8 Glutamate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2051 PE=3 SV=1                                      | Amuc_2051 | 14 | 14 | 41.70 | 49.57  | 451  | 226.25 | 7.E+09 | 417 | 2.E+08 |
| B2UQH2 | trjB2UQH2 B2UQH2_AKKM8 Elongation factor P OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=efp PE=3 SV=1  | Amuc_0874 | 4  | 4  | 23.40 | 20.91  | 188  | 93.81  | 2.E+09 | 50  | 2.E+08 |
| B2UPN4 | trjB2UPN4 B2UPN4_AKKM8 Methionine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2103 PE=3 SV=1                                      | Amuc_2103 | 9  | 9  | 19.30 | 62.13  | 550  | 235.75 | 5.E+09 | 320 | 2.E+08 |
| B2UPY9 | trjB2UPY9 B2UPY9_AKKM8 Outer membrane autotransporter barrel domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0687 PE=4 SV=1         | Amuc_0687 | 13 | 13 | 27.30 | 107.54 | 1044 | 323.31 | 8.E+09 | 284 | 2.E+08 |
| B2UQ32 | trjB2UQ32 B2UQ32_AKKM8 ATP-grasp domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0730 PE=4 SV=1                          | Amuc_0730 | 9  | 9  | 33.70 | 38.30  | 341  | 127.29 | 4.E+09 | 366 | 2.E+08 |
| B2UQB4 | trjB2UQB4 B2UQB4_AKKM8 Beta sliding clamp OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0816 PE=3 SV=1   | Amuc_0816 | 11 | 11 | 42.30 | 40.54  | 366  | 168.71 | 5.E+09 | 246 | 2.E+08 |
| B2UQ98 | trjB2UQ98 B2UQ98_AKKM8 Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0799 PE=3 SV=1 | Amuc_0799 | 22 | 22 | 27.50 | 129.66 | 1192 | 323.31 | 1.E+10 | 737 | 2.E+08 |
| B2ULC0 | trjB2ULC0 B2ULC0_AKKM8 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0064 PE=4 SV=1           | Amuc_0064 | 7  | 7  | 36.00 | 31.33  | 292  | 130.07 | 3.E+09 | 226 | 2.E+08 |
| B2UN16 | trjB2UN16 B2UN16_AKKM8 NAD(P)H dehydrogenase (Quinone) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1809 PE=4 SV=1                              | Amuc_1809 | 5  | 5  | 26.50 | 20.95  | 185  | 48.54  | 2.E+09 | 122 | 2.E+08 |
| B2UQ84 | trjB2UQ84 B2UQ84_AKKM8 3-isopropylmalate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=leuB PE=3 SV=1                                   | Amuc_0785 | 10 | 10 | 29.00 | 39.80  | 369  | 148.93 | 4.E+09 | 271 | 2.E+08 |
| B2UNN8 | trjB2UNN8 B2UNN8_AKKM8 Adenylosuccinate lyase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1941 PE=3 SV=1                                       | Amuc_1941 | 12 | 12 | 33.50 | 52.42  | 474  | 272.31 | 5.E+09 | 378 | 2.E+08 |
| B2UNE7 | trjB2UNE7 B2UNE7_AKKM8 Glutamine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glnS PE=3 SV=1  | Amuc_0421 | 13 | 13 | 32.20 | 64.11  | 559  | 251.66 | 6.E+09 | 305 | 2.E+08 |
| B2UMG2 | trjB2UMG2 B2UMG2_AKKM8 Histidine triad (HIT) protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0268 PE=4 SV=1                                | Amuc_0268 | 2  | 2  | 21.90 | 12.49  | 114  | 22.34  | 1.E+09 | 82  | 2.E+08 |
| B2UM17 | spjB2UM17 FOLD_AKKM8 Bifunctional protein FoId OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=foId PE=3 SV=1   | Amuc_1641 | 10 | 10 | 51.20 | 30.85  | 291  | 136.95 | 3.E+09 | 230 | 2.E+08 |
| B2UPP6 | spjB2UPP6 SYS_AKKM8 Serine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=serS PE=3 SV=1  | Amuc_2115 | 7  | 7  | 21.60 | 47.90  | 426  | 128.81 | 3.E+09 | 208 | 2.E+08 |

|        |   |           |    |    |       |       |     |        |        |     |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|-----|--------|
| B2UPN2 | tr B2UPN2 B2UPN2_AKKM8 D-ribose pyranase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2101 PE=4 SV=1                           | Amuc_2101 | 4  | 4  | 36.70 | 15.08 | 139 | 39.18  | 8.E+08 | 69  | 2.E+08 |
| B2UQ02 | tr B2UQ02 B2UQ02_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0700 PE=4 SV=1                     | Amuc_0700 | 2  | 2  | 13.70 | 15.12 | 139 | 51.76  | 5.E+08 | 26  | 2.E+08 |
| B2UNE0 | sp B2UNE0 GMHA_AKKM8 Phosphoheptose isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gmhA PE=3 SV=1                           | Amuc_0414 | 3  | 3  | 20.60 | 20.11 | 189 | 73.52  | 1.E+09 | 132 | 2.E+08 |
| B2UQT2 | tr B2UQT2 B2UQT2_AKKM8 TatD-related deoxyribonuclease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0988 PE=4 SV=1              | Amuc_0988 | 6  | 6  | 32.50 | 30.79 | 271 | 102.11 | 3.E+09 | 192 | 2.E+08 |
| B2UMM5 | tr B2UMM5 B2UMM5_AKKM8 Pyridoxal phosphate homeostasis protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1763 PE=3 SV=1     | Amuc_1763 | 5  | 5  | 27.70 | 25.63 | 231 | 63.66  | 2.E+09 | 246 | 1.E+08 |
| B2UN34 | tr B2UN34 B2UN34_AKKM8 Pirin domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1827 PE=3 SV=1                        | Amuc_1827 | 4  | 4  | 12.10 | 26.34 | 232 | 15.68  | 2.E+09 | 105 | 1.E+08 |
| B2UNI4 | tr B2UNI4 B2UNI4_AKKM8 Glutamine amidotransferase class-II OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0458 PE=4 SV=1         | Amuc_0458 | 18 | 18 | 33.30 | 72.22 | 639 | 236.68 | 4.E+09 | 410 | 1.E+08 |
| B2UM77 | tr B2UM77 B2UM77_AKKM8 Ferritin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1703 PE=3 SV=1                                    | Amuc_1703 | 3  | 3  | 17.10 | 18.97 | 164 | 16.60  | 1.E+09 | 84  | 1.E+08 |
| B2ULR5 | tr B2ULR5 B2ULR5_AKKM8 N5-carboxyaminoimidazole ribonucleotide mutase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=purE PE=3 SV=1   | Amuc_0114 | 4  | 4  | 40.40 | 14.14 | 136 | 30.20  | 8.E+08 | 69  | 1.E+08 |
| B2ULP8 | tr B2ULP8 B2ULP8_AKKM8 ROK family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0097 PE=4 SV=1                          | Amuc_0097 | 5  | 5  | 22.60 | 33.91 | 319 | 76.81  | 2.E+09 | 164 | 1.E+08 |
| B2UME9 | tr B2UME9 B2UME9_AKKM8 3-methyl-2-oxobutanoate hydroxymethyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=panB PE=3 SV=1 | Amuc_0255 | 6  | 6  | 30.50 | 27.64 | 262 | 65.83  | 1.E+09 | 180 | 1.E+08 |
| B2UR09 | sp B2UR09 METK_AKKM8 S-adenosylmethionine synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=metK PE=3 SV=1                      | Amuc_1068 | 9  | 9  | 29.20 | 43.52 | 394 | 58.07  | 3.E+09 | 145 | 1.E+08 |
| B2UQ68 | tr B2UQ68 B2UQ68_AKKM8 Ferrityochelin binding protein (Fbp) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0768 PE=4 SV=1        | Amuc_0768 | 2  | 2  | 14.00 | 19.07 | 178 | 8.97   | 5.E+08 | 108 | 1.E+08 |
| B2UPW8 | sp B2UPW8 LEUC_AKKM8 3-isopropylmalate dehydratase large subunit OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=leuC PE=3 SV=1        | Amuc_0666 | 9  | 9  | 27.00 | 50.53 | 470 | 94.34  | 3.E+09 | 166 | 1.E+08 |
| B2UPA8 | tr B2UPA8 B2UPA8_AKKM8 Catalase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2070 PE=3 SV=1                                    | Amuc_2070 | 17 | 17 | 29.60 | 84.03 | 751 | 146.98 | 4.E+09 | 296 | 1.E+08 |
| B2UR10 | tr B2UR10 B2UR10_AKKM8 Adenosylhomocysteinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ahcY PE=3 SV=1                           | Amuc_1069 | 7  | 7  | 23.10 | 52.07 | 471 | 123.87 | 3.E+09 | 214 | 1.E+08 |
| B2UPH1 | tr B2UPH1 B2UPH1_AKKM8 Phosphoribosyl-AMP cyclohydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=hisI PE=3 SV=1                | Amuc_0611 | 3  | 3  | 23.30 | 17.86 | 163 | 9.66   | 8.E+08 | 52  | 1.E+08 |
| B2UN13 | tr B2UN13 B2UN13_AKKM8 Carboxymuconolactone decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 /   | Amuc_1806 | 6  | 6  | 29.40 | 28.21 | 255 | 94.40  | 2.E+09 | 161 | 1.E+08 |

|        |   |           |    |    |       |        |     |        |        |     |        |  |
|--------|---|-----------|----|----|-------|--------|-----|--------|--------|-----|--------|--|
|        | BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1806 PE=4 SV=1  |           |    |    |       |        |     |        |        |     |        |  |
| B2ULU8 | tr B2ULU8 B2ULU8_AKKM8 Saccharopine dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0148 PE=4 SV=1                  | Amuc_0148 | 7  | 7  | 28.10 | 45.82  | 409 | 119.97 | 2.E+09 | 185 | 1.E+08 |  |
| B2UKV6 | sp B2UKV6 DNAK_AKKM8 Chaperone protein DnaK OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=dnaK PE=3 SV=1                             | Amuc_1406 | 13 | 13 | 29.30 | 68.85  | 642 | 196.07 | 3.E+09 | 365 | 1.E+08 |  |
| B2UR52 | sp B2UR52 ILVD_AKKM8 Dihydroxy-acid dehydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ilvd PE=3 SV=1                         | Amuc_1111 | 9  | 9  | 24.60 | 59.48  | 558 | 87.53  | 2.E+09 | 96  | 1.E+08 |  |
| B2UPP1 | tr B2UPP1 B2UPP1_AKKM8 Orotate phosphoribosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pyrE PE=3 SV=1                | Amuc_2110 | 4  | 4  | 33.90 | 20.13  | 189 | 46.38  | 9.E+08 | 30  | 1.E+08 |  |
| B2UQ23 | tr B2UQ23 B2UQ23_AKKM8 Fructose-bisphosphate aldolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0721 PE=3 SV=1              | Amuc_0721 | 7  | 7  | 33.20 | 36.92  | 343 | 133.49 | 2.E+09 | 164 | 1.E+08 |  |
| B2UPS6 | tr B2UPS6 B2UPS6_AKKM8 6-carboxy-5,6,7,8-tetrahydropterin synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2146 PE=3 SV=1 | Amuc_2146 | 4  | 4  | 32.70 | 17.24  | 150 | 29.24  | 9.E+08 | 74  | 1.E+08 |  |
| B2UNH4 | sp B2UNH4 GCSP_AKKM8 Glycine dehydrogenase (decarboxylating) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gcvP PE=3 SV=1            | Amuc_0448 | 12 | 12 | 15.80 | 102.65 | 948 | 167.26 | 4.E+09 | 140 | 1.E+08 |  |
| B2UM95 | tr B2UM95 B2UM95_AKKM8 Methylmalonyl-CoA epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0200 PE=3 SV=1                 | Amuc_0200 | 2  | 2  | 19.30 | 15.05  | 140 | 16.76  | 8.E+08 | 49  | 1.E+08 |  |
| B2UL88 | tr B2UL88 B2UL88_AKKM8 APH domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0030 PE=4 SV=1               | Amuc_0030 | 10 | 10 | 31.60 | 41.66  | 364 | 98.24  | 3.E+09 | 286 | 1.E+08 |  |
| B2UQP6 | tr B2UQP6 B2UQP6_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0949 PE=3 SV=1         | Amuc_0949 | 2  | 2  | 12.70 | 20.97  | 197 | 47.03  | 6.E+08 | 127 | 1.E+08 |  |
| B2UM88 | tr B2UM88 B2UM88_AKKM8 Cysteine desulfurase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0193 PE=3 SV=1                        | Amuc_0193 | 10 | 10 | 37.30 | 44.14  | 408 | 88.82  | 2.E+09 | 151 | 1.E+08 |  |
| B2UL59 | tr B2UL59 B2UL59_AKKM8 NUDIX hydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0001 PE=4 SV=1                             | Amuc_0001 | 3  | 3  | 27.40 | 20.60  | 186 | 60.00  | 7.E+08 | 60  | 9.E+07 |  |
| B2UNG5 | sp B2UNG5 RS13_AKKM8 30S ribosomal protein S13 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsM PE=3 SV=1                          | Amuc_0439 | 3  | 3  | 31.20 | 14.21  | 125 | 31.36  | 6.E+08 | 29  | 9.E+07 |  |
| B2UMU1 | sp B2UMU1 RS10_AKKM8 30S ribosomal protein S10 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsJ PE=3 SV=1                          | Amuc_0305 | 2  | 2  | 21.60 | 11.71  | 102 | 13.75  | 4.E+08 | 35  | 9.E+07 |  |
| B2UN72 | tr B2UN72 B2UN72_AKKM8 Glycosyl transferase group 1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1869 PE=4 SV=1                | Amuc_1869 | 12 | 12 | 30.10 | 47.87  | 432 | 120.81 | 2.E+09 | 139 | 9.E+07 |  |
| B2UM63 | tr B2UM63 B2UM63_AKKM8 Dihydrolypoyl dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1689 PE=3 SV=1                 | Amuc_1689 | 9  | 9  | 25.30 | 48.95  | 462 | 92.78  | 2.E+09 | 159 | 9.E+07 |  |

|        |   |           |    |    |       |       |     |        |        |     |        |
|--------|---|-----------|----|----|-------|-------|-----|--------|--------|-----|--------|
| B2ULD3 | trjB2ULD3 B2ULD3_AKKM8 2-amino-3-ketobutyrate coenzyme A ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=kbl PE=3 SV=1                    | Amuc_0077 | 8  | 8  | 27.60 | 43.36 | 399 | 102.03 | 2.E+09 | 156 | 9.E+07 |
| B2UQY3 | sp B2UQY3 RL7_AKKM8 50S ribosomal protein L7/L12 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpL PE=3 SV=1                                   | Amuc_1042 | 3  | 3  | 27.40 | 12.64 | 124 | 57.71  | 6.E+08 | 60  | 9.E+07 |
| B2UP74 | trjB2UP74 B2UP74_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2035 PE=4 SV=1                               | Amuc_2035 | 4  | 4  | 22.30 | 27.43 | 251 | 116.43 | 1.E+09 | 59  | 9.E+07 |
| B2UNZ8 | trjB2UNZ8 B2UNZ8_AKKM8 Transketolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0530 PE=3 SV=1   | Amuc_0530 | 17 | 17 | 33.50 | 72.86 | 677 | 157.84 | 3.E+09 | 296 | 8.E+07 |
| B2UP35 | trjB2UP35 B2UP35_AKKM8 Tryptophanase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1995 PE=3 SV=1   | Amuc_1995 | 7  | 7  | 17.90 | 54.00 | 487 | 107.46 | 2.E+09 | 195 | 8.E+07 |
| B2UP77 | trjB2UP77 B2UP77_AKKM8 PUR-alpha/beta/gamma DNA/RNA-binding OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2038 PE=4 SV=1                  | Amuc_2038 | 4  | 4  | 52.90 | 8.11  | 70  | 11.84  | 2.E+08 | 51  | 8.E+07 |
| B2URK3 | trjB2URK3 B2URK3_AKKM8 Quinolate phosphoribosyltransferase [decarboxylating] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1263 PE=3 SV=1 | Amuc_1263 | 3  | 3  | 13.90 | 30.91 | 287 | 48.31  | 8.E+08 | 108 | 8.E+07 |
| B2UPP7 | trjB2UPP7 B2UPP7_AKKM8 Alcohol dehydrogenase zinc-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2116 PE=3 SV=1     | Amuc_2116 | 7  | 7  | 26.80 | 40.38 | 373 | 64.36  | 1.E+09 | 184 | 8.E+07 |
| B2UKV8 | sp B2UKV8 CH60_AKKM8 60 kDa chaperonin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=groL PE=3 SV=1  | Amuc_1408 | 11 | 11 | 29.10 | 58.44 | 550 | 157.91 | 3.E+09 | 247 | 7.E+07 |
| B2UM62 | trjB2UM62 B2UM62_AKKM8 Amidohydrolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1688 PE=4 SV=1  | Amuc_1688 | 4  | 4  | 15.20 | 47.60 | 440 | 55.44  | 1.E+09 | 55  | 7.E+07 |
| B2UPW3 | trjB2UPW3 B2UPW3_AKKM8 D-alanine--D-alanine ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ddl PE=3 SV=1                                 | Amuc_0661 | 3  | 3  | 10.30 | 33.30 | 311 | 23.44  | 1.E+09 | 89  | 7.E+07 |
| B2UNP4 | trjB2UNP4 B2UNP4_AKKM8 N-acetylglucosamine 2-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1947 PE=4 SV=1                       | Amuc_1947 | 6  | 6  | 20.60 | 45.60 | 393 | 31.79  | 1.E+09 | 124 | 6.E+07 |
| B2URQ1 | trjB2URQ1 B2URQ1_AKKM8 Peptidase M16 domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1312 PE=4 SV=1                          | Amuc_1312 | 9  | 9  | 14.90 | 93.01 | 840 | 150.12 | 2.E+09 | 211 | 6.E+07 |
| B2UQL1 | trjB2UQL1 B2UQL1_AKKM8 Cupin 2 conserved barrel domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0914 PE=4 SV=1               | Amuc_0914 | 2  | 2  | 18.80 | 12.31 | 112 | 11.16  | 3.E+08 | 34  | 6.E+07 |
| B2UNJ7 | trjB2UNJ7 B2UNJ7_AKKM8 Flavodoxin/nitric oxide synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1899 PE=4 SV=1                      | Amuc_1899 | 2  | 2  | 14.60 | 15.84 | 144 | 16.15  | 3.E+08 | 31  | 6.E+07 |
| B2UN86 | trjB2UN86 B2UN86_AKKM8 Beta-lactamase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1883 PE=4 SV=1                         | Amuc_1883 | 7  | 7  | 20.20 | 50.21 | 456 | 38.43  | 1.E+09 | 90  | 6.E+07 |
| B2UPT0 | trjB2UPT0 B2UPT0_AKKM8 Quinolate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2150 PE=4 SV=1                                    | Amuc_2150 | 3  | 3  | 15.80 | 34.45 | 311 | 47.91  | 1.E+09 | 59  | 6.E+07 |

|        |   |           |    |    |       |        |      |        |        |     |        |
|--------|---|-----------|----|----|-------|--------|------|--------|--------|-----|--------|
| B2UKP4 | tr B2UKP4 B2UKP4_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1343 PE=4 SV=1                       | Amuc_1343 | 2  | 2  | 13.30 | 20.32  | 188  | 12.68  | 4.E+08 | 41  | 5.E+07 |
| B2UNX2 | tr B2UNX2 B2UNX2_AKKM8 DUF5069 domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0504 PE=4 SV=1             | Amuc_0504 | 2  | 2  | 14.40 | 21.45  | 187  | 13.69  | 5.E+08 | 100 | 5.E+07 |
| B2UMI8 | tr B2UMI8 B2UMI8_AKKM8 UDP-glucuronate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1726 PE=3 SV=1                 | Amuc_1726 | 6  | 6  | 20.60 | 35.03  | 310  | 47.48  | 8.E+08 | 163 | 5.E+07 |
| B2UPX3 | tr B2UPX3 B2UPX3_AKKM8 3-dehydroquinase synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0671 PE=4 SV=1                     | Amuc_0671 | 4  | 4  | 13.20 | 42.15  | 387  | 47.64  | 1.E+09 | 121 | 5.E+07 |
| B2URI5 | tr B2URI5 B2URI5_AKKM8 Mannose-6-phosphate isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1245 PE=3 SV=1                 | Amuc_1245 | 8  | 8  | 32.70 | 34.83  | 306  | 39.99  | 7.E+08 | 60  | 5.E+07 |
| B2UNZ3 | tr B2UNZ3 B2UNZ3_AKKM8 Cycloartenol synthase-like protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0525 PE=4 SV=1            | Amuc_0525 | 8  | 8  | 30.40 | 43.36  | 392  | 42.09  | 1.E+09 | 69  | 5.E+07 |
| B2UM18 | tr B2UM18 B2UM18_AKKM8 Enoyl-[acyl-carrier-protein] reductase [NADH] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1642 PE=3 SV=1 | Amuc_1642 | 5  | 5  | 19.60 | 27.88  | 260  | 26.48  | 8.E+08 | 75  | 5.E+07 |
| B2UKX4 | tr B2UKX4 B2UKX4_AKKM8 Kelch repeat-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1425 PE=4 SV=1               | Amuc_1425 | 2  | 2  | 9.20  | 35.13  | 327  | 29.39  | 7.E+08 | 56  | 5.E+07 |
| B2UQX4 | tr B2UQX4 B2UQX4_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1033 PE=3 SV=1                                     | Amuc_1033 | 9  | 9  | 18.20 | 67.00  | 581  | 42.47  | 2.E+09 | 103 | 5.E+07 |
| B2UM28 | tr B2UM28 B2UM28_AKKM8 Ribulose-phosphate 3-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpe PE=3 SV=1                      | Amuc_1653 | 3  | 3  | 12.40 | 23.63  | 217  | 15.85  | 2.E+08 | 12  | 5.E+07 |
| B2UPD6 | tr B2UPD6 B2UPD6_AKKM8 Peptidase M16 domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0576 PE=3 SV=1                  | Amuc_0576 | 22 | 22 | 16.90 | 160.48 | 1442 | 199.61 | 4.E+09 | 264 | 5.E+07 |
| B2UQ36 | tr B2UQ36 B2UQ36_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0735 PE=4 SV=1                             | Amuc_0735 | 23 | 23 | 19.20 | 212.82 | 1938 | 161.17 | 4.E+09 | 172 | 4.E+07 |
| B2UQY5 | tr B2UQY5 B2UQY5_AKKM8 50S ribosomal protein L1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rplA PE=3 SV=1                           | Amuc_1044 | 4  | 4  | 26.60 | 24.67  | 233  | 41.16  | 5.E+08 | 34  | 4.E+07 |
| B2UQJ3 | tr B2UQJ3 B2UQJ3_AKKM8 PepSY-like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0895 PE=4 SV=1          | Amuc_0895 | 3  | 3  | 24.30 | 16.87  | 152  | 8.63   | 3.E+08 | 24  | 4.E+07 |
| B2UMU3 | sp B2UMU3 RS7_AKKM8 30S ribosomal protein S7 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsG PE=3 SV=1                              | Amuc_0307 | 2  | 2  | 25.50 | 17.94  | 157  | 28.58  | 3.E+08 | 42  | 4.E+07 |
| B2UL08 | tr B2UL08 B2UL08_AKKM8 Protein GrpE OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=grpE PE=3 SV=1                                       | Amuc_1459 | 2  | 2  | 17.90 | 20.67  | 184  | 32.19  | 2.E+08 | 16  | 4.E+07 |
| B2UP30 | tr B2UP30 B2UP30_AKKM8 Pyrroline-5-carboxylate reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=proC PE=3 SV=1                  | Amuc_1990 | 3  | 3  | 15.70 | 27.92  | 268  | 30.52  | 5.E+08 | 43  | 4.E+07 |
| B2URK5 | tr B2URK5 B2URK5_AKKM8 Aspartate-semialdehyde dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=asd PE=3 SV=1                | Amuc_1265 | 4  | 4  | 16.70 | 36.06  | 336  | 98.04  | 7.E+08 | 38  | 4.E+07 |



|               |   |           |    |    |       |        |         |        |        |     |        |
|---------------|---|-----------|----|----|-------|--------|---------|--------|--------|-----|--------|
| B2UKZ7        | trjB2UKZ7 B2UKZ7_AKKM8 Arginine biosynthesis bifunctional protein ArgJ OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=argJ PE=3 SV=1  | Amuc_1448 | 6  | 6  | 19.70 | 44.44  | 417     | 35.58  | 9.E+08 | 51  | 4.E+07 |
| B2UQI1        | trjB2UQI1 B2UQI1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0883 PE=4 SV=1   | Amuc_0883 | 2  | 2  | 21.00 | 6.74   | 62      | 29.80  | 8.E+07 | 4   | 4.E+07 |
| B2UN37        | trjB2UN37 B2UN37_AKKM8 L-fuculokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fuck PE=3 SV=1   | Amuc_1830 | 6  | 6  | 20.50 | 51.25  | 474     | 46.09  | 7.E+08 | 85  | 4.E+07 |
| B2UP85        | trjB2UP85 B2UP85_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2046 PE=4 SV=1   | Amuc_2046 | 4  | 4  | 27.70 | 22.81  | 206     | 27.75  | 5.E+08 | 93  | 4.E+07 |
| B2UNN9        | trjB2UNN9 B2UNN9_AKKM8 Peptidase T OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pepT PE=3 SV=1  | Amuc_1942 | 5  | 5  | 17.70 | 45.12  | 417     | 37.50  | 6.E+08 | 48  | 4.E+07 |
| B2URI3        | sp B2URI3 ISPF_AKKM8 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ispF PE=3 SV=1                                      | Amuc_1243 | 3  | 3  | 21.30 | 17.69  | 169     | 15.18  | 3.E+08 | 15  | 4.E+07 |
| B2UL30        | trjB2UL30 B2UL30_AKKM8 ATP-dependent 6-phosphofructokinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pfkA PE=3 SV=1  | Amuc_1481 | 5  | 5  | 15.90 | 37.95  | 359     | 14.12  | 7.E+08 | 53  | 4.E+07 |
| B2UMH5        | sp B2UMH5 SUCC_AKKM8 Succinate--CoA ligase [ADP-forming] subunit beta OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=sucC PE=3 SV=1   | Amuc_1713 | 6  | 6  | 20.40 | 42.34  | 393     | 102.02 | 1.E+09 | 77  | 4.E+07 |
| B2UMH4        | trjB2UMH4 B2UMH4_AKKM8 Succinate--CoA ligase [ADP-forming] subunit alpha OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=sucD PE=3 SV=1  | Amuc_1712 | 4  | 4  | 18.60 | 30.57  | 295     | 20.75  | 5.E+08 | 39  | 4.E+07 |
| B2UP52        | trjB2UP52 B2UP52_AKKM8 O-acetylhomoserine/O-acetylserine sulfhydrylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2013 PE=3 SV=1                                     | Amuc_2013 | 3  | 3  | 8.40  | 46.41  | 428     | 32.68  | 7.E+08 | 51  | 4.E+07 |
| B2UQI4        | trjB2UQI4 B2UQI4_AKKM8 Transketolase central region OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0886 PE=4 SV=1  | Amuc_0886 | 7  | 7  | 30.90 | 35.59  | 324     | 53.97  | 6.E+08 | 81  | 4.E+07 |
| B2UQG5        | trjB2UQG5 B2UQG5_AKKM8 Peptidase M42 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0867 PE=3 SV=1  | Amuc_0867 | 5  | 5  | 19.10 | 41.20  | 382     | 37.51  | 7.E+08 | 38  | 3.E+07 |
| B2UNI3        | trjB2UNI3 B2UNI3_AKKM8 AIR synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0457 PE=3 SV=1  | Amuc_0457 | 5  | 5  | 20.10 | 36.49  | 333     | 66.15  | 6.E+08 | 55  | 3.E+07 |
| B2UN30;B2UQW1 | trjB2UN30 B2UN30_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1823 PE=4 SV=1; trjB2UQW1 B2UQW1_AKKM8 Uncharacterized protein OS=Akkerman | Amuc_1823 | 6  | 6  | 15.40 | 61.69  | 545;546 | 132.90 | 9.E+08 | 75  | 3.E+07 |
| B2UQC2        | trjB2UQC2 B2UQC2_AKKM8 Lactase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0824 PE=3 SV=1   | Amuc_0824 | 20 | 20 | 18.00 | 142.05 | 1264    | 124.73 | 2.E+09 | 273 | 3.E+07 |
| B2UNT6        | trjB2UNT6 B2UNT6_AKKM8 Transcriptional regulator, DeoR family OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0468 PE=4 SV=1  | Amuc_0468 | 3  | 3  | 14.10 | 27.12  | 249     | 15.20  | 4.E+08 | 30  | 3.E+07 |
| B2UQG3        | trjB2UQG3 B2UQG3_AKKM8 Rubrerythrin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0865 PE=4 SV=1  | Amuc_0865 | 4  | 4  | 29.70 | 19.53  | 182     | 35.11  | 3.E+08 | 31  | 3.E+07 |
| B2URJ1        | trjB2URJ1 B2URJ1_AKKM8 Carbamoyl-phosphate synthase large chain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=carB PE=3 SV=1   | Amuc_1251 | 16 | 16 | 21.00 | 117.47 | 1067    | 120.87 | 2.E+09 | 230 | 3.E+07 |

|        |  |           |    |    |       |       |     |       |        |     |        |
|--------|--|-----------|----|----|-------|-------|-----|-------|--------|-----|--------|
| B2UQE2 | trjB2UQE2 B2UQE2_AKKM8 Enolase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=eno PE=3 SV=1   | Amuc_0844 | 6  | 4  | 19.30 | 45.97 | 429 | 25.17 | 5.E+08 | 26  | 3.E+07 |
| B2UP25 | sp B2UP25 RS14_AKKM8 30S ribosomal protein S14 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsN PE=3 SV=1                                | Amuc_0557 | 2  | 2  | 25.80 | 10.28 | 89  | 7.50  | 6.E+07 | 15  | 3.E+07 |
| B2UL21 | sp B2UL21 RL25_AKKM8 50S ribosomal protein L25 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=rplY PE=3 SV=1                                | Amuc_1472 | 2  | 2  | 15.40 | 21.01 | 201 | 14.15 | 2.E+08 | 31  | 3.E+07 |
| B2UN14 | trjB2UN14 B2UN14_AKKM8 Aldo/keto reductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1807 PE=4 SV=1                               | Amuc_1807 | 7  | 7  | 33.40 | 34.57 | 314 | 25.97 | 5.E+08 | 86  | 3.E+07 |
| B2UQC0 | trjB2UQC0 B2UQC0_AKKM8 TatD-related deoxyribonuclease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0822 PE=4 SV=1                    | Amuc_0822 | 4  | 4  | 19.20 | 30.49 | 271 | 25.97 | 5.E+08 | 44  | 3.E+07 |
| B2UQQ6 | trjB2UQQ6 B2UQQ6_AKKM8 dTTP/XTP pyrophosphatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0959 PE=3 SV=1                          | Amuc_0959 | 3  | 3  | 21.00 | 23.54 | 214 | 12.43 | 2.E+08 | 34  | 3.E+07 |
| B2UNA9 | sp B2UNA9 PNP_AKKM8 Polyribonucleotide nucleotidyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=pnp PE=3 SV=1                  | Amuc_0382 | 8  | 8  | 15.80 | 77.48 | 714 | 35.83 | 9.E+08 | 84  | 3.E+07 |
| B2URG3 | trjB2URG3 B2URG3_AKKM8 Orotidine-5-phosphate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1223 PE=4 SV=1               | Amuc_1223 | 4  | 4  | 22.70 | 28.31 | 264 | 47.74 | 4.E+08 | 49  | 3.E+07 |
| B2UN11 | trjB2UN11 B2UN11_AKKM8 Flavodoxin-like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1804 PE=4 SV=1         | Amuc_1804 | 2  | 2  | 14.00 | 19.22 | 178 | 8.61  | 3.E+08 | 16  | 3.E+07 |
| B2URD0 | trjB2URD0 B2URD0_AKKM8 Alcohol dehydrogenase zinc-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1190 PE=4 SV=1 | Amuc_1190 | 6  | 6  | 25.50 | 36.08 | 333 | 43.43 | 5.E+08 | 62  | 3.E+07 |
| B2ULH7 | trjB2ULH7 B2ULH7_AKKM8 Formate C-acetyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1543 PE=3 SV=1                       | Amuc_1543 | 11 | 11 | 20.70 | 85.23 | 755 | 80.99 | 1.E+09 | 158 | 2.E+07 |
| B2ULM1 | trjB2ULM1 B2ULM1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1588 PE=4 SV=1                           | Amuc_1588 | 4  | 4  | 27.80 | 18.54 | 169 | 21.44 | 2.E+08 | 29  | 2.E+07 |
| B2UQI5 | trjB2UQI5 B2UQI5_AKKM8 Dehydrogenase E1 component OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0887 PE=4 SV=1                        | Amuc_0887 | 7  | 7  | 23.70 | 33.92 | 312 | 28.90 | 4.E+08 | 50  | 2.E+07 |
| B2ULE0 | trjB2ULE0 B2ULE0_AKKM8 PA14 domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0084 PE=4 SV=1                    | Amuc_0084 | 3  | 3  | 9.90  | 61.62 | 547 | 47.40 | 7.E+08 | 49  | 2.E+07 |
| B2URI2 | trjB2URI2 B2URI2_AKKM8 Inositol-1-monophosphatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1242 PE=3 SV=1                        | Amuc_1242 | 3  | 3  | 14.20 | 28.52 | 254 | 11.42 | 2.E+08 | 27  | 2.E+07 |
| B2UKU8 | trjB2UKU8 B2UKU8_AKKM8 Histidine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1397 PE=3 SV=1                            | Amuc_1397 | 7  | 7  | 20.50 | 47.05 | 424 | 40.52 | 5.E+08 | 66  | 2.E+07 |
| B2UN97 | sp B2UN97 AROA_AKKM8 3-phosphoshikimate 1-carboxyvinyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCG 64013 / CIP 107961 / Muc) OX=349741 GN=aroA PE=3 SV=1             | Amuc_1894 | 3  | 3  | 11.50 | 46.11 | 435 | 19.31 | 3.E+08 | 17  | 2.E+07 |

|               |  |           |    |    |       |        |           |        |        |     |        |
|---------------|--|-----------|----|----|-------|--------|-----------|--------|--------|-----|--------|
| B2UL94        | tr B2UL94 B2UL94_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0036 PE=4 SV=1  | Amuc_0036 | 26 | 26 | 19.70 | 214.69 | 1957      | 147.05 | 2.E+09 | 211 | 2.E+07 |
| B2UR15        | tr B2UR15 B2UR15_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1074 PE=3 SV=1  | Amuc_1074 | 5  | 5  | 10.10 | 62.82  | 552       | 18.05  | 5.E+08 | 74  | 2.E+07 |
| B2UN71        | tr B2UN71 B2UN71_AKKM8 Glycoside hydrolase family 57 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1868 PE=4 SV=1  | Amuc_1868 | 5  | 5  | 15.70 | 45.10  | 395       | 13.43  | 3.E+08 | 14  | 2.E+07 |
| B2UPB5        | tr B2UPB5 B2UPB5_AKKM8 Polysaccharide export protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2077 PE=4 SV=1  | Amuc_2077 | 4  | 4  | 20.40 | 28.03  | 260       | 35.78  | 3.E+08 | 35  | 2.E+07 |
| B2UM84        | tr B2UM84 B2UM84_AKKM8 Isoleucine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ileS PE=3 SV=1   | Amuc_0189 | 12 | 12 | 16.80 | 102.39 | 909       | 47.91  | 9.E+08 | 189 | 2.E+07 |
| B2UNL2        | tr B2UNL2 B2UNL2_AKKM8 Site-specific DNA-methyltransferase (adenine-specific) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1915 PE=3 SV=1                             | Amuc_1915 | 12 | 12 | 15.00 | 95.77  | 853       | 40.70  | 8.E+08 | 86  | 2.E+07 |
| B2ULS7        | tr B2ULS7 B2ULS7_AKKM8 Transposase IS3/IS911 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0127 PE=4 SV=1   | Amuc_0127 | 3  | 3  | 31.70 | 13.95  | 126       | 16.53  | 1.E+08 | 9   | 2.E+07 |
| B2URJ0        | sp B2URJ0 CARA_AKKM8 Carbamoyl-phosphate synthase small chain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=carA PE=3 SV=1  | Amuc_1250 | 4  | 4  | 17.70 | 40.19  | 372       | 13.16  | 2.E+08 | 34  | 2.E+07 |
| B2UPP9        | tr B2UPP9 B2UPP9_AKKM8 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2118 PE=4 SV=1                   | Amuc_2118 | 3  | 3  | 11.90 | 32.04  | 285       | 14.89  | 2.E+08 | 23  | 2.E+07 |
| B2UL26        | tr B2UL26 B2UL26_AKKM8 4-hydroxythreonine-4-phosphate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1477 PE=4 SV=1                                       | Amuc_1477 | 3  | 3  | 17.30 | 31.16  | 289       | 16.71  | 2.E+08 | 27  | 2.E+07 |
| B2UPT2;B2UQS7 | tr B2UPT2 B2UPT2_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2152 PE=4 SV=1;tr B2UQS7 B2UQS7_AKKM8 YD repeat protein OS=Akkermansia muciniph | Amuc_2152 | 19 | 19 | 14.20 | 208.44 | 1912;1929 | 76.75  | 1.E+09 | 112 | 2.E+07 |
| B2UPC8        | tr B2UPC8 B2UPC8_AKKM8 Thioesterase superfamily protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0568 PE=3 SV=1   | Amuc_0568 | 2  | 2  | 18.90 | 16.61  | 143       | 14.15  | 1.E+08 | 6   | 1.E+07 |
| B2UM07        | tr B2UM07 B2UM07_AKKM8 Carboxyl-terminal protease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1631 PE=3 SV=1   | Amuc_1631 | 8  | 8  | 13.60 | 83.86  | 748       | 47.61  | 4.E+08 | 31  | 1.E+07 |
| B2UP66        | tr B2UP66 B2UP66_AKKM8 Dihydroorotase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pyrC PE=3 SV=1  | Amuc_2027 | 5  | 5  | 16.80 | 36.40  | 333       | 11.33  | 2.E+08 | 14  | 1.E+07 |
| B2UN04        | tr B2UN04 B2UN04_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1797 PE=4 SV=1  | Amuc_1797 | 2  | 2  | 9.70  | 33.10  | 290       | 6.38   | 2.E+08 | 33  | 1.E+07 |
| B2UR35        | tr B2UR35 B2UR35_AKKM8 ROK family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1094 PE=4 SV=1   | Amuc_1094 | 2  | 2  | 8.70  | 35.76  | 332       | 12.46  | 2.E+08 | 34  | 1.E+07 |
| B2UMD2        | tr B2UMD2 B2UMD2_AKKM8 Beta-lactamase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0238 PE=4 SV=1  | Amuc_0238 | 5  | 5  | 13.00 | 52.42  | 468       | 14.04  | 3.E+08 | 43  | 1.E+07 |

|        |   |           |   |   |       |       |     |       |        |    |        |
|--------|---|-----------|---|---|-------|-------|-----|-------|--------|----|--------|
| B2ULD1 | tr B2ULD1 B2ULD1_AKKM8 PfkB domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0075 PE=4 SV=1                                    | Amuc_0075 | 3 | 3 | 11.80 | 39.38 | 355 | 15.84 | 2.E+08 | 7  | 1.E+07 |
| B2UQN1 | tr B2UQN1 B2UQN1_AKKM8 Adenylate kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=adk PE=3 SV=1   | Amuc_0934 | 2 | 2 | 12.00 | 24.69 | 216 | 8.73  | 1.E+08 | 22 | 1.E+07 |
| B2URF3 | tr B2URF3 B2URF3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1213 PE=4 SV=1                                | Amuc_1213 | 2 | 2 | 19.70 | 16.13 | 147 | 5.45  | 7.E+07 | 2  | 9.E+06 |
| B2UL75 | sp B2UL75 G1091_AKKM8 Glycosyl hydrolase family 109 protein 1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0017 PE=3 SV=1                 | Amuc_0017 | 4 | 4 | 11.40 | 53.80 | 481 | 43.96 | 2.E+08 | 14 | 9.E+06 |
| B2UQ57 | tr B2UQ57 B2UQ57_AKKM8 ADP-L-glycero-D-manno-heptose-6-epimerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=hldD PE=3 SV=1                   | Amuc_0756 | 4 | 4 | 16.20 | 36.86 | 328 | 14.77 | 2.E+08 | 13 | 9.E+06 |
| B2UNI9 | tr B2UNI9 B2UNI9_AKKM8 Phosphopantothenoylcysteine decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0463 PE=4 SV=1              | Amuc_0463 | 2 | 2 | 14.00 | 19.18 | 179 | 7.73  | 6.E+07 | 13 | 9.E+06 |
| B2ULS2 | tr B2ULS2 B2ULS2_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0121 PE=3 SV=1  | Amuc_0121 | 6 | 6 | 16.20 | 57.46 | 526 | 22.83 | 3.E+08 | 36 | 9.E+06 |
| B2UN08 | tr B2UN08 B2UN08_AKKM8 Peptidase S15 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1801 PE=4 SV=1  | Amuc_1801 | 5 | 5 | 20.10 | 39.75 | 359 | 23.41 | 2.E+08 | 18 | 9.E+06 |
| B2UN18 | tr B2UN18 B2UN18_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1811 PE=4 SV=1                                | Amuc_1811 | 3 | 3 | 22.00 | 17.22 | 150 | 9.25  | 8.E+07 | 15 | 9.E+06 |
| B2UKV7 | tr B2UKV7 B2UKV7_AKKM8 10 kDa chaperonin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=groS PE=3 SV=1   | Amuc_1407 | 2 | 2 | 29.20 | 10.31 | 96  | 7.25  | 4.E+07 | 3  | 8.E+06 |
| B2UQQ5 | tr B2UQQ5 B2UQQ5_AKKM8 Exodeoxyribonuclease III OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0958 PE=3 SV=1                               | Amuc_0958 | 2 | 2 | 7.10  | 28.58 | 253 | 6.92  | 1.E+08 | 18 | 8.E+06 |
| B2UKW1 | tr B2UKW1 B2UKW1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1411 PE=4 SV=1                                | Amuc_1411 | 2 | 2 | 16.10 | 21.91 | 224 | 5.25  | 4.E+07 | 2  | 7.E+06 |
| B2UMT3 | sp B2UMT3 RS3_AKKM8 30S ribosomal protein S3 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpsC PE=3 SV=1                                       | Amuc_0297 | 3 | 3 | 18.80 | 25.87 | 229 | 19.13 | 1.E+08 | 29 | 7.E+06 |
| B2UNL1 | tr B2UNL1 B2UNL1_AKKM8 Restriction modification system DNA specificity domain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1914 PE=4 SV=1 | Amuc_1914 | 2 | 2 | 9.80  | 43.90 | 386 | 11.72 | 1.E+08 | 12 | 6.E+06 |
| B2URC9 | sp B2URC9 RL28_AKKM8 50S ribosomal protein L28 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpmB PE=3 SV=1                                     | Amuc_1189 | 2 | 2 | 23.00 | 9.85  | 87  | 4.41  | 2.E+07 | 3  | 6.E+06 |
| B2UKX6 | tr B2UKX6 B2UKX6_AKKM8 Histidinol-phosphatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1427 PE=3 SV=1                                 | Amuc_1427 | 2 | 2 | 6.30  | 30.87 | 269 | 2.45  | 7.E+07 | 2  | 5.E+06 |
| B2UQK6 | tr B2UQK6 B2UQK6_AKKM8 3-phosphate/5-hydroxy nucleic acid ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0909 PE=3 SV=1              | Amuc_0909 | 4 | 4 | 13.70 | 41.25 | 371 | 8.23  | 1.E+08 | 10 | 5.E+06 |
| B2UNM5 | tr B2UNM5 B2UNM5_AKKM8 Periplasmic binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1928 PE=4 SV=1                            | Amuc_1928 | 3 | 3 | 14.00 | 32.90 | 307 | 6.88  | 1.E+08 | 22 | 5.E+06 |

|        |   |           |   |   |       |        |      |       |        |    |        |
|--------|---|-----------|---|---|-------|--------|------|-------|--------|----|--------|
| B2URM0 | trjB2URM0 B2URM0_AKKM8 Aminopeptidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1280 PE=4 SV=1  | Amuc_1280 | 2 | 2 | 8.40  | 40.49  | 369  | 7.98  | 9.E+07 | 5  | 5.E+06 |
| B2UQ85 | trjB2UQ85 B2UQ85_AKKM8 FAD dependent oxidoreductase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0786 PE=4 SV=1  | Amuc_0786 | 2 | 2 | 10.10 | 38.46  | 346  | 6.14  | 9.E+07 | 17 | 5.E+06 |
| B2UPK9 | trjB2UPK9 B2UPK9_AKKM8 Transcriptional regulator MraZ OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=mraZ PE=3 SV=1   | Amuc_0649 | 3 | 3 | 24.50 | 17.05  | 151  | 5.24  | 5.E+07 | 9  | 5.E+06 |
| B2UPI5 | trjB2UPI5 B2UPI5_AKKM8 Exo-alpha-sialidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0625 PE=4 SV=1   | Amuc_0625 | 2 | 2 | 5.70  | 45.59  | 419  | 3.33  | 1.E+08 | 6  | 5.E+06 |
| B2UQH0 | trjB2UQH0 B2UQH0_AKKM8 Acetylmornithine and succinylornithine aminotransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0872 PE=3 SV=1                   | Amuc_0872 | 4 | 4 | 12.20 | 45.36  | 418  | 12.23 | 1.E+08 | 23 | 5.E+06 |
| B2URI8 | trjB2URI8 B2URI8_AKKM8 GDP-L-fucose synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fcl PE=3 SV=1   | Amuc_1248 | 3 | 3 | 13.50 | 40.65  | 362  | 10.52 | 7.E+07 | 12 | 4.E+06 |
| B2URJ3 | trjB2URJ3 B2URJ3_AKKM8 Glutamate synthase (Ferredoxin) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1253 PE=3 SV=1   | Amuc_1253 | 6 | 6 | 5.70  | 161.75 | 1479 | 44.35 | 2.E+08 | 17 | 4.E+06 |
| B2URE6 | trjB2URE6 B2URE6_AKKM8 Bifunctional purine biosynthesis protein PurH OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=purH PE=3 SV=1                                  | Amuc_1206 | 2 | 2 | 4.50  | 56.36  | 515  | 5.65  | 1.E+08 | 16 | 3.E+06 |
| B2UL15 | trjB2UL15 B2UL15_AKKM8 FAD linked oxidase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1466 PE=4 SV=1   | Amuc_1466 | 4 | 4 | 12.90 | 48.88  | 458  | 8.03  | 8.E+07 | 10 | 3.E+06 |
| B2UMH6 | trjB2UMH6 B2UMH6_AKKM8 Histidinol dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1714 PE=3 SV=1  | Amuc_1714 | 2 | 2 | 5.30  | 46.29  | 432  | 8.97  | 6.E+07 | 7  | 3.E+06 |
| B2UKT9 | sp B2UKT9 ISPG_AKKM8 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ispG PE=3 SV=1                | Amuc_1388 | 5 | 5 | 13.20 | 64.49  | 585  | 15.11 | 1.E+08 | 26 | 3.E+06 |
| B2ULH3 | trjB2ULH3 B2ULH3_AKKM8 Homoserine O-acetyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=metXA PE=3 SV=1  | Amuc_1539 | 2 | 2 | 7.50  | 42.86  | 387  | 13.92 | 6.E+07 | 21 | 3.E+06 |
| B2UQU9 | trjB2UQU9 B2UQU9_AKKM8 Glycoside hydrolase family 31 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1008 PE=3 SV=1   | Amuc_1008 | 4 | 4 | 5.30  | 146.26 | 1311 | 11.39 | 2.E+08 | 15 | 3.E+06 |
| B2UND5 | trjB2UND5 B2UND5_AKKM8 Putative substrate-binding protein of aliphatic sulfonate ABC transporter OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0409 PE=4 SV=1 | Amuc_0409 | 2 | 2 | 8.30  | 38.40  | 348  | 3.16  | 5.E+07 | 13 | 3.E+06 |
| B2UQE7 | sp B2UQE7 MIAB_AKKM8 tRNA-2-methylthio-N(6)-dimethylallyl adenosine synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=miaB PE=3 SV=1                          | Amuc_0849 | 2 | 2 | 6.80  | 51.96  | 458  | 6.71  | 7.E+07 | 16 | 3.E+06 |
| B2ULC6 | trjB2ULC6 B2ULC6_AKKM8 Tryptophan--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=trpS PE=3 SV=1  | Amuc_0070 | 2 | 2 | 10.00 | 35.86  | 321  | 6.09  | 4.E+07 | 3  | 2.E+06 |
| B2UQX2 | trjB2UQX2 B2UQX2_AKKM8 Cysteine--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=cysS PE=3 SV=1  | Amuc_1031 | 3 | 3 | 7.00  | 53.02  | 471  | 8.35  | 5.E+07 | 16 | 2.E+06 |

|        |   |           |   |   |       |        |      |      |        |    |        |
|--------|---|-----------|---|---|-------|--------|------|------|--------|----|--------|
| B2UN50 | tr B2UN50 B2UN50_AKKM8 PDZ/DHR/GLGF domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1844 PE=4 SV=1           | Amuc_1844 | 2 | 2 | 10.00 | 34.08  | 319  | 5.79 | 2.E+07 | 3  | 1.E+06 |
| B2ULN0 | tr B2ULN0 B2ULN0_AKKM8 Polyprenyl synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1597 PE=3 SV=1                 | Amuc_1597 | 2 | 2 | 5.70  | 37.33  | 336  | 2.80 | 2.E+07 | 10 | 1.E+06 |
| B2UQJ6 | tr B2UQJ6 B2UQJ6_AKKM8 DNA topoisomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0898 PE=3 SV=1                     | Amuc_0898 | 4 | 4 | 4.90  | 97.19  | 869  | 7.12 | 5.E+07 | 8  | 9.E+05 |
| B2ULZ9 | sp B2ULZ9 RIMO_AKKM8 Ribosomal protein S12 methyltransferase RimO OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rimO PE=3 SV=1 | Amuc_1623 | 4 | 4 | 10.00 | 50.86  | 452  | 5.59 | 2.E+07 | 5  | 9.E+05 |
| B2UQE3 | sp B2UQE3 END4_AKKM8 Probable endonuclease 4 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=info PE=3 SV=1                      | Amuc_0845 | 3 | 3 | 14.10 | 30.78  | 277  | 4.26 | 1.E+07 | 1  | 8.E+05 |
| B2UN91 | sp B2UN91 SYE_AKKM8 Glutamate--tRNA ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=gltx PE=3 SV=1                        | Amuc_1888 | 2 | 2 | 7.60  | 48.61  | 433  | 6.33 | 2.E+07 | 7  | 8.E+05 |
| B2UNY2 | tr B2UNY2 B2UNY2_AKKM8 Peptidoglycan glycosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0514 PE=4 SV=1     | Amuc_0514 | 2 | 2 | 4.10  | 89.28  | 822  | 7.04 | 3.E+07 | 3  | 7.E+05 |
| B2UR84 | tr B2UR84 B2UR84_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1143 PE=4 SV=1                     | Amuc_1143 | 3 | 3 | 2.40  | 217.62 | 1991 | 2.39 | 6.E+07 | 4  | 7.E+05 |
| B2UKU3 | tr B2UKU3 B2UKU3_AKKM8 Beta-ketoacyl synthase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1392 PE=3 SV=1                | Amuc_1392 | 2 | 2 | 6.40  | 40.31  | 390  | 2.93 | 4.E+06 | 1  | 2.E+05 |
| B2URL5 | tr B2URL5 B2URL5_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1275 PE=4 SV=1               | Amuc_1275 | 2 | 2 | 6.60  | 38.86  | 348  | 3.84 | 2.E+06 | 2  | 1.E+05 |
| B2UL46 | tr B2UL46 B2UL46_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1497 PE=4 SV=1               | Amuc_1497 | 2 | 2 | 6.60  | 38.92  | 349  | 2.63 | 0.E+00 | 2  | 0.E+00 |

**Supplementary Table 3. List of signal peptide-containing proteins identified in secretome of *A. muciniphila* cultivated under basal medium.**

| Majority protein IDs | Fasta headers  | Gene locus | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Score  | Intensity | MS/MS count | iBAQ   | SignalP                  |             | Secretome P (Probability) | PSORTb 3.0 (subcellular localization) |
|----------------------|--|------------|----------|-----------------|-----------------------|-------------------|--------|-----------|-------------|--------|--------------------------|-------------|---------------------------|---------------------------------------|
|                      |  |            |          |                 |                       |                   |        |           |             |        | Signal peptide           | Probability |                           |                                       |
| B2UMR7               | tr B2UMR7 B2UMR7_AKKM8 Histone family protein DNA-binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0281 PE=3 SV=1 | Amuc_0281  | 4        | 4               | 50.50                 | 11.25             | 210.98 | 6.E+10    | 587         | 2.E+10 | -                        | -           | 0.540                     | Cytoplasm                             |
| B2URF0               | tr B2URF0 B2URF0_AKKM8 Phosphoenolpyruvate carboxykinase [GTP] OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pcpG PE=3 SV=1         | Amuc_1210  | 22       | 22              | 48.40                 | 67.52             | 323.31 | 2.E+11    | 2108        | 8.E+09 | -                        | -           | 0.817                     | Cytoplasm                             |
| B2UKV9               | tr B2UKV9 B2UKV9_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1409 PE=4 SV=1       | Amuc_1409  | 8        | 8               | 52.00                 | 16.52             | 245.16 | 4.E+10    | 538         | 5.E+09 | Signal peptide (Sec/SPI) | 0.998       | -                         | Unknown                               |
| B2UL96               | sp B2UL96 GLSA_AKKM8 Glutaminase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=glSA PE=3 SV=1                                       | Amuc_0038  | 7        | 7               | 31.00                 | 33.13             | 186.41 | 3.E+10    | 391         | 3.E+09 | -                        | -           | 0.875                     | Cytoplasm                             |
| B2UKY5               | sp B2UKY5 MDH_AKKM8 Malate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=mdh PE=3 SV=1                                | Amuc_1436  | 13       | 13              | 47.10                 | 35.10             | 323.31 | 4.E+10    | 548         | 2.E+09 | -                        | -           | 0.571                     | Cytoplasm                             |
| B2UQW7               | tr B2UQW7 B2UQW7_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1026 PE=3 SV=1        | Amuc_1026  | 5        | 5               | 47.90                 | 17.92             | 260.88 | 6.E+09    | 192         | 8.E+08 | -                        | -           | 0.888                     | Cytoplasm                             |
| B2UMX5               | tr B2UMX5 B2UMX5_AKKM8 OsmC family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0342 PE=4 SV=1                        | Amuc_0342  | 7        | 7               | 65.20                 | 14.48             | 113.32 | 5.E+09    | 262         | 8.E+08 | -                        | -           | 0.660                     | Unknown                               |
| B2UPJ1               | tr B2UPJ1 B2UPJ1_AKKM8 FAD-binding domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0631 PE=4 SV=1                 | Amuc_0631  | 13       | 13              | 53.50                 | 41.44             | 323.31 | 1.E+10    | 521         | 7.E+08 | -                        | -           | 0.614                     | Cytoplasmic Membrane                  |
| B2UP16               | tr B2UP16 B2UP16_AKKM8 MotA/TolQ/ExbB proton channel OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0548 PE=3 SV=1              | Amuc_0548  | 2        | 2               | 11.80                 | 28.34             | 12.58  | 3.E+09    | 44          | 6.E+08 | Signal peptide (Sec/SPI) | 0.964       | -                         | Cytoplasmic Membrane                  |

|        |  |           |    |    |       |        |        |        |      |        |                                       |       |       |               |
|--------|--|-----------|----|----|-------|--------|--------|--------|------|--------|---------------------------------------|-------|-------|---------------|
| B2UNP3 | tr B2UNP3 B2UNP3_AKKM8 Dihydrodipicolinate synthetase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1946 PE=3 SV=1                       | Amuc_1946 | 6  | 6  | 25.60 | 33.03  | 119.27 | 8.E+09 | 463  | 5.E+08 | -                                     | -     | 0.881 | Cytoplasm     |
| B2UQK1 | tr B2UQK1 B2UQK1_AKKM8 Aconitate hydratase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0904 PE=3 SV=1                                  | Amuc_0904 | 23 | 23 | 38.40 | 99.01  | 323.31 | 2.E+10 | 1077 | 4.E+08 | -                                     | -     | 0.575 | Cytoplasm     |
| B2UKP3 | tr B2UKP3 B2UKP3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1342 PE=4 SV=1                              | Amuc_1342 | 4  | 4  | 17.30 | 34.98  | 90.38  | 5.E+09 | 235  | 3.E+08 | -                                     | -     | 0.743 | Cytoplasm     |
| B2UMM9 | tr B2UMM9 B2UMM9_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1767 PE=4 SV=1                              | Amuc_1767 | 11 | 11 | 47.60 | 32.22  | 317.01 | 4.E+09 | 236  | 2.E+08 | Signal peptide (Sec/SPI)              | 0.982 | -     | Unknown       |
| B2UP96 | tr B2UP96 B2UP96_AKKM8 Thioredoxin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2057 PE=4 SV=1                | Amuc_2057 | 4  | 4  | 29.30 | 18.12  | 48.08  | 2.E+09 | 144  | 2.E+08 | Signal peptide (Sec/SPI)              | 0.936 | 0.934 | Unknown       |
| B2ULU7 | tr B2ULU7 B2ULU7_AKKM8 Thioredoxin domain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0147 PE=4 SV=1                                   | Amuc_0147 | 9  | 9  | 29.60 | 34.97  | 86.17  | 4.E+09 | 274  | 2.E+08 | Signal peptide (Sec/SPI)              | 0.981 | 0.914 | Unknown       |
| B2UPY9 | tr B2UPY9 B2UPY9_AKKM8 Outer membrane autotransporter barrel domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0687 PE=4 SV=1 | Amuc_0687 | 13 | 13 | 27.30 | 107.54 | 323.31 | 8.E+09 | 284  | 2.E+08 | Signal peptide (Sec/SPI)              | 0.996 | 0.950 | OuterMembrane |
| B2ULC0 | tr B2ULC0 B2ULC0_AKKM8 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0064 PE=4 SV=1   | Amuc_0064 | 7  | 7  | 36.00 | 31.33  | 130.07 | 3.E+09 | 226  | 2.E+08 | -                                     | -     | 0.763 | Cytoplasm     |
| B2UQ02 | tr B2UQ02 B2UQ02_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0700 PE=4 SV=1                              | Amuc_0700 | 2  | 2  | 13.70 | 15.12  | 51.76  | 5.E+08 | 26   | 2.E+08 | Lipoprotein signal peptide (Sec/SPII) | 0.999 | 0.934 | Unknown       |
| B2UPA8 | tr B2UPA8 B2UPA8_AKKM8 Catalase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2070 PE=3 SV=1   | Amuc_2070 | 17 | 17 | 29.60 | 84.03  | 146.98 | 4.E+09 | 296  | 1.E+08 | -                                     | -     | 0.842 | Cytoplasm     |



|        |   |           |    |    |       |        |        |        |     |        |                          |       |       |                      |
|--------|---|-----------|----|----|-------|--------|--------|--------|-----|--------|--------------------------|-------|-------|----------------------|
| B2UQP6 | tr B2UQP6 B2UQP6_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0949 PE=3 SV=1 | Amuc_0949 | 2  | 2  | 12.70 | 20.97  | 47.03  | 6.E+08 | 127 | 1.E+08 | Signal peptide (Sec/SPI) | 0.807 | 0.786 | Unknown              |
| B2UP74 | tr B2UP74 B2UP74_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2035 PE=4 SV=1             | Amuc_2035 | 4  | 4  | 22.30 | 27.43  | 116.43 | 1.E+09 | 59  | 9.E+07 | -                        | -     | 0.891 | Periplasmic space    |
| B2UPW3 | tr B2UPW3 B2UPW3_AKKM8 D-alanine-D-alanine ligase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=ddl PE=3 SV=1                | Amuc_0661 | 3  | 3  | 10.30 | 33.30  | 23.44  | 1.E+09 | 89  | 7.E+07 | -                        | -     | 0.515 | Cytoplasm            |
| B2UKP4 | tr B2UKP4 B2UKP4_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1343 PE=4 SV=1             | Amuc_1343 | 2  | 2  | 13.30 | 20.32  | 12.68  | 4.E+08 | 41  | 5.E+07 | Signal peptide (Sec/SPI) | 0.946 | -     | Cytoplasmic Membrane |
| B2UNZ3 | tr B2UNZ3 B2UNZ3_AKKM8 Cycloartenol synthase-like protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0525 PE=4 SV=1  | Amuc_0525 | 8  | 8  | 30.40 | 43.36  | 42.09  | 1.E+09 | 69  | 5.E+07 | Signal peptide (Sec/SPI) | 0.967 | 0.936 | Unknown              |
| B2UKX4 | tr B2UKX4 B2UKX4_AKKM8 Kelch repeat-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1425 PE=4 SV=1     | Amuc_1425 | 2  | 2  | 9.20  | 35.13  | 29.39  | 7.E+08 | 56  | 5.E+07 | -                        | -     | 0.910 | Unknown              |
| B2UQX4 | tr B2UQX4 B2UQX4_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1033 PE=3 SV=1                           | Amuc_1033 | 9  | 9  | 18.20 | 67.00  | 42.47  | 2.E+09 | 103 | 5.E+07 | Signal peptide (Sec/SPI) | 0.745 | 0.922 | Periplasmic space    |
| B2UPD6 | tr B2UPD6 B2UPD6_AKKM8 Peptidase M16 domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0576 PE=3 SV=1        | Amuc_0576 | 22 | 22 | 16.90 | 160.48 | 199.61 | 4.E+09 | 264 | 5.E+07 | -                        | -     | 0.794 | Unknown              |
| B2UQ36 | tr B2UQ36 B2UQ36_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0735 PE=4 SV=1                   | Amuc_0735 | 23 | 23 | 19.20 | 212.82 | 161.17 | 4.E+09 | 172 | 4.E+07 | -                        | -     | 0.932 | Unknown              |
| B2UQY5 | tr B2UQY5 B2UQY5_AKKM8 50S ribosomal protein L1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpIA PE=3 SV=1                 | Amuc_1044 | 4  | 4  | 26.60 | 24.67  | 41.16  | 5.E+08 | 34  | 4.E+07 | -                        | -     | 0.956 | Cytoplasm            |
| B2UQJ3 | tr B2UQJ3 B2UQJ3_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG   | Amuc_0895 | 3  | 3  | 24.30 | 16.87  | 8.63   | 3.E+08 | 24  | 4.E+07 | Signal peptide (Sec/SPI) | 0.982 | 0.591 | Unknown              |

|        |  |           |    |    |       |        |        |        |     |        |   |       |       |                      |  |
|--------|--|-----------|----|----|-------|--------|--------|--------|-----|--------|---|-------|-------|----------------------|--|
|        | 64013 / CIP 107961 / Muc) OX=349741<br>GN=Amuc_0895 PE=4 SV=1  |           |    |    |       |        |        |        |     |        |   |       |       |                      |  |
| B2UQ11 | tr B2UQ11 B2UQ11_AKKM8<br>Uncharacterized protein OS=Akkermansia<br>muciniphila (strain ATCC BAA-835 / DSM<br>22959 / JCM 33894 / BCRC 81048 / CCUG<br>64013 / CIP 107961 / Muc) OX=349741<br>GN=Amuc_0883 PE=4 SV=1                       | Amuc_0883 | 2  | 2  | 21.00 | 6.74   | 29.80  | 8.E+07 | 4   | 4.E+07 | -   | -     | 0.683 | Unknown              |  |
| B2UMH4 | tr B2UMH4 B2UMH4_AKKM8 Succinate--<br>CoA ligase [ADP-forming] subunit alpha<br>OS=Akkermansia muciniphila (strain ATCC<br>BAA-835 / DSM 22959 / JCM 33894 /<br>BCRC 81048 / CCUG 64013 / CIP 107961 /<br>Muc) OX=349741 GN=sucD PE=3 SV=1 | Amuc_1712 | 4  | 4  | 18.60 | 30.57  | 20.75  | 5.E+08 | 39  | 4.E+07 | -   | -     | 0.805 | Cytoplasm            |  |
| B2UQC2 | tr B2UQC2 B2UQC2_AKKM8 Lactase<br>OS=Akkermansia muciniphila (strain ATCC<br>BAA-835 / DSM 22959 / JCM 33894 /<br>BCRC 81048 / CCUG 64013 / CIP 107961 /<br>Muc) OX=349741 GN=Amuc_0824 PE=3<br>SV=1                                       | Amuc_0824 | 20 | 20 | 18.00 | 142.05 | 124.73 | 2.E+09 | 273 | 3.E+07 | Lipoprotein<br>signal peptide<br>(Sec/SPII) | 0.712 | 0.936 | Periplasmic<br>space |  |
| B2URJ1 | tr B2URJ1 B2URJ1_AKKM8 Carbamoyl-<br>phosphate synthase large chain<br>OS=Akkermansia muciniphila (strain ATCC<br>BAA-835 / DSM 22959 / JCM 33894 /<br>BCRC 81048 / CCUG 64013 / CIP 107961 /<br>Muc) OX=349741 GN=carB PE=3 SV=1          | Amuc_1251 | 16 | 16 | 21.00 | 117.47 | 120.87 | 2.E+09 | 230 | 3.E+07 | Lipoprotein<br>signal peptide<br>(Sec/SPII) | 0.713 | -     | Unknown              |  |
| B2UP25 | sp B2UP25 RS14_AKKM8 30S ribosomal<br>protein S14 OS=Akkermansia muciniphila<br>(strain ATCC BAA-835 / DSM 22959 / JCM<br>33894 / BCRC 81048 / CCUG 64013 / CIP<br>107961 / Muc) OX=349741 GN=rpsN PE=3<br>SV=1                            | Amuc_0557 | 2  | 2  | 25.80 | 10.28  | 7.50   | 6.E+07 | 15  | 3.E+07 | -   | -     | 0.568 | Cytoplasm            |  |
| B2UN14 | tr B2UN14 B2UN14_AKKM8 Aldo/keto<br>reductase OS=Akkermansia muciniphila<br>(strain ATCC BAA-835 / DSM 22959 / JCM<br>33894 / BCRC 81048 / CCUG 64013 / CIP<br>107961 / Muc) OX=349741<br>GN=Amuc_1807 PE=4 SV=1                           | Amuc_1807 | 7  | 7  | 33.40 | 34.57  | 25.97  | 5.E+08 | 86  | 3.E+07 | Signal peptide<br>(Sec/SPI)                 | 0.507 | -     | Cytoplasm            |  |
| B2UN11 | tr B2UN11 B2UN11_AKKM8 Flavodoxin-like<br>domain-containing protein OS=Akkermansia<br>muciniphila (strain ATCC BAA-835 / DSM<br>22959 / JCM 33894 / BCRC 81048 / CCUG<br>64013 / CIP 107961 / Muc) OX=349741<br>GN=Amuc_1804 PE=4 SV=1     | Amuc_1804 | 2  | 2  | 14.00 | 19.22  | 8.61   | 3.E+08 | 16  | 3.E+07 | -   | -     | 0.813 | Unknown              |  |
| B2ULE0 | tr B2ULE0 B2ULE0_AKKM8 PA14 domain-<br>containing protein OS=Akkermansia<br>muciniphila (strain ATCC BAA-835 / DSM<br>22959 / JCM 33894 / BCRC 81048 / CCUG<br>64013 / CIP 107961 / Muc) OX=349741<br>GN=Amuc_0084 PE=4 SV=1               | Amuc_0084 | 3  | 3  | 9.90  | 61.62  | 47.40  | 7.E+08 | 49  | 2.E+07 | -   | -     | 0.771 | Cytoplasm            |  |
| B2UL94 | tr B2UL94 B2UL94_AKKM8 YD repeat<br>protein OS=Akkermansia muciniphila (strain<br>ATCC BAA-835 / DSM 22959 / JCM 33894<br>/ BCRC 81048 / CCUG 64013 / CIP 107961<br>/ Muc) OX=349741 GN=Amuc_0036 PE=4<br>SV=1                             | Amuc_0036 | 26 | 26 | 19.70 | 214.69 | 147.05 | 2.E+09 | 211 | 2.E+07 | -   | -     | 0.937 | Unknown              |  |
| B2UR15 | tr B2UR15 B2UR15_AKKM8 Sulfatase<br>OS=Akkermansia muciniphila (strain ATCC<br>BAA-835 / DSM 22959 / JCM 33894 /<br>BCRC 81048 / CCUG 64013 / CIP 107961 /<br>Muc) OX=349741 GN=Amuc_1074 PE=3<br>SV=1                                     | Amuc_1074 | 5  | 5  | 10.10 | 62.82  | 18.05  | 5.E+08 | 74  | 2.E+07 | Signal peptide<br>(Sec/SPI)                 | 0.982 | 0.930 | Periplasmic<br>space |  |

|               |  |           |    |    |       |        |       |        |     |        |                                       |       |       |                      |
|---------------|--|-----------|----|----|-------|--------|-------|--------|-----|--------|---------------------------------------|-------|-------|----------------------|
| B2UPB5        | tr B2UPB5 B2UPB5_AKKM8 Polysaccharide export protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2077 PE=4 SV=1  | Amuc_2077 | 4  | 4  | 20.40 | 28.03  | 35.78 | 3.E+08 | 35  | 2.E+07 | Lipoprotein signal peptide (Sec/SPII) | 0.960 | 0.726 | Unknown              |
| B2ULS7        | tr B2ULS7 B2ULS7_AKKM8 Transposase IS3/IS911 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0127 PE=4 SV=1   | Amuc_0127 | 3  | 3  | 31.70 | 13.95  | 16.53 | 1.E+08 | 9   | 2.E+07 | -                                     | -     | 0.739 | Unknown              |
| B2UPT2;B2UQS7 | tr B2UPT2 B2UPT2_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2152 PE=4 SV=1;tr B2UQS7 B2UQS7_AKKM8 YD repeat protein OS=Akkermansia muciniph | Amuc_2152 | 19 | 19 | 14.20 | 208.44 | 76.75 | 1.E+09 | 112 | 2.E+07 | -                                     | -     | 0.940 | OuterMembrane        |
| B2UM07        | tr B2UM07 B2UM07_AKKM8 Carboxyl-terminal protease OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1631 PE=3 SV=1   | Amuc_1631 | 8  | 8  | 13.60 | 83.86  | 47.61 | 4.E+08 | 31  | 1.E+07 | Lipoprotein signal peptide (Sec/SPII) | 0.524 | -     | Cytoplasmic Membrane |
| B2UP66        | tr B2UP66 B2UP66_AKKM8 Dihydroorotase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=pyrC PE=3 SV=1  | Amuc_2027 | 5  | 5  | 16.80 | 36.40  | 11.33 | 2.E+08 | 14  | 1.E+07 | TAT signal peptide (Tat/SPI)          | 0.811 | -     | Cytoplasm            |
| B2URF3        | tr B2URF3 B2URF3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1213 PE=4 SV=1  | Amuc_1213 | 2  | 2  | 19.70 | 16.13  | 5.45  | 7.E+07 | 2   | 9.E+06 | Signal peptide (Sec/SPI)              | 0.989 | -     | Unknown              |
| B2UL75        | sp B2UL75 G1091_AKKM8 Glycosyl hydrolase family 109 protein 1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0017 PE=3 SV=1   | Amuc_0017 | 4  | 4  | 11.40 | 53.80  | 43.96 | 2.E+08 | 14  | 9.E+06 | TAT signal peptide (Tat/SPI)          | 0.999 | -     | Unknown              |
| B2UNI9        | tr B2UNI9 B2UNI9_AKKM8 Phosphopantothenoylcysteine decarboxylase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0463 PE=4 SV=1  | Amuc_0463 | 2  | 2  | 14.00 | 19.18  | 7.73  | 6.E+07 | 13  | 9.E+06 | Signal peptide (Sec/SPI)              | 0.530 | -     | Cytoplasm            |
| B2ULS2        | tr B2ULS2 B2ULS2_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0121 PE=3 SV=1  | Amuc_0121 | 6  | 6  | 16.20 | 57.46  | 22.83 | 3.E+08 | 36  | 9.E+06 | Lipoprotein signal peptide (Sec/SPII) | 0.765 | 0.779 | Unknown              |
| B2UN08        | tr B2UN08 B2UN08_AKKM8 Peptidase S15 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1801 PE=4 SV=1  | Amuc_1801 | 5  | 5  | 20.10 | 39.75  | 23.41 | 2.E+08 | 18  | 9.E+06 | Signal peptide (Sec/SPI)              | 0.810 | 0.609 | Unknown              |

|        |   |           |   |   |       |        |       |        |    |        |                                       |       |       |                      |
|--------|---|-----------|---|---|-------|--------|-------|--------|----|--------|---------------------------------------|-------|-------|----------------------|
| B2UKW1 | tr B2UKW1 B2UKW1_AKKM8<br>Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1411 PE=4 SV=1  | Amuc_1411 | 2 | 2 | 16.10 | 21.91  | 5.25  | 4.E+07 | 2  | 7.E+06 | Signal peptide (Sec/SPI)              | 0.964 | 0.950 | Unknown              |
| B2URC9 | sp B2URC9 RL28_AKKM8 50S ribosomal protein L28 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpMB PE=3 SV=1  | Amuc_1189 | 2 | 2 | 23.00 | 9.85   | 4.41  | 2.E+07 | 3  | 6.E+06 | -                                     | -     | 0.549 | Unknown              |
| B2UNM5 | tr B2UNM5 B2UNM5_AKKM8 Periplasmic binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1928 PE=4 SV=1   | Amuc_1928 | 3 | 3 | 14.00 | 32.90  | 6.88  | 1.E+08 | 22 | 5.E+06 | Signal peptide (Sec/SPI)              | 0.996 | -     | Unknown              |
| B2UPI5 | tr B2UPI5 B2UPI5_AKKM8 Exo-alpha-sialidase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0625 PE=4 SV=1   | Amuc_0625 | 2 | 2 | 5.70  | 45.59  | 3.33  | 1.E+08 | 6  | 5.E+06 | Signal peptide (Sec/SPI)              | 0.917 | 0.945 | Periplasmic space    |
| B2UQU9 | tr B2UQU9 B2UQU9_AKKM8 Glycoside hydrolase family 31 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1008 PE=3 SV=1   | Amuc_1008 | 4 | 4 | 5.30  | 146.26 | 11.39 | 2.E+08 | 15 | 3.E+06 | Signal peptide (Sec/SPI)              | 0.856 | 0.860 | Unknown              |
| B2UND5 | tr B2UND5 B2UND5_AKKM8 Putative substrate-binding protein of aliphatic sulfonate ABC transporter OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0409 PE=4 SV=1 | Amuc_0409 | 2 | 2 | 8.30  | 38.40  | 3.16  | 5.E+07 | 13 | 3.E+06 | Lipoprotein signal peptide (Sec/SPII) | 0.997 | -     | Cytoplasm            |
| B2UN50 | tr B2UN50 B2UN50_AKKM8 PDZ/DHR/GLGF domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1844 PE=4 SV=1   | Amuc_1844 | 2 | 2 | 10.00 | 34.08  | 5.79  | 2.E+07 | 3  | 1.E+06 | Lipoprotein signal peptide (Sec/SPII) | 0.632 | 0.951 | Unknown              |
| B2UNY2 | tr B2UNY2 B2UNY2_AKKM8 Peptidoglycan glycosyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0514 PE=4 SV=1   | Amuc_0514 | 2 | 2 | 4.10  | 89.28  | 7.04  | 3.E+07 | 3  | 7.E+05 | Signal peptide (Sec/SPI)              | 0.861 | 0.823 | Cytoplasmic Membrane |
| B2UR84 | tr B2UR84 B2UR84_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1143 PE=4 SV=1   | Amuc_1143 | 3 | 3 | 2.40  | 217.62 | 2.39  | 6.E+07 | 4  | 7.E+05 | -                                     | -     | 0.943 | Unknown              |
| B2URL5 | tr B2URL5 B2URL5_AKKM8<br>Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1275 PE=4 SV=1  | Amuc_1275 | 2 | 2 | 6.60  | 38.86  | 3.84  | 2.E+06 | 2  | 1.E+05 | Signal peptide (Sec/SPI)              | 0.786 | -     | Unknown              |

**Supplementary Table 4. List of putative extracellular proteins secreted from *A. muciniphila* cultivated under basal medium.**

| Majority protein IDs | Fasta headers   | Gene locus | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Score  | Intensity | MS/MS count | iBAQ   | SignalP                               |             | Secretome P (Probability) | PSORTb 3.0 (subcellular localization) |
|----------------------|---|------------|----------|-----------------|-----------------------|-------------------|--------|-----------|-------------|--------|---------------------------------------|-------------|---------------------------|---------------------------------------|
|                      |   |            |          |                 |                       |                   |        |           |             |        | Signal peptide                        | Probability |                           |                                       |
| B2UKV9               | tr[B2UKV9]B2UKV9_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1409 PE=4 SV=1  | Amuc_1409  | 8        | 8               | 52.00                 | 16.52             | 245.16 | 4.E+10    | 538         | 5.E+09 | Signal peptide (Sec/SPI)              | 0.998       | -                         | Unknown                               |
| B2UMX5               | tr[B2UMX5]B2UMX5_AKKM8 OsmC family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0342 PE=4 SV=1                   | Amuc_0342  | 7        | 7               | 65.20                 | 14.48             | 113.32 | 5.E+09    | 262         | 8.E+08 | -                                     | -           | 0.660                     | Unknown                               |
| B2UMM9               | tr[B2UMM9]B2UMM9_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1767 PE=4 SV=1               | Amuc_1767  | 11       | 11              | 47.60                 | 32.22             | 317.01 | 4.E+09    | 236         | 2.E+08 | Signal peptide (Sec/SPI)              | 0.982       | -                         | Unknown                               |
| B2UP96               | tr[B2UP96]B2UP96_AKKM8 Thioredoxin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2057 PE=4 SV=1 | Amuc_2057  | 4        | 4               | 29.30                 | 18.12             | 48.08  | 2.E+09    | 144         | 2.E+08 | Signal peptide (Sec/SPI)              | 0.936       | 0.934                     | Unknown                               |
| B2ULU7               | tr[B2ULU7]B2ULU7_AKKM8 Thioredoxin domain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0147 PE=4 SV=1                    | Amuc_0147  | 9        | 9               | 29.60                 | 34.97             | 86.17  | 4.E+09    | 274         | 2.E+08 | Signal peptide (Sec/SPI)              | 0.981       | 0.914                     | Unknown                               |
| B2UQ02               | tr[B2UQ02]B2UQ02_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0700 PE=4 SV=1               | Amuc_0700  | 2        | 2               | 13.70                 | 15.12             | 51.76  | 5.E+08    | 26          | 2.E+08 | Lipoprotein signal peptide (Sec/SPII) | 0.999       | 0.934                     | Unknown                               |
| B2UQP6               | tr[B2UQP6]B2UQP6_AKKM8 Peptidyl-prolyl cis-trans isomerase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0949 PE=3 SV=1   | Amuc_0949  | 2        | 2               | 12.70                 | 20.97             | 47.03  | 6.E+08    | 127         | 1.E+08 | Signal peptide (Sec/SPI)              | 0.807       | 0.786                     | Unknown                               |
| B2UNZ3               | tr[B2UNZ3]B2UNZ3_AKKM8 Cycloartenol synthase-like protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0525 PE=4 SV=1    | Amuc_0525  | 8        | 8               | 30.40                 | 43.36             | 42.09  | 1.E+09    | 69          | 5.E+07 | Signal peptide (Sec/SPI)              | 0.967       | 0.936                     | Unknown                               |
| B2UKX4               | tr[B2UKX4]B2UKX4_AKKM8 Kelch repeat-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1425 PE=4 SV=1       | Amuc_1425  | 2        | 2               | 9.20                  | 35.13             | 29.39  | 7.E+08    | 56          | 5.E+07 | -                                     | -           | 0.910                     | Unknown                               |
| B2UPD6               | tr[B2UPD6]B2UPD6_AKKM8 Peptidase M16 domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0576 PE=3 SV=1          | Amuc_0576  | 22       | 22              | 16.90                 | 160.48            | 199.61 | 4.E+09    | 264         | 5.E+07 | -                                     | -           | 0.794                     | Unknown                               |
| B2UQ36               | tr[B2UQ36]B2UQ36_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0735 PE=4 SV=1                     | Amuc_0735  | 23       | 23              | 19.20                 | 212.82            | 161.17 | 4.E+09    | 172         | 4.E+07 | -                                     | -           | 0.932                     | Unknown                               |

|        |   |           |    |    |       |        |        |        |     |        |                                       |       |       |         |
|--------|---|-----------|----|----|-------|--------|--------|--------|-----|--------|---------------------------------------|-------|-------|---------|
| B2UQJ3 | trjB2UQJ3 B2UQJ3_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0895 PE=4 SV=1      | Amuc_0895 | 3  | 3  | 24.30 | 16.87  | 8.63   | 3.E+08 | 24  | 4.E+07 | Signal peptide (Sec/SPI)              | 0.982 | 0.591 | Unknown |
| B2UQI1 | trjB2UQI1 B2UQI1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0883 PE=4 SV=1                   | Amuc_0883 | 2  | 2  | 21.00 | 6.74   | 29.80  | 8.E+07 | 4   | 4.E+07 | -                                     | -     | 0.683 | Unknown |
| B2URJ1 | trjB2URJ1 B2URJ1_AKKM8 Carbamoyl-phosphate synthase large chain OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=carB PE=3 SV=1       | Amuc_1251 | 16 | 16 | 21.00 | 117.47 | 120.87 | 2.E+09 | 230 | 3.E+07 | Lipoprotein signal peptide (Sec/SPII) | 0.713 | -     | Unknown |
| B2UN11 | trjB2UN11 B2UN11_AKKM8 Flavodoxin-like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1804 PE=4 SV=1 | Amuc_1804 | 2  | 2  | 14.00 | 19.22  | 8.61   | 3.E+08 | 16  | 3.E+07 | -                                     | -     | 0.813 | Unknown |
| B2UL94 | trjB2UL94 B2UL94_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0036 PE=4 SV=1                         | Amuc_0036 | 26 | 26 | 19.70 | 214.69 | 147.05 | 2.E+09 | 211 | 2.E+07 | -                                     | -     | 0.937 | Unknown |
| B2UPB5 | trjB2UPB5 B2UPB5_AKKM8 Polysaccharide export protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2077 PE=4 SV=1             | Amuc_2077 | 4  | 4  | 20.40 | 28.03  | 35.78  | 3.E+08 | 35  | 2.E+07 | Lipoprotein signal peptide (Sec/SPII) | 0.960 | 0.726 | Unknown |
| B2ULS7 | trjB2ULS7 B2ULS7_AKKM8 Transposase IS3/IS911 family protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0127 PE=4 SV=1      | Amuc_0127 | 3  | 3  | 31.70 | 13.95  | 16.53  | 1.E+08 | 9   | 2.E+07 | -                                     | -     | 0.739 | Unknown |
| B2URF3 | trjB2URF3 B2URF3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1213 PE=4 SV=1                   | Amuc_1213 | 2  | 2  | 19.70 | 16.13  | 5.45   | 7.E+07 | 2   | 9.E+06 | Signal peptide (Sec/SPI)              | 0.989 | -     | Unknown |
| B2UL75 | spjB2UL75 G1091_AKKM8 Glycosyl hydrolase family 109 protein 1 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0017 PE=3 SV=1    | Amuc_0017 | 4  | 4  | 11.40 | 53.80  | 43.96  | 2.E+08 | 14  | 9.E+06 | TAT signal peptide (Tat/SPI)          | 0.999 | -     | Unknown |
| B2ULS2 | trjB2ULS2 B2ULS2_AKKM8 Sulfatase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0121 PE=3 SV=1                                 | Amuc_0121 | 6  | 6  | 16.20 | 57.46  | 22.83  | 3.E+08 | 36  | 9.E+06 | Lipoprotein signal peptide (Sec/SPII) | 0.765 | 0.779 | Unknown |
| B2UN08 | trjB2UN08 B2UN08_AKKM8 Peptidase S15 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1801 PE=4 SV=1                             | Amuc_1801 | 5  | 5  | 20.10 | 39.75  | 23.41  | 2.E+08 | 18  | 9.E+06 | Signal peptide (Sec/SPI)              | 0.810 | 0.609 | Unknown |
| B2UKW1 | trjB2UKW1 B2UKW1_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1411 PE=4 SV=1                   | Amuc_1411 | 2  | 2  | 16.10 | 21.91  | 5.25   | 4.E+07 | 2   | 7.E+06 | Signal peptide (Sec/SPI)              | 0.964 | 0.950 | Unknown |

|        |  |           |   |   |       |        |       |        |    |        |                                      |       |       |         |
|--------|--|-----------|---|---|-------|--------|-------|--------|----|--------|--------------------------------------|-------|-------|---------|
| B2URC9 | sp B2URC9 RL28_AKKM8 50S ribosomal protein L28 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpmb PE=3 SV=1             | Amuc_1189 | 2 | 2 | 23.00 | 9.85   | 4.41  | 2.E+07 | 3  | 6.E+06 | -                                    | -     | 0.549 | Unknown |
| B2UNM5 | trj B2UNM5 B2UNM5_AKKM8 Periplasmic binding protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1928 PE=4 SV=1   | Amuc_1928 | 3 | 3 | 14.00 | 32.90  | 6.88  | 1.E+08 | 22 | 5.E+06 | Signal peptide (Sec/SPI)             | 0.996 | -     | Unknown |
| B2UQU9 | trj B2UQU9 B2UQU9_AKKM8 Glycoside hydrolase family 31 OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1008 PE=3 SV=1 | Amuc_1008 | 4 | 4 | 5.30  | 146.26 | 11.39 | 2.E+08 | 15 | 3.E+06 | Signal peptide (Sec/SPI)             | 0.856 | 0.860 | Unknown |
| B2UN50 | trj B2UN50 B2UN50_AKKM8 PDZ/DHR/GLGF domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1844 PE=4 SV=1   | Amuc_1844 | 2 | 2 | 10.00 | 34.08  | 5.79  | 2.E+07 | 3  | 1.E+06 | Lipoprotein signal peptide (Sec/SPI) | 0.632 | 0.951 | Unknown |
| B2UR84 | trj B2UR84 B2UR84_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1143 PE=4 SV=1             | Amuc_1143 | 3 | 3 | 2.40  | 217.62 | 2.39  | 6.E+07 | 4  | 7.E+05 | -                                    | -     | 0.943 | Unknown |
| B2URL5 | trj B2URL5 B2URL5_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1275 PE=4 SV=1       | Amuc_1275 | 2 | 2 | 6.60  | 38.86  | 3.84  | 2.E+06 | 2  | 1.E+05 | Signal peptide (Sec/SPI)             | 0.786 | -     | Unknown |

**Supplementary Table 5. List of proteins identified in secretome of *A. muciniphila* cultivated under BHI medium.**

| Majority protein IDs | Fasta headers  | Gene locus | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Sequence lengths | Score  | Intensity | MS/MS count | iBAQ   |
|----------------------|--|------------|----------|-----------------|-----------------------|-------------------|------------------|--------|-----------|-------------|--------|
| B2UKV9               | trjB2UKV9 B2UKV9_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1409 PE=4 SV=1             | Amuc_1409  | 5        | 5               | 32.7                  | 16.523            | 150              | 122.63 | 3.E+08    | 70          | 5.E+07 |
| B2UP96               | trjB2UP96 B2UP96_AKKM8 Thioredoxin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2057 PE=4 SV=1            | Amuc_2057  | 3        | 3               | 22.8                  | 18.123            | 167              | 53.52  | 2.E+08    | 62          | 3.E+07 |
| B2UKW7               | trjB2UKW7 B2UKW7_AKKM8 Glyceraldehyde-3-phosphate dehydrogenase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1417 PE=3 SV=1         | Amuc_1417  | 6        | 6               | 30.5                  | 36.743            | 341              | 208.11 | 4.E+08    | 56          | 2.E+07 |
| B2UQS2               | spjB2UQS2 ACP_AKKM8 Acyl carrier protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=acpP PE=3 SV=1                                     | Amuc_0975  | 2        | 2               | 32.5                  | 8.8206            | 80               | 138.88 | 2.E+08    | 53          | 8.E+07 |
| B2URH0               | trjB2URH0 B2URH0_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1230 PE=4 SV=1                          | Amuc_1883  | 1        | 1               | 3.3                   | 30.038            | 271              | 4.4739 | 3.E+08    | 40          | 3.E+07 |
| B2UPZ3               | trjB2UPZ3 B2UPZ3_AKKM8 Thioredoxin OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0691 PE=3 SV=1                                      | Amuc_0691  | 3        | 3               | 38.1                  | 11.49             | 105              | 225.24 | 7.E+08    | 22          | 1.E+08 |
| B2UMF9               | spjB2UMF9 PLSX_AKKM8 Phosphate acyltransferase OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=plsx PE=3 SV=1                               | Amuc_0265  | 1        | 1               | 4.3                   | 37.054            | 349              | 20.287 | 3.E+08    | 18          | 2.E+07 |
| B2URF3               | trjB2URF3 B2URF3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1213 PE=4 SV=1                          | Amuc_1213  | 1        | 1               | 5.4                   | 16.131            | 147              | 38.257 | 6.E+07    | 18          | 9.E+06 |
| B2UR84               | trjB2UR84 B2UR84_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1143 PE=4 SV=1                                | Amuc_1143  | 2        | 2               | 1                     | 217.62            | 1991             | 8.7575 | 4.E+07    | 17          | 5.E+05 |
| B2ULB8               | trjB2ULB8 B2ULB8_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0062 PE=4 SV=1                          | Amuc_0062  | 1        | 1               | 3.4                   | 26.955            | 235              | 4.9961 | 8.E+07    | 15          | 6.E+06 |
| B2UMU2               | trjB2UMU2 B2UMU2_AKKM8 Elongation factor G OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=fusA PE=3 SV=1                                   | Amuc_0306  | 1        | 1               | 3.8                   | 78.782            | 715              | 85.686 | 7.E+07    | 8           | 2.E+06 |
| B2UN03               | trjB2UN03 B2UN03_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0370 PE=4 SV=1                          | Amuc_0370  | 1        | 1               | 5.1                   | 20.257            | 176              | 3.5135 | 3.E+07    | 7           | 3.E+06 |
| B2UKP3               | trjB2UKP3 B2UKP3_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1342 PE=4 SV=1                          | Amuc_1342  | 1        | 1               | 5.4                   | 34.981            | 312              | 9.6821 | 4.E+07    | 5           | 3.E+06 |
| B2UPI3               | trjB2UPI3 B2UPI3_AKKM8 Glycosyl hydrolase BNR repeat-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0623 PE=4 SV=1 | Amuc_0623  | 1        | 1               | 2.1                   | 48.372            | 436              | 3.2438 | 3.E+07    | 5           | 2.E+06 |
| B2UQY2               | trjB2UQY2 B2UQY2_AKKM8 DNA-directed RNA polymerase subunit beta OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=rpoB PE=3 SV=1              | Amuc_1041  | 1        | 1               | 1.8                   | 146.23            | 1312             | 323.31 | 6.E+07    | 5           | 9.E+05 |
| B2ULW5               | trjB2ULW5 B2ULW5_AKKM8 Twitching motility protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0165 PE=3 SV=1                       | Amuc_0165  | 1        | 1               | 8.1                   | 40.417            | 360              | 163.34 | 4.E+07    | 3           | 2.E+06 |
| B2UM02               | trjB2UM02 B2UM02_AKKM8 RNA polymerase sigma factor SigA OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=sigA PE=3 SV=1                      | Amuc_1626  | 2        | 2               | 2.6                   | 78.262            | 688              | 3.328  | 3.E+07    | 3           | 1.E+06 |
| B2UN86               | trjB2UN86 B2UN86_AKKM8 Beta-lactamase domain protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1883 PE=4 SV=1                    | Amuc_1883  | 1        | 1               | 4.2                   | 50.21             | 456              | 3.422  | 7.E+08    | 2           | 4.E+07 |



|        |  |           |   |   |      |        |         |        |        |   |        |
|--------|--|-----------|---|---|------|--------|---------|--------|--------|---|--------|
| B2UN30 | trjB2UN30 B2UN30_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1823 PE=4 SV=1;trjB2UQW1 B2UQW1_AKKM8 Uncharacterized protein OS=Akkerman | Amuc_1823 | 1 | 1 | 3.7  | 61.69  | 545;546 | 40.295 | 9.E+06 | 2 | 3.E+05 |
| B2UL03 | trjB2UL03 B2UL03_AKKM8 Uncharacterized protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1454 PE=4 SV=1  | Amuc_1454 | 1 | 1 | 21.5 | 20.058 | 195     | 223.29 | 4.E+07 | 1 | 4.E+06 |
| B2UMN9 | trjB2UMN9 B2UMN9_AKKM8 von Willebrand factor type A OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1777 PE=4 SV=1   | Amuc_1777 | 1 | 1 | 2.1  | 85.513 | 754     | 3.3214 | 3.E+07 | 1 | 1.E+06 |
| B2ULW6 | trjB2ULW6 B2ULW6_AKKM8 Twitching motility protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_0166 PE=3 SV=1   | Amuc_0166 | 1 | 1 | 8    | 39.925 | 364     | 46.086 | 1.E+07 | 1 | 7.E+05 |

**Supplementary Table 6. List of putative extracellular proteins secreted from *A. muciniphila* cultivated under BHI medium.**

| Majority protein IDs | Fasta headers   | Gene locus | Peptides | Unique peptides | Sequence coverage [%] | Mol. weight [kDa] | Sequence lengths | Score  | Intensity | MS/MS count | iBAQ   | SignalP                  |             | Secretome P (Probability) | PSORTb 3.0 (subcellular localization) |
|----------------------|---|------------|----------|-----------------|-----------------------|-------------------|------------------|--------|-----------|-------------|--------|--------------------------|-------------|---------------------------|---------------------------------------|
|                      |   |            |          |                 |                       |                   |                  |        |           |             |        | Signal peptide           | Probability |                           |                                       |
| B2UKV9               | tr B2UKV9 B2UKV9_AKKM8 PepSY_like domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1409 PE=4 SV=1  | Amuc_1409  | 5        | 5               | 32.7                  | 16.523            | 150              | 122.63 | 3.E+08    | 70          | 5.E+07 | Signal peptide (Sec/SPI) | 0.998       | -                         | Unknown                               |
| B2UP96               | tr B2UP96 B2UP96_AKKM8 Thioredoxin domain-containing protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_2057 PE=4 SV=1 | Amuc_2057  | 3        | 3               | 22.8                  | 18.123            | 167              | 53.52  | 2.E+08    | 62          | 3.E+07 | Signal peptide (Sec/SPI) | 0.936       | 0.934                     | Unknown                               |
| B2UR84               | tr B2UR84 B2UR84_AKKM8 YD repeat protein OS=Akkermansia muciniphila (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) OX=349741 GN=Amuc_1143 PE=4 SV=1                     | Amuc_1143  | 2        | 2               | 1                     | 217.62            | 1991             | 8.7575 | 4.E+07    | 17          | 5.E+05 | -                        | -           | 0.943                     | Unknown                               |

**Supplementary Table 7. Sequences of qRT-PCR primers used in this study.**

| Gene          | Primer sequence (5'-3') |                          |
|---------------|-------------------------|--------------------------|
| <i>Mist1</i>  | Forward                 | AGAGCAATGAGCGAGAGAGG     |
|               | Reverse                 | GTGAGGGTCTCGATCTTGGA     |
| <i>Atoh1</i>  | Forward                 | GCCAGTTAGGAAGGCAACAG     |
|               | Reverse                 | ACAACGATCACCACAGACCA     |
| <i>Dll1</i>   | Forward                 | GTTGTCTCCATGGCACCTG      |
|               | Reverse                 | TGCACGGCTTATGGTGAGTA     |
| <i>Tph1</i>   | Forward                 | GCCTGTGGCTGGTTACCTC      |
|               | Reverse                 | GCTCTGGAGTGTAGAGGGGA     |
| <i>Chga</i>   | Forward                 | CCCCTGCAGCATCCAGTT       |
|               | Reverse                 | CCGACTGACCATCATCTTTCTG   |
| <i>Gpr119</i> | Forward                 | CCGTGGCTGATACCTTGATT     |
|               | Reverse                 | AGAGGCAGCTGCAGAAGAAG     |
| <i>Gpr120</i> | Forward                 | AGAGGCTTACGCTGAGCTTG     |
|               | Reverse                 | GAAGGAAACCATGAGCAGGA     |
| <i>Prox1</i>  | Forward                 | TGAATCCCCAAGGTTTCAGAG    |
|               | Reverse                 | AAAGGCATCATGGCATCTTC     |
| <i>Lyz1</i>   | Forward                 | ATGGCTACCGTGGTGTCAAG     |
|               | Reverse                 | ATCCCATAGTCGGTGCTTCG     |
| <i>Defa24</i> | Forward                 | TGTAGAGCAAGAGGCTGCAA     |
|               | Reverse                 | CAGCATCAGTGGCCTCAGTA     |
| <i>Cd24a</i>  | Forward                 | CTTCTGGCACTGCTCCTACC     |
|               | Reverse                 | TACTTGGATTTGGGGAAGCA     |
| <i>Sox9</i>   | Forward                 | CGACTACGCTGACCATCAGA     |
|               | Reverse                 | AGACTGGTTGTTCCAGTGC      |
| <i>Spdef</i>  | Forward                 | TTGGATGAGCACTCGCTAGA     |
|               | Reverse                 | AAAAGCCACTTCTGCACGTT     |
| <i>Tff3</i>   | Forward                 | GATTACGTTGGCCTGTGTCC     |
|               | Reverse                 | CAGGGCACATTTGGGATACT     |
| <i>Agr2</i>   | Forward                 | CAAATCTGGAGCCAAAAAGG     |
|               | Reverse                 | CCATCAAGGGTCTGTTGCTT     |
| <i>Manf</i>   | Forward                 | CCACCATATCCCTGTGGAAA     |
|               | Reverse                 | CGTCCAGGATCTTCTTCAGC     |
| <i>Muc2</i>   | Forward                 | CTGACCAAGAGCGAACACAA     |
|               | Reverse                 | CATGACTGGAAGCAACTGGA     |
| <i>Muc3</i>   | Forward                 | GCTGGCTTTCATCCTCCACT     |
|               | Reverse                 | GCTGTCGTCTTGGGTGCTAT     |
| <i>Muc4</i>   | Forward                 | GAGGGCTACTGTCACAATGGAGGC |
|               | Reverse                 | AGGGTTCCGAAGAGGATCCCGTAG |

|               |         |                        |
|---------------|---------|------------------------|
| <i>Muc13</i>  | Forward | CTGCAACCCTAACCCCTGTA   |
|               | Reverse | CGTTCCTTTCACACATGACG   |
| <i>Fabp1</i>  | Forward | ATTCATGAAGGCAATAGGTCTG |
|               | Reverse | TCATGCACGATTTCTGACAC   |
| <i>Fabp2</i>  | Forward | GTGGAAAGTAGACCGGAACGA  |
|               | Reverse | CCATCCTGTGTGATTGTCAGTT |
| <i>Apoc3</i>  | Forward | CGTAGGTGCCATGCAGCCCC   |
|               | Reverse | CAGCTCGGGCAGATGCCAGG   |
| <i>Alpi</i>   | Forward | ATCATCTTCCTGGGAGACGG   |
|               | Reverse | CGCCGATGGTCTTGTAGTTG   |
| <i>Ki67</i>   | Forward | ATCCAGATGATGGAGCCAAG   |
|               | Reverse | ATTTCTGCAGCTGGTTTGCT   |
| <i>Pcna</i>   | Forward | CAAAGACCTCATCAATGAGG   |
|               | Reverse | GAGGTTACGCCCATGGCTA    |
| <i>Ccnd1</i>  | Forward | CCAGCTCCTGTGCTGCGAAG   |
|               | Reverse | CATGGATGGCACAATCTCCT   |
| <i>Lgr5</i>   | Forward | CAGGTCAATACCGGAGCGAG   |
|               | Reverse | GCGAGGCACCATTCAAAGTC   |
| <i>Olfm4</i>  | Forward | GCCAGATCTTGGCTCTGAAG   |
|               | Reverse | GCCAGTTGAGCTGAATCACA   |
| <i>Msi1</i>   | Forward | GAGGACTCAGTTGGCAGACC   |
|               | Reverse | CGCCTGGTCCATGAAAGTGA   |
| <i>Bmi1</i>   | Forward | TGCTGGAGAGCTGGAAAGTG   |
|               | Reverse | GTGAGGGAAGTGTGGGTGAG   |
| <i>Hopx</i>   | Forward | ACCAGGTGGAGATCCTGGAGTA |
|               | Reverse | CCAGGCGCTGCTTAAACCAT   |
| <i>Axin2</i>  | Forward | CTCCCCACCTTGAATGAAGA   |
|               | Reverse | ACTGGGTCGCTTCTCTTGAA   |
| <i>Myc</i>    | Forward | GCTGTTTGAAGGCTGGATTTC  |
|               | Reverse | GATGAAATAGGGCTGTACGGAG |
| <i>Ctnnb1</i> | Forward | CCCAGTCCTTACGCAAGAG    |
|               | Reverse | CATCTAGCGTCTCAGGGAACA  |
| <i>Prom1</i>  | Forward | GAAAAGTTGCTCTGCGAACC   |
|               | Reverse | TCTCAAGCTGAAAAGCAGCA   |
| <i>Tert</i>   | Forward | ACTCAGCAACCTCCAGCCTA   |
|               | Reverse | CATATTGGCACTCTGCATGG   |
| <i>Cd44</i>   | Forward | GTGGGCAGAAGAAAAAGCTG   |
|               | Reverse | TGATGGTTCCTTGTTACCA    |
| <i>Ephb3</i>  | Forward | CGTGAAAGTGGACACCATTG   |
|               | Reverse | CCAAGTAGAAGCCAGCCTTG   |

|                 |         |                              |
|-----------------|---------|------------------------------|
| <i>Rnf43</i>    | Forward | ATGTAACCTCGTGGGTCTGC         |
|                 | Reverse | GCCAACTTTCTGCTCCACTC         |
| <i>Znf3</i>     | Forward | AGAAGCCATCGACCAGCTAA         |
|                 | Reverse | AAGTACTCGGTGGGTTGTCG         |
| <i>18s rRNA</i> | Forward | GACACGGACAGGATTGACAGATTGATAG |
|                 | Reverse | GTTAGCATGCCAGAGTCTCGTTCGTT   |
| <i>MKI67</i>    | Forward | TGACCCTGATGAGAAAGCTCAA       |
|                 | Reverse | CCCTGAGCAACACTGTCTTTT        |
| <i>LGR5</i>     | Forward | TGCTCTCACCAACTGCATC          |
|                 | Reverse | CTCAGGCTCACCAGATCCTC         |
| <i>LRIG1</i>    | Forward | GACCCTTCTGACCGACAA           |
|                 | Reverse | CGCTTCCACGGCTCTT             |
| <i>CD166</i>    | Forward | TCAAGGTGTTCAAGCAACCA         |
|                 | Reverse | CTGAAATGCAGTCACCCAAC         |
| <i>ASCL2</i>    | Forward | CGTGAAGCTGGTGAAGTGG          |
|                 | Reverse | GGATGTACTCCACGGCTGAG         |
| <i>OLFM4</i>    | Forward | ACCTTCCCCTGGACAGAGT          |
|                 | Reverse | TGGACATATTCCCTCACTTTGGA      |
| <i>AXIN2</i>    | Forward | CTCCCCACCTTGAATGAAGA         |
|                 | Reverse | GTTTCCGTGGACCTCACACT         |
| <i>CTNNB</i>    | Forward | TCTGAGGACAAGCCACAAGATTACA    |
|                 | Reverse | TGGGCACCAATATCAAGTCCAA       |
| <i>SOX9</i>     | Forward | GGAGAGCGAGGAGGACAAGTTC       |
|                 | Reverse | TTGAAGATGGCGTTGGGGG          |
| <i>TERT</i>     | Forward | CTACTCCTCAGGCGACAAGG         |
|                 | Reverse | TGGAACCCAGAAAGATGGTC         |
| <i>WNT3</i>     | Forward | CGCCTCGGAGATGGTAGTAG         |
|                 | Reverse | AAAGTTGGGGGAGTTCTCGT         |
| <i>CCND1</i>    | Forward | TGTTTGCAAGCAGGACTTTG         |
|                 | Reverse | TCATCCTGGCAATGTGAGAA         |
| <i>GAPDH</i>    | Forward | GAAGGTGAAGGTCGGAGTC          |
|                 | Reverse | GAAGATGGTGATGGGATTTTC        |

**Supplementary Table 8. List of antibodies used in this study.**

| Name of Antibody   | Catalog No.   | Company        | Dilution used       |
|--|---------------|----------------|---------------------|
| E-Cadherin   | BD-610181     | BD Biosciences | 1:1000 WB           |
| Frizzled 7   | ab64636       | Abcam          | 1:1000 WB           |
| LRP5 (D80F2)   | 5731S         | Cell Signaling | 1:1000 WB           |
| LRP6 (C47E12)  | 3395S         | Cell Signaling | 1:1000 WB           |
| $\beta$ -catenin   | BD-610153     | BD Biosciences | 1:1000 WB           |
| Active $\beta$ -catenin  | 19807S        | Cell Signaling | 1:1000 WB           |
| $\beta$ -Actin   | 4967S         | Cell Signaling | 1:1000 WB           |
| 6X His tag   | ab9108        | Abcam          | 1:1000 WB           |
| Strep-tag  | 34850         | QIAGEN         | 1:3000 WB           |
| Amuc_1409  | in-house-made | AbClon         | 1:1000 WB           |
| Ki67   | ab15580       | Abcam          | 1:100 IF, 1:200 IHC |
| Chromogranin A   | ab199192      | Abcam          | 1:200 IF            |
| Lysozyme   | ab108508      | Abcam          | 1:200 IF            |
| MUC2   | GTX100664     | GeneTex        | 1:100 IF            |
| Ki67   | AB9260        | Millipore      | 1:100 IF            |
| Ki67   | 556003        | BD Biosciences | 1:100 IF            |
| Brdu   | B2531         | Sigma Aldrich  | 1:100 IF            |
| E-Cadherin   | 610182        | BD Biosciences | 1:200 IF            |
| E-Cadherin   | AF648         | R&D systems    | 1:200 IF            |
| ASCL2  | MAB4418       | Millipore      | 1:100 IF            |
| GFP  | ab13970       | Abcam          | 1:100 IF            |
| OLFM4  | ab85046       | Abcam          | 1:100 IF            |
| OLFM4 (D6Y5A)  | 39141S        | Cell Signaling | 1:100 IHC           |
| Western blot (WB), Immunofluorescence (IF), Immunohistochemistry (IHC) |               |                |                     |

**Supplementary Table 9. List of primer sequence used for E-cadherin cloning.**

| Primers         | Primer sequence (5'-3')*   |
|-----------------|----------------------------|
| CDH1-F-SacII    | TCCCCGCGGTCCAGGAGCCGGAG    |
| CDH1-R-XhoI     | CCGCTCGAGGGCTAGTCGTCCTCGCC |
| CDH1-EC-F-SacII | TCCCCGCGGTCGACTGGGTATT     |
| CDH1-EC-R-XhoI  | CCGCTCGAGGGCTACAATCCTGCTTC |
| CDH1-IC-F-SacII | TCCCCGCGGTCAGAGCGGTGGTC    |
| CDH1-IC-R-XhoI  | CCGCTCGAGGGCTAGTCGTCCTCGCC |

\*Sites for restrictive endonucleases are underlined.