

Changes in intestinal proteins induced by colostrum uptake in neonatal calves: analysis by two-dimensional gel electrophoresis-based proteomics analysis

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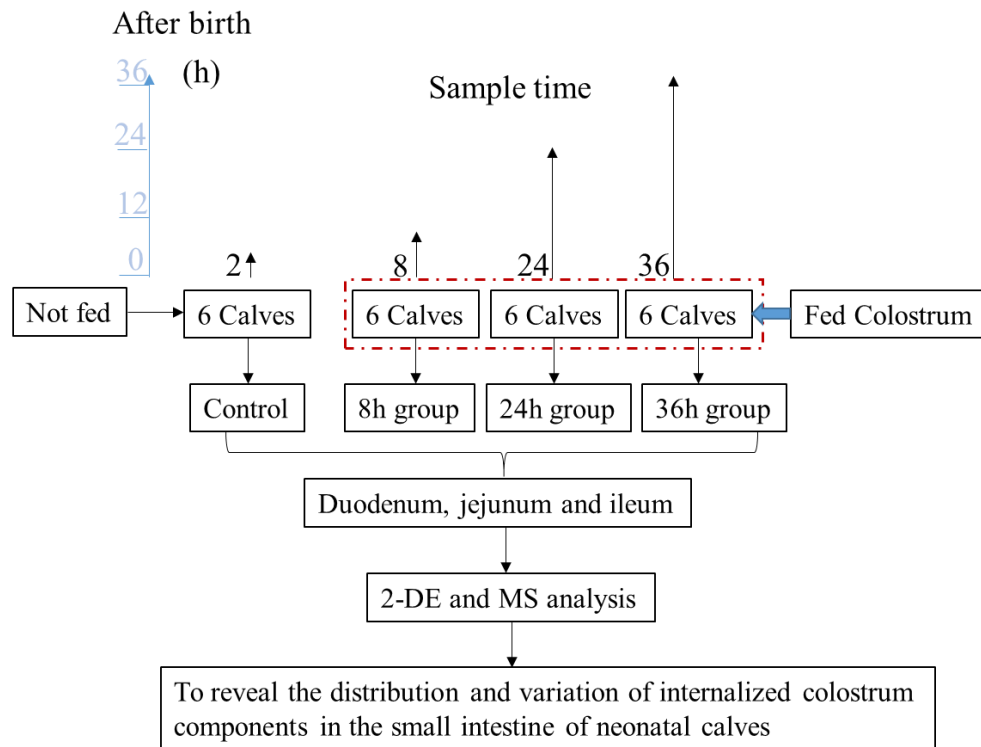


Figure S1. An overview of the strategy used to reveal colostrum components internalized in the small intestine of neonatal calves.

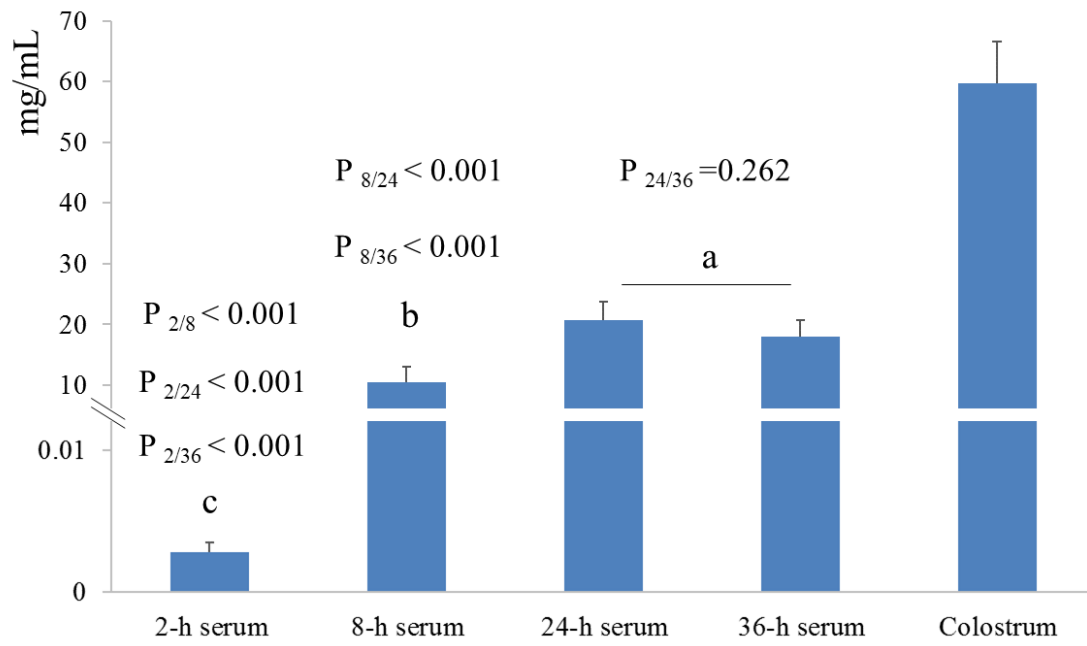


Figure S2. Contents of serum and colostral IgG quantified using an ELISA kit. Different letters mean significant difference.

Table S1. Peptide information of the differential expressed proteins among the duodenum, jejunum and ileum segments of the calves not fed colostrum by mass spectrometry

| No. | Peptide Information | | | | | | | Ion Score | C. I. % | Modification * |
|-----|-------------------------------------|-------------|----------|-----------|------------|----------|------------------------|-----------|---------|----------------|
| | Calc. Mass | Obsrv. Mass | \pm da | \pm ppm | Start Seq. | End Seq. | Sequence | | | |
| s1 | Malate dehydrogenase, mitochondrial | | | | | | | | | |
| | 1130.6125 | 1130.5923 | -0.0202 | -18 | 315 | 324 | MIAEAIPELK | | | M |
| | 1233.7202 | 1233.7163 | -0.0039 | -3 | 166 | 176 | IFGVTTLDIVR | 16 | 0 | |
| | 1338.7198 | 1338.71 | -0.0098 | -7 | 92 | 104 | GCDVVVIPAGVPR | | | C |
| | 1417.7686 | 1417.7134 | -0.0552 | -39 | 302 | 314 | NLGIGKVSPFEEK | | | |
| | 1470.7006 | 1470.6862 | -0.0144 | -10 | 242 | 257 | AGAGSATLSMAYAGAR | | | M |
| | 1604.8279 | 1604.8289 | 0.001 | 1 | 216 | 229 | VEFPQDQLTTLTGR | 118 | 100 | |
| | 2143.166 | 2143.0063 | -0.1597 | -75 | 158 | 176 | HGVYNPNKIFGVTTLDIVR | | | |
| | 2393.2461 | 2393.2454 | -0.0007 | 0 | 53 | 74 | LTLYDIAHTPGVAADLSHIETR | | | |
| s2 | Cofilin 1 | | | | | | | | | |
| | 815.3967 | 815.3997 | 0.003 | 4 | 115 | 121 | MIYASSK | | | M |
| | 876.4309 | 876.4398 | 0.0089 | 10 | 23 | 30 | SSTPEEVK | | | |
| | 915.5145 | 915.5151 | 0.0006 | 1 | 46 | 53 | NIILEEGK | | | |
| | 1004.5258 | 1004.5252 | -0.0006 | -1 | 23 | 31 | SSTPEEVKK | | | |
| | 1024.5244 | 1024.4924 | -0.032 | -31 | 14 | 21 | VFNDMKVR | | | M |

| | | | | | | | | | | |
|----|-------------------------------|-----------|---------|-----|-----|-----|------------------------------|-----|--------|------|
| | 1050.4707 | 1050.4792 | 0.0085 | 8 | 74 | 81 | MLPKDCR | 27 | 7.461 | C, M |
| | 1309.6821 | 1309.6849 | 0.0028 | 2 | 35 | 45 | AVLFCLSEDKK | 96 | 100 | C |
| | 1337.626 | 1337.621 | -0.005 | -4 | 82 | 92 | YALYDATYETK | 88 | 100 | |
| | 1340.7784 | 1340.7026 | -0.0758 | -57 | 153 | 166 | LGGSAVISLEGKPL | | | |
| | 1519.6846 | 1519.6909 | 0.0063 | 4 | 133 | 144 | HELQANCYEEVK | 79 | 100 | C |
| | 1790.8126 | 1790.8163 | 0.0037 | 2 | 133 | 146 | HELQANCYEEVKDR | 95 | 100 | C |
| | 2166.0967 | 2166.0818 | -0.0149 | -7 | 54 | 73 | EILVGDVGQTVDDPYATFVK | | | |
| | 3062.5933 | 3062.6023 | 0.009 | 3 | 46 | 73 | NIILEEGKEILVGDVGQTVDDPYATFVK | | | |
| s3 | actin, alpha cardiac muscle 1 | | | | | | | | | |
| | 923.5672 | 923.6104 | 0.0432 | 47 | 331 | 338 | IIAPPERK | | | |
| | 1036.6514 | 1036.6104 | -0.041 | -40 | 329 | 337 | IKIIAPPER | | | |
| | 1130.5477 | 1130.593 | 0.0453 | 40 | 199 | 208 | GYSFVTTAER | 76 | 99.999 | |
| | 1161.6184 | 1161.6591 | 0.0407 | 35 | 318 | 328 | EITALAPSTMK | | | |
| | 1177.6133 | 1177.6514 | 0.0381 | 32 | 318 | 328 | EITALAPSTMK | | | M |
| | 1500.7078 | 1500.7578 | 0.05 | 33 | 362 | 374 | QEYDEAGPSIVHR | 100 | 100 | |
| | 1790.892 | 1790.9564 | 0.0644 | 36 | 241 | 256 | SYELPDGQVITIGNER | 153 | 100 | |
| | 2228.0652 | 2228.158 | 0.0928 | 42 | 294 | 314 | DLYANNVLSGGTTMYPGIADR | | | |
| | 2229.9309 | 2229.731 | -0.1999 | -90 | 1 | 20 | MCDDEETTALVCDNGSGLVK | | | C, M |
| | 2356.1602 | 2356.2488 | 0.0886 | 38 | 293 | 314 | KDLYANNVLSGGTTMYPGIADR | 79 | 100 | |

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|----|------------------------|-----------|---------|-----|-----|-----|------------------------------|-----|--------|------|
| | 2372.155 | 2372.2397 | 0.0847 | 36 | 293 | 314 | KDLYANNVLSGGTTMYPGIADR | | | M |
| | 2536.1582 | 2536.2524 | 0.0942 | 37 | 218 | 240 | LCYVALDFENEMATAASSSSLEK | | | C |
| | 3220.4636 | 3220.603 | 0.1394 | 43 | 259 | 286 | CPETLFQPSFIGMESAGIHETTYNSIMK | | | C, M |
| s4 | hemoglobin alpha chain | | | | | | | | | |
| | 818.4407 | 818.4644 | 0.0237 | 29 | 94 | 100 | VDPVNFK | | | |
| | 1071.5543 | 1071.5791 | 0.0248 | 23 | 33 | 41 | MFLSFPTTK | 60 | 99.957 | |
| | 1087.6259 | 1087.6434 | 0.0175 | 16 | 92 | 100 | LRVDPVNFK | 41 | 96.252 | |
| | 1101.6263 | 1101.6128 | -0.0135 | -12 | 2 | 12 | VLSAADKGNVK | | | |
| | 1232.6667 | 1232.6315 | -0.0352 | -29 | 1 | 12 | MVLSAADKGNVK | | | |
| | 1529.7344 | 1529.7557 | 0.0213 | 14 | 18 | 32 | VGGHAAEYGAEALER | | | |
| | 1529.7344 | 1529.7557 | 0.0213 | 14 | 18 | 32 | VGGHAAEYGAEALER | 108 | 100 | |
| | 1571.8792 | 1571.8057 | -0.0735 | -47 | 129 | 142 | FLASVSTVLTSKYR | | | |
| | 1833.892 | 1833.9165 | 0.0245 | 13 | 42 | 57 | TYFPHFDLSHGSAQVK | 117 | 100 | |
| | 2367.1938 | 2367.2327 | 0.0389 | 16 | 70 | 91 | AVEHLDDLPGALSELSDLHAHK | 180 | 100 | |
| s5 | Hemoglobin, gamma | | | | | | | | | |
| | 907.5247 | 907.5417 | 0.017 | 19 | 8 | 16 | AAVTSLFAK | | | |
| | 1101.5536 | 1101.5808 | 0.0272 | 25 | 19 | 29 | VDEVGGEALGR | | | |
| | 1126.5641 | 1126.5819 | 0.0178 | 16 | 95 | 103 | LHVDPENFR | 83 | 100 | |
| | 1167.5715 | 1167.59 | 0.0185 | 16 | 66 | 75 | VLDSFCEGLK | 65 | 99.984 | C |

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|----|-------------------|-----------|---------|-----|-----|-----|------------------------|-----|--------|---|
| | 1207.6907 | 1207.7117 | 0.021 | 17 | 132 | 143 | VVTGVANALAHR | 91 | 100 | |
| | 1265.8304 | 1265.861 | 0.0306 | 24 | 104 | 115 | LLGNVLVVVLAR | | | |
| | 1274.7256 | 1274.7518 | 0.0262 | 21 | 30 | 39 | LLVVYPWTQR | 62 | 99.965 | |
| | 1295.6665 | 1295.6945 | 0.028 | 22 | 65 | 75 | KVLDSFCEGLK | 50 | 99.485 | C |
| | 1328.7169 | 1328.7357 | 0.0188 | 14 | 17 | 29 | VKVDEVGGEALGR | | | |
| | 1434.6682 | 1434.6934 | 0.0252 | 18 | 82 | 94 | GAFASLSELHCDK | 87 | 100 | C |
| | 1507.8129 | 1507.8335 | 0.0206 | 14 | 132 | 145 | VVTGVANALAHRYH | | | |
| | 1701.8119 | 1701.8341 | 0.0222 | 13 | 117 | 131 | FGSEFSPELQASFQK | | | |
| | 1857.9131 | 1857.9408 | 0.0277 | 15 | 116 | 131 | RFGSEFSPELQASFQK | 100 | 100 | |
| | 1879.947 | 1879.9215 | -0.0255 | -14 | 66 | 81 | VLDSFCEGLKQLDDLK | | | C |
| | 2014.9757 | 2014.9976 | 0.0219 | 11 | 40 | 58 | FFESFGDLSSADAILGNPK | | | |
| | 2542.2144 | 2542.2612 | 0.0468 | 18 | 82 | 103 | GAFASLSELHCDKLHVDPENFR | | | C |
| s6 | Hemoglobin, gamma | | | | | | | | | |
| | 907.5247 | 907.5384 | 0.0137 | 15 | 8 | 16 | AAVTSLFAK | | | |
| | 1101.5536 | 1101.5739 | 0.0203 | 18 | 19 | 29 | VDEVGGEALGR | | | |
| | 1126.5641 | 1126.5764 | 0.0123 | 11 | 95 | 103 | LHVDPENFR | 73 | 99.998 | |
| | 1167.5715 | 1167.587 | 0.0155 | 13 | 66 | 75 | VLDSFCEGLK | 67 | 99.99 | C |
| | 1207.6907 | 1207.709 | 0.0183 | 15 | 132 | 143 | VVTGVANALAHR | 91 | 100 | |
| | 1265.8304 | 1265.8519 | 0.0215 | 17 | 104 | 115 | LLGNVLVVVLAR | | | |

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|----|----------------------|-----------|---------|-----|-----|-----|------------------------|-----|--------|---|
| | 1274.7256 | 1274.7498 | 0.0242 | 19 | 30 | 39 | LLVVYPWTQR | 48 | 99.288 | |
| | 1295.6665 | 1295.6871 | 0.0206 | 16 | 65 | 75 | KVLDSFCEGLK | | | C |
| | 1328.7169 | 1328.7321 | 0.0152 | 11 | 17 | 29 | VKVDEVGGEALGR | | | |
| | 1434.6682 | 1434.6841 | 0.0159 | 11 | 82 | 94 | GAFASLSELHCDK | 91 | 100 | C |
| | 1507.8129 | 1507.7812 | -0.0317 | -21 | 132 | 145 | VVTGVANALAHRYH | | | |
| | 1701.8119 | 1701.8262 | 0.0143 | 8 | 117 | 131 | FGSEFSPELQASFQK | 114 | 100 | |
| | 1857.9131 | 1857.9348 | 0.0217 | 12 | 116 | 131 | RFGSEFSPELQASFQK | 88 | 100 | |
| | 1879.947 | 1879.9114 | -0.0356 | -19 | 66 | 81 | VLDSFCEGLKQLDDLK | | | C |
| | 2014.9757 | 2014.9832 | 0.0075 | 4 | 40 | 58 | FFESFGDLSSADAILGNPK | | | |
| | 2542.2144 | 2542.2378 | 0.0234 | 9 | 82 | 103 | GAFASLSELHCDKLHVDPENFR | | | C |
| s7 | actin, cytoplasmic 2 | | | | | | | | | |
| | 923.5672 | 923.5628 | -0.0044 | -5 | 329 | 336 | IIAPPERK | | | |
| | 976.4483 | 976.4464 | -0.0019 | -2 | 19 | 28 | AGFAGDDAPR | 35 | 82.332 | |
| | 998.4863 | 998.4516 | -0.0347 | -35 | 184 | 191 | DLTDYLMK | | | |
| | 1132.527 | 1132.5247 | -0.0023 | -2 | 197 | 206 | GYSFTTTAER | 39 | 92.126 | |
| | 1171.5712 | 1171.5692 | -0.002 | -2 | 40 | 50 | HQGVMVGMGQK | | | |
| | 1187.566 | 1187.5829 | 0.0169 | 14 | 40 | 50 | HQGVMVGMGQK | | | M |
| | 1198.7056 | 1198.6984 | -0.0072 | -6 | 29 | 39 | AVFPSIVGRPR | 10 | 0 | |
| | 1203.5609 | 1203.5863 | 0.0254 | 21 | 40 | 50 | HQGVMVGMGQK | | | M |

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|----|------------|-----------|---------|-----|-----|-----|--------------------------------|-----|--------|------|
| | 1354.6234 | 1354.624 | 0.0006 | 0 | 51 | 62 | DSYVGDEAQSQR | | | |
| | 1516.7028 | 1516.7059 | 0.0031 | 2 | 360 | 372 | QEYDESGPSIVHR | 70 | 99.994 | |
| | 1644.7976 | 1644.7231 | -0.0745 | -45 | 360 | 373 | QEYDESGPSIVHRK | | | |
| | 1778.83 | 1778.8212 | -0.0088 | -5 | 2 | 18 | EEEIAALVIDNGSGMCK | | | |
| | 1790.892 | 1790.8772 | -0.0148 | -8 | 239 | 254 | SYELPDGQVITIGNER | 149 | 100 | |
| | 1954.0645 | 1954.0295 | -0.035 | -18 | 96 | 113 | VAPEEHPVLLTEAPLNPK | 74 | 99.998 | |
| | 1982.8868 | 1983.0021 | 0.1153 | 58 | 1 | 18 | MEEEIAALVIDNGSGMCK | | | C, M |
| | 2215.0701 | 2215.0588 | -0.0113 | -5 | 292 | 312 | DLYANTVLSGGTTMYPGIADR | 95 | 100 | |
| | 2231.0649 | 2231.042 | -0.0229 | -10 | 292 | 312 | DLYANTVLSGGTTMYPGIADR | | | M |
| | 2343.165 | 2343.1514 | -0.0136 | -6 | 291 | 312 | KDLYANTVLSGGTTMYPGIADR | | | |
| | 2359.1599 | 2359.1294 | -0.0305 | -13 | 291 | 312 | KDLYANTVLSGGTTMYPGIADR | | | M |
| | 2550.1738 | 2550.145 | -0.0288 | -11 | 216 | 238 | LCYVALDFEQEMATAASSSSLEK | | | C |
| | 2730.4324 | 2730.2896 | -0.1428 | -52 | 336 | 359 | KYSVWIGGSILASLSTFQQMWISK | | | |
| | 3183.6145 | 3183.6292 | 0.0147 | 5 | 148 | 177 | TTGIVMDSGDGVTHTVPIYEGYALPHAILR | | | |
| | 3199.6094 | 3199.6147 | 0.0053 | 2 | 148 | 177 | TTGIVMDSGDGVTHTVPIYEGYALPHAILR | | | M |
| s8 | Transgelin | | | | | | | | | |
| | 870.3774 | 870.4021 | 0.0247 | 28 | 8 | 15 | GPSYGMSR | | | M |
| | 1010.44 | 1010.4601 | 0.0201 | 20 | 150 | 157 | GDPNWFMK | | | M |
| | 1082.4636 | 1082.488 | 0.0244 | 23 | 25 | 32 | YDEELEER | 43 | 97.695 | |
| | 1203.6997 | 1203.6372 | -0.0625 | -52 | 51 | 60 | GRLGFQVWLK | | | |

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|----|--|-----------|---------|-----|-----|-----|--------------------|----|--------|---|
| | 1204.697 | 1204.6276 | -0.0694 | -58 | 132 | 143 | TLMALGSLAVTK | | | |
| | 1210.5586 | 1210.5808 | 0.0222 | 18 | 24 | 32 | KYDEELEER | 59 | 99.939 | |
| | 1220.6919 | 1220.6543 | -0.0376 | -31 | 132 | 143 | TLMALGSLAVTK | | | M |
| | 1221.6296 | 1221.647 | 0.0174 | 14 | 93 | 102 | QMEQVAQFLK | | | |
| | 1237.6246 | 1237.6385 | 0.0139 | 11 | 93 | 102 | QMEQVAQFLK | | | M |
| | 1244.6344 | 1244.6492 | 0.0148 | 12 | 82 | 92 | VPENPPSMVFK | 51 | 99.621 | |
| | 1260.6293 | 1260.6359 | 0.0066 | 5 | 82 | 92 | VPENPPSMVFK | | | M |
| | 1295.6115 | 1295.6283 | 0.0168 | 13 | 165 | 175 | EFTESQLQEGK | | | |
| | 1451.7125 | 1451.7378 | 0.0253 | 17 | 164 | 175 | REFTESQLQEGK | | | |
| | 1516.837 | 1516.8566 | 0.0196 | 13 | 68 | 81 | LVNSLYPDGSKPVK | 87 | 100 | |
| | 1530.7145 | 1530.7303 | 0.0158 | 10 | 112 | 124 | TDMFQTVDLFEGK | 95 | 100 | |
| | 1546.7095 | 1546.7234 | 0.0139 | 9 | 112 | 124 | TDMFQTVDLFEGK | | | M |
| | 1963.0066 | 1963.0184 | 0.0118 | 6 | 132 | 149 | TLMALGSLAVTKNDGHYR | | | M |
| | 2127.0474 | 2127.0845 | 0.0371 | 17 | 33 | 50 | LVEWIVMQCGPDVGRPDR | | | C |
| s9 | fatty acid-binding protein, intestinal | | | | | | | | | |
| | 881.4839 | 881.5135 | 0.0296 | 34 | 31 | 38 | LAAHDNLK | | | |
| | 1009.5789 | 1009.604 | 0.0251 | 25 | 30 | 38 | KLAAHDNLK | | | |
| | 1015.5782 | 1015.601 | 0.0228 | 22 | 39 | 47 | LIITQEGNK | 34 | 80.095 | |
| | 1166.5437 | 1166.5814 | 0.0377 | 32 | 9 | 17 | VDRNENYEK | 34 | 80.459 | |

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|-----|-------------------|-----------|--------|----|-----|-----|---------------------|----|--------|---|
| | 1186.6176 | 1186.6523 | 0.0347 | 29 | 97 | 107 | LDNGNALNTRV | | | |
| | 1194.5902 | 1194.6373 | 0.0471 | 39 | 2 | 11 | AFDGTWKVDR | | | |
| | 1201.6212 | 1201.6676 | 0.0464 | 39 | 48 | 57 | FTVKESSTFR | | | |
| | 1295.6851 | 1295.6934 | 0.0083 | 6 | 18 | 28 | FMEKMGINVVK | | | |
| | 1325.6307 | 1325.731 | 0.1003 | 76 | 1 | 11 | MAFDGTWKVDR | | | |
| | 1342.7186 | 1342.75 | 0.0314 | 23 | 96 | 107 | RLDNGNALNTRV | | | |
| | 2117.0107 | 2117.0349 | 0.0242 | 11 | 108 | 126 | EIIGGEMVQTYTYEGVEAK | | | |
| s10 | Hemoglobin, gamma | | | | | | | | | |
| | 907.5247 | 907.5384 | 0.0137 | 15 | 8 | 16 | AAVTSLFAK | | | |
| | 1101.5536 | 1101.5739 | 0.0203 | 18 | 19 | 29 | VDEVGGEALGR | | | |
| | 1126.5641 | 1126.5764 | 0.0123 | 11 | 95 | 103 | LHVPENFR | 73 | 99.998 | |
| | 1167.5715 | 1167.587 | 0.0155 | 13 | 66 | 75 | VLDSFCEGLK | 67 | 99.99 | C |
| | 1207.6907 | 1207.709 | 0.0183 | 15 | 132 | 143 | VVTGVANALHR | 91 | 100 | |
| | 1265.8304 | 1265.8519 | 0.0215 | 17 | 104 | 115 | LLGNVLVVVLAR | | | |
| | 1274.7256 | 1274.7498 | 0.0242 | 19 | 30 | 39 | LLVVYPWTQR | 48 | 99.288 | |
| | 1295.6665 | 1295.6871 | 0.0206 | 16 | 65 | 75 | KVLDSFCEGLK | | | C |
| | 1328.7169 | 1328.7321 | 0.0152 | 11 | 17 | 29 | VKVDEVGGEALGR | | | |
| | 1434.6682 | 1434.6841 | 0.0159 | 11 | 82 | 94 | GAFASLSELHCDK | | | C |
| | 1434.6682 | 1434.6841 | 0.0159 | 11 | 82 | 94 | GAFASLSELHCDK | 91 | 100 | C |

| | | | | | | | | | | |
|-----|---------------|-----------|---------|-----|-----|-----|------------------------|-----|--------|---|
| | 1507.8129 | 1507.7812 | -0.0317 | -21 | 132 | 145 | VVTGVANALAHRYH | | | |
| | 1701.8119 | 1701.8262 | 0.0143 | 8 | 117 | 131 | FGSEFSPELQASFQK | 114 | 100 | |
| | 1857.9131 | 1857.9348 | 0.0217 | 12 | 116 | 131 | RFGSEFSPELQASFQK | 88 | 100 | |
| | 1879.947 | 1879.9114 | -0.0356 | -19 | 66 | 81 | VLDSFCEGLKQLDDLK | | | C |
| | 2014.9757 | 2014.9832 | 0.0075 | 4 | 40 | 58 | FFESFGDLSSADAILGNPK | | | |
| | 2542.2144 | 2542.2378 | 0.0234 | 9 | 82 | 103 | GAFASLSELHCDKLHVDPENFR | | | C |
| s11 | serum albumin | | | | | | | | | |
| | 818.4254 | 818.4598 | 0.0344 | 42 | 431 | 437 | ATEEQLK | | | |
| | 898.4815 | 898.5201 | 0.0386 | 43 | 352 | 358 | LCVLHEK | | | C |
| | 1014.6193 | 1014.656 | 0.0367 | 36 | 418 | 426 | QTALVELLK | | | |
| | 1107.5139 | 1107.5535 | 0.0396 | 36 | 457 | 466 | EACFAVEGPK | | | C |
| | 1138.498 | 1138.543 | 0.045 | 40 | 368 | 376 | CCTESLVNR | 60 | 99.958 | C |
| | 1142.7144 | 1142.7549 | 0.0405 | 35 | 417 | 426 | KQTALVELLK | | | |
| | 1145.6426 | 1145.5947 | -0.0479 | -42 | 105 | 114 | AWSVARLSQK | | | |
| | 1166.4929 | 1166.5837 | 0.0908 | 78 | 329 | 337 | CCTKPESER | | | C |
| | 1399.6926 | 1399.7349 | 0.0423 | 30 | 438 | 449 | TVMENFVAFVDK | 57 | 99.903 | |
| | 1415.6876 | 1415.7296 | 0.042 | 30 | 438 | 449 | TVMENFVAFVDK | 79 | 100 | M |
| | 1880.9211 | 1880.9841 | 0.063 | 33 | 377 | 392 | RPCFSALTPDETYVPK | 119 | 100 | C |
| | 1907.9208 | 1907.973 | 0.0522 | 27 | 398 | 413 | LFTFHADICTLPDETEK | | | C |

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|-----|---------------|-----------|---------|-----|-----|-----|-------------------|-----|--------|---|
| | 1909.0007 | 1908.9951 | -0.0056 | -3 | 37 | 52 | SHPQFFAPLLLYYANK | | | |
| | 1927.7983 | 1927.8441 | 0.0458 | 24 | 450 | 466 | CCAADDKEACFAVEGPK | 132 | 100 | C |
| | 1941.9222 | 1941.8521 | -0.0701 | -36 | 150 | 166 | ADLAKYICDNQDTISSK | | | C |
| s12 | alpha-enolase | | | | | | | | | |
| | 800.3825 | 800.4056 | 0.0231 | 29 | 257 | 262 | YDLDFK | | | |
| | 806.4519 | 806.4707 | 0.0188 | 23 | 407 | 412 | YNQILR | | | |
| | 810.4468 | 810.4644 | 0.0176 | 22 | 65 | 71 | AVEHINK | | | |
| | 815.4872 | 815.4947 | 0.0075 | 9 | 222 | 228 | EAELELLK | | | |
| | 958.5203 | 958.5245 | 0.0042 | 4 | 82 | 89 | LNVVEQEK | | | |
| | 1007.5012 | 1007.5123 | 0.0111 | 11 | 336 | 343 | SCNCLLLK | | | C |
| | 1072.531 | 1072.5474 | 0.0164 | 15 | 254 | 262 | SGKYDLDFK | | | |
| | 1086.6154 | 1086.6328 | 0.0174 | 16 | 81 | 89 | KLNVVEQEK | | | |
| | 1143.6157 | 1143.6283 | 0.0126 | 11 | 184 | 193 | IGAEVYHNLK | | | |
| | 1143.6157 | 1143.6283 | 0.0126 | 11 | 184 | 193 | IGAEVYHNLK | 71 | 99.996 | |
| | 1390.7213 | 1390.7272 | 0.0059 | 4 | 16 | 28 | GNPTVEVDLFTAK | | | |
| | 1439.7417 | 1439.7491 | 0.0074 | 5 | 270 | 281 | YITPDELANLYK | | | |
| | 1541.7642 | 1541.7762 | 0.012 | 8 | 359 | 372 | LAQSNGWGMVSHR | | | |
| | 1554.7072 | 1554.77 | 0.0628 | 40 | 257 | 269 | YDLDFKSPDDPSR | | | |
| | 1556.7778 | 1556.7928 | 0.015 | 10 | 240 | 253 | VVIGMDVAASEFYR | 64 | 99.982 | |

| | | | | | | | | | | |
|-----|-----------|-----------|---------|-----|-----|-----|------------------------|-----|--------|---|
| | 1572.7727 | 1572.7764 | 0.0037 | 2 | 240 | 253 | VVIGMDVAASEFYR | 86 | 100 | M |
| | 1630.837 | 1630.7753 | -0.0617 | -38 | 180 | 193 | EAMRIGAEVYHNLK | | | |
| | 1633.8214 | 1633.8167 | -0.0047 | -3 | 344 | 358 | VNQIGSVTESLQACK | | | C |
| | 1668.7819 | 1668.7997 | 0.0178 | 11 | 90 | 103 | IDKLMIEMDGTENK | | | M |
| | 1804.944 | 1804.9514 | 0.0074 | 4 | 33 | 50 | AAVPSGASTGIYEALELR | 178 | 100 | |
| | 1960.9247 | 1960.9236 | -0.0011 | -1 | 203 | 221 | DATNVGDEGGFAPNILENK | | | |
| | 1965.9926 | 1966.0059 | 0.0133 | 7 | 163 | 179 | LAMQEFMILPVGAENFR | | | |
| | 1981.9874 | 1981.9913 | 0.0039 | 2 | 163 | 179 | LAMQEFMILPVGAENFR | 69 | 99.994 | M |
| | 1997.9824 | 1997.9795 | -0.0029 | -1 | 163 | 179 | LAMQEFMILPVGAENFR | 40 | 95.024 | M |
| | 2033.0551 | 2033.0441 | -0.011 | -5 | 307 | 326 | FTASAGIQVVGDDLTVTNPK | | | |
| | 2277.1357 | 2277.1648 | 0.0291 | 13 | 33 | 54 | AAVPSGASTGIYEALELRDNDK | | | |
| | 2353.1592 | 2353.1624 | 0.0032 | 1 | 373 | 394 | SGETEDTFIADLVVGLCTGQIK | | | C |
| | 2582.1357 | 2582.127 | -0.0087 | -3 | 286 | 306 | DYPVVSIEDPFDQDDWEAWQK | | | |
| s13 | Desmin | | | | | | | | | |
| | 884.4512 | 884.4877 | 0.0365 | 41 | 119 | 125 | FANYIEK | | | |
| | 911.4581 | 911.4928 | 0.0347 | 38 | 242 | 248 | VHEEEIR | | | |
| | 986.407 | 986.4319 | 0.0249 | 25 | 319 | 325 | QEMMEYR | | | |
| | 1002.4019 | 1002.4307 | 0.0288 | 29 | 319 | 325 | QEMMEYR | | | M |
| | 1002.5214 | 1002.5533 | 0.0319 | 32 | 213 | 222 | ADVDAATLAR | | | |

| | | | | | | | | | |
|------------|---------------------------|---------|-------|------------|----------|--------------|-----------|---------|--------------|
| 1016.5483 | 1016.5807 | 0.0324 | 32 | 59 | 70 | TSGGAGGLGALR | 3 | 0 | |
| 1018.3968 | 1018.4411 | 0.0443 | 43 | 319 | 325 | QEMMEYR | | | M |
| 1039.5531 | 1039.5883 | 0.0352 | 34 | 241 | 248 | KVHEEEIR | | | |
| 1060.5634 | 1060.5966 | 0.0332 | 31 | 407 | 415 | KLLEGEESR | | | |
| 1086.5902 | 1086.6288 | 0.0386 | 36 | 165 | 173 | QVEVLTNQR | 67 | 99.989 | |
| 1101.5535 | 1101.5946 | 0.0411 | 37 | 181 | 189 | DNLLDDLQR | 39 | 93.658 | |
| 1115.5692 | 1115.6084 | 0.0392 | 35 | 110 | 118 | VELQELNDR | 35 | 82.533 | |
| 1121.5837 | 1121.5764 | -0.0073 | -7 | 387 | 395 | EYQDLLNVK | | | |
| 1242.6914 | 1242.7279 | 0.0365 | 29 | 164 | 173 | RQVEVLTNQR | | | |
| 1250.6263 | 1250.6647 | 0.0384 | 31 | 151 | 160 | VAEIYEEELR | 51 | 99.536 | |
| s14 | heat shock protein beta-1 | | | | | | | | |
| Calc. Mass | Obsrv. Mass | ± da | ± ppm | Start Seq. | End Seq. | Sequence | Ion Score | C. I. % | Modification |
| 831.5087 | 831.5466 | 0.0379 | 46 | 6 | 12 | VPFSLLR | | | |
| 961.4526 | 961.4915 | 0.0389 | 40 | 13 | 20 | GPSWDPFR | | | |
| 961.4526 | 961.4915 | 0.0389 | 40 | 13 | 20 | GPSWDPFR | 59 | 99.93 | |
| 1031.4694 | 1031.5094 | 0.04 | 39 | 21 | 28 | DWYPAHSR | 65 | 99.98 | |
| 1104.507 | 1104.5502 | 0.0432 | 39 | 124 | 132 | QDEHGYISR | 32 | 59.169 | |
| 1146.6365 | 1146.6403 | 0.0038 | 3 | 109 | 119 | TKDGVVEITGK | | | |
| 1163.6208 | 1163.6658 | 0.045 | 39 | 29 | 38 | LFDQAFGLPR | 91 | 100 | |

| | | | | | | | | | | |
|-----|------------------------|-----------|---------|-----|-----|-----|-------------------|-----|--------|---|
| | 1413.7485 | 1413.8003 | 0.0518 | 37 | 58 | 71 | ALPAAAIEGPAYNR | 126 | 100 | |
| | 1618.8031 | 1618.8594 | 0.0563 | 35 | 76 | 90 | QLSSGVSEIQQTADR | 142 | 100 | |
| | 1797.9382 | 1797.9912 | 0.053 | 29 | 93 | 108 | VSLDVNHFAPEELTVK | 85 | 100 | |
| | 1819.955 | 1819.9807 | 0.0257 | 14 | 168 | 184 | SATQSAEITIPVTFQAR | | | |
| s15 | tropomyosin beta chain | | | | | | | | | |
| | 822.4025 | 822.384 | -0.0185 | -22 | 199 | 205 | TMDQALK | | | M |
| | 846.4679 | 846.4667 | -0.0012 | -1 | 232 | 238 | LKEAETR | | | |
| | 894.4679 | 894.4626 | -0.0053 | -6 | 162 | 168 | YEEVARK | | | |
| | 906.4097 | 906.4313 | 0.0216 | 24 | 31 | 37 | QAEDRCK | | | C |
| | 916.4734 | 916.4666 | -0.0068 | -7 | 192 | 198 | QLEEELR | 30 | 33.808 | |
| | 942.4276 | 942.4222 | -0.0054 | -6 | 153 | 160 | HIAEDSDR | | | |
| | 989.4897 | 989.4917 | 0.002 | 2 | 22 | 30 | AEQAEADKK | | | |
| | 1070.5226 | 1070.5142 | -0.0084 | -8 | 153 | 161 | HIAEDSDRK | | | |
| | 1073.5586 | 1073.551 | -0.0076 | -7 | 13 | 21 | LDKENAIDR | | | |
| | 1170.6729 | 1170.6655 | -0.0074 | -6 | 169 | 178 | LVILEGELER | 33 | 63.372 | |
| | 1181.5541 | 1181.5356 | -0.0185 | -16 | 141 | 149 | MELQEMQLK | | | M |
| | 1182.5525 | 1182.5394 | -0.0131 | -11 | 218 | 226 | EDKYEEEIK | | | |
| | 1243.6528 | 1243.6449 | -0.0079 | -6 | 92 | 101 | IQLVEEELDR | 72 | 99.996 | |
| | 1262.5972 | 1262.6038 | 0.0066 | 5 | 179 | 189 | SEERA EVAESR | | | |
| | 1283.6115 | 1283.6945 | 0.083 | 65 | 60 | 70 | YSESVKDAQEK | | | |

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|-----|---------------|-----------|---------|-----|-----|-----|----------------|-----|--------|---|
| | 1298.7678 | 1298.7583 | -0.0095 | -7 | 168 | 178 | KLVILEGELER | 100 | 100 | |
| | 1308.6179 | 1308.6429 | 0.025 | 19 | 234 | 244 | EAETRAEFAER | | | |
| | 1332.639 | 1332.6398 | 0.0008 | 1 | 78 | 90 | ATDAEADVASLNR | | | |
| | 1343.6802 | 1343.6593 | -0.0209 | -16 | 38 | 48 | QLEEEQALQK | 49 | 99.254 | |
| | 1390.6042 | 1390.5861 | -0.0181 | -13 | 206 | 217 | SLMASEEEYSTK | | | M |
| | 1399.754 | 1399.738 | -0.016 | -11 | 91 | 101 | RIQLVEEELDR | 18 | 0 | |
| | 1460.734 | 1460.7249 | -0.0091 | -6 | 77 | 90 | KATDAEADVASLNR | | | |
| | 1488.7401 | 1488.7234 | -0.0167 | -11 | 78 | 91 | ATDAEADVASLNRR | | | |
| | 1727.8922 | 1727.8528 | -0.0394 | -23 | 92 | 105 | IQLVEEELDRAQER | | | |
| s16 | tropomyosin 1 | | | | | | | | | |
| | 846.4679 | 846.4445 | -0.0234 | -28 | 232 | 238 | LKEAETR | | | |
| | 847.4155 | 847.4174 | 0.0019 | 2 | 134 | 140 | AQKDEEK | | | |
| | 875.4468 | 875.4301 | -0.0167 | -19 | 206 | 213 | SLEAQA EK | | | |
| | 894.4679 | 894.4575 | -0.0104 | -12 | 162 | 168 | YEEVARK | | | |
| | 926.4326 | 926.4187 | -0.0139 | -15 | 153 | 160 | HIAEDADR | 19 | 0 | |
| | 989.4897 | 989.4675 | -0.0222 | -22 | 22 | 30 | AEQAEADKK | | | |
| | 1054.5276 | 1054.5078 | -0.0198 | -19 | 153 | 161 | HIAEDADRK | | | |
| | 1073.5586 | 1073.538 | -0.0206 | -19 | 13 | 21 | LDKENALDR | 30 | 47.467 | |
| | 1093.4943 | 1093.4987 | 0.0044 | 4 | 119 | 128 | AADESERGMK | | | |
| | 1120.519 | 1120.4998 | -0.0192 | -17 | 190 | 198 | CAELEELK | | | C |

| | | | | | | | | | | |
|-----|---------------------------------------|-----------|---------|-----|-----|-----|---------------|----|--------|---|
| | 1131.6078 | 1131.5668 | -0.041 | -36 | 141 | 149 | MEIQEIQLK | | | |
| | 1147.6028 | 1147.5601 | -0.0427 | -37 | 141 | 149 | MEIQEIQLK | 59 | 99.927 | M |
| | 1161.5997 | 1161.5745 | -0.0252 | -22 | 50 | 59 | LKATEDELDK | | | |
| | 1182.5525 | 1182.5349 | -0.0176 | -15 | 218 | 226 | EDKYEEEIK | | | |
| | 1186.6678 | 1186.6462 | -0.0216 | -18 | 169 | 178 | LVIIESDLER | 13 | 0 | |
| | 1243.6528 | 1243.6383 | -0.0145 | -12 | 92 | 101 | IQLVEEELDR | 44 | 97.474 | |
| | 1254.6073 | 1254.6493 | 0.042 | 33 | 150 | 160 | EAKHIAEDADR | | | |
| | 1301.6947 | 1301.6907 | -0.004 | -3 | 38 | 48 | QLEDELVSLQK | | | |
| | 1314.7627 | 1314.7462 | -0.0165 | -13 | 168 | 178 | KLVIIESDLER | 23 | 0 | |
| | 1381.6958 | 1381.7311 | 0.0353 | 26 | 206 | 217 | SLEAQAEKYSQK | | | |
| | 1399.754 | 1399.7229 | -0.0311 | -22 | 91 | 101 | RIQLVEEELDR | | | |
| | 1648.8098 | 1648.7523 | -0.0575 | -35 | 137 | 149 | DEEKMEIQEIQLK | | | M |
| s17 | myosin regulatory light polypeptide 9 | | | | | | | | | |
| | 1035.5139 | 1035.5563 | 0.0424 | 41 | 121 | 129 | ELLTTMGDR | | | |
| | 1051.5089 | 1051.5516 | 0.0427 | 41 | 121 | 129 | ELLTTMGDR | | | M |
| | 1228.6168 | 1228.6614 | 0.0446 | 36 | 90 | 100 | LNGTDPEDVIR | | | |
| | 1237.563 | 1237.6134 | 0.0504 | 41 | 32 | 41 | EAFNMIDQNR | 65 | 99.982 | |
| | 1246.5852 | 1246.6338 | 0.0486 | 39 | 148 | 157 | GNFNHYVEFTR | 79 | 100 | |
| | 1253.558 | 1253.6045 | 0.0465 | 37 | 32 | 41 | EAFNMIDQNR | | | M |
| | 1374.6802 | 1374.7338 | 0.0536 | 39 | 147 | 157 | KGNFNHYVEFTR | | | |

| | | | | | | | | | | |
|-----|----------------------------|-----------|--------|----|-----|-----|----------------------|-----|--------|------|
| | 1433.589 | 1433.6469 | 0.0579 | 40 | 130 | 140 | FTDEEVDEMYR | 89 | 100 | |
| | 1449.5839 | 1449.637 | 0.0531 | 37 | 130 | 140 | FTDEEVDEMYR | | | M |
| | 1449.5839 | 1449.637 | 0.0531 | 37 | 130 | 140 | FTDEEVDEMYR | 70 | 99.995 | M |
| | 2037.9257 | 2037.9882 | 0.0625 | 31 | 42 | 59 | DGFIDKEDLHDMLASMGK | | | M |
| | 2053.9207 | 2053.9773 | 0.0566 | 28 | 42 | 59 | DGFIDKEDLHDMLASMGK | | | M |
| | 2090.9851 | 2091.0574 | 0.0723 | 35 | 14 | 31 | ATSNVFAMFDQSQIQEFK | | | |
| | 2106.9802 | 2107.0405 | 0.0603 | 29 | 14 | 31 | ATSNVFAMFDQSQIQEFK | | | M |
| | 2365.0303 | 2365.1155 | 0.0852 | 36 | 101 | 120 | NAFACFDEEASGFIHEDHLR | 143 | 100 | C |
| s18 | Myosin light polypeptide 6 | | | | | | | | | |
| | 838.3611 | 838.398 | 0.0369 | 44 | 57 | 63 | SDEMNVK | | | M |
| | 995.5884 | 995.611 | 0.0226 | 23 | 111 | 119 | HVLVTLGEK | 68 | 99.993 | |
| | 1025.5051 | 1025.5345 | 0.0294 | 29 | 14 | 21 | EAFQLFDR | | | |
| | 1025.5051 | 1025.5345 | 0.0294 | 29 | 14 | 21 | EAFQLFDR | 60 | 99.949 | |
| | 1249.5841 | 1249.6246 | 0.0405 | 32 | 99 | 110 | EGNGTVMGAEIR | | | M |
| | 1341.629 | 1341.6757 | 0.0467 | 35 | 27 | 37 | ILYSQCGDVMR | | | C |
| | 1354.7325 | 1354.7665 | 0.034 | 25 | 38 | 50 | ALGQNPTNAEVLK | | | |
| | 1357.6239 | 1357.6592 | 0.0353 | 26 | 27 | 37 | ILYSQCGDVMR | 15 | 0 | C, M |
| | 1544.6864 | 1544.7332 | 0.0468 | 30 | 82 | 94 | DQGTIEDYVEGLR | 82 | 100 | |
| | 1738.8429 | 1738.8865 | 0.0436 | 25 | 95 | 110 | VFDKEGNGTVMGAEIR | | | M |

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|-----|------------|-----------|---------|-----|-----|-----|------------------------------|-----|--------|---|
| | 1786.8242 | 1786.8765 | 0.0523 | 29 | 80 | 94 | NKDQGTIEDYVEGLR | 146 | 100 | |
| | 1903.9987 | 1904.0371 | 0.0384 | 20 | 64 | 79 | VLD FEHFLPMLQTVAK | | | M |
| | 3312.4202 | 3312.4355 | 0.0153 | 5 | 120 | 148 | MTEEEVEMLVAGHEDSNGCINYEGERTR | | | C |
| s19 | Transgelin | | | | | | | | | |
| | 854.3825 | 854.412 | 0.0295 | 35 | 8 | 15 | GPSYGMSR | | | |
| | 870.3774 | 870.4062 | 0.0288 | 33 | 8 | 15 | GPSYGMSR | | | M |
| | 953.4575 | 953.4813 | 0.0238 | 25 | 103 | 111 | AAEDYGVTK | | | |
| | 994.4451 | 994.4675 | 0.0224 | 23 | 150 | 157 | GDPNWFMK | 62 | 99.968 | |
| | 1010.44 | 1010.4594 | 0.0194 | 19 | 150 | 157 | GDPNWFMK | | | M |
| | 1082.4636 | 1082.4938 | 0.0302 | 28 | 25 | 32 | YDEELEER | 63 | 99.975 | |
| | 1138.535 | 1138.5488 | 0.0138 | 12 | 150 | 158 | GDPNWFMKK | | | M |
| | 1203.6997 | 1203.6509 | -0.0488 | -41 | 51 | 60 | GRLGFQVWLK | | | |
| | 1204.697 | 1204.6351 | -0.0619 | -51 | 132 | 143 | TLMALGSLAVTK | | | |
| | 1210.5586 | 1210.5856 | 0.027 | 22 | 24 | 32 | KYDEELEER | 54 | 99.808 | |
| | 1220.6919 | 1220.6327 | -0.0592 | -48 | 132 | 143 | TLMALGSLAVTK | | | M |
| | 1221.6296 | 1221.6488 | 0.0192 | 16 | 93 | 102 | QMEQVAQFLK | | | |
| | 1237.6246 | 1237.64 | 0.0154 | 12 | 93 | 102 | QMEQVAQFLK | | | M |
| | 1244.6344 | 1244.6521 | 0.0177 | 14 | 82 | 92 | VPENPPSMVFK | 48 | 99.23 | |
| | 1260.6293 | 1260.6429 | 0.0136 | 11 | 82 | 92 | VPENPPSMVFK | 54 | 99.768 | M |
| | 1516.837 | 1516.8661 | 0.0291 | 19 | 68 | 81 | LVNSLYPDGSKPVK | 98 | 100 | |

| | | | | | | | | | | |
|-----|------------|-----------|---------|----|-----|-----|--------------------|-----|--------|---|
| | 1530.7145 | 1530.7407 | 0.0262 | 17 | 112 | 124 | TDMFQTVDLFEGK | 98 | 100 | |
| | 1546.7095 | 1546.7285 | 0.019 | 12 | 112 | 124 | TDMFQTVDLFEGK | 82 | 100 | M |
| | 2127.0474 | 2127.1057 | 0.0583 | 27 | 33 | 50 | LVEWIVMQCGPDVGRPDR | | | C |
| s20 | galectin-1 | | | | | | | | | |
| | 891.5298 | 891.5539 | 0.0241 | 27 | 29 | 36 | SFLLNLGK | | | |
| | 968.4724 | 968.4964 | 0.024 | 25 | 100 | 107 | LPDGYEFK | 58 | 99.922 | |
| | 1015.553 | 1015.5757 | 0.0227 | 22 | 19 | 28 | VRGEVAADAK | | | |
| | 1060.4807 | 1060.5054 | 0.0247 | 23 | 64 | 73 | DAGAWGAEQR | 81 | 100 | |
| | 1482.7377 | 1482.7252 | -0.0125 | -8 | 100 | 111 | LPDGYEFKFPNR | | | |
| | 1514.6805 | 1514.7112 | 0.0307 | 20 | 37 | 48 | DDNNLCLHFNPR | 96 | 100 | C |
| | 1675.7858 | 1675.8141 | 0.0283 | 17 | 49 | 63 | FNAHGDVNTIVCNSK | 104 | 100 | C |
| | 1724.8854 | 1724.9102 | 0.0248 | 14 | 112 | 127 | LNLEAINYLSAGGDFK | 84 | 100 | |
| | 1972.0103 | 1972.0652 | 0.0549 | 28 | 1 | 18 | ACGLVASNLNLKPGECL | | | C |

*M means oxidation of methionine; C means carbamidomethylation of cysteine.

Table S2. Peptide information of the differential expressed proteins in the small intestine of the calves without or with colostrum by mass spectrometry

| No. | Peptide Information | | | | | | | Ion Score | C. I. % | Modification* |
|-----|---------------------|-------------|----------|-----------|------------|----------|------------------------|-----------|---------|---------------|
| | Calc. Mass | Obsrv. Mass | \pm da | \pm ppm | Start Seq. | End Seq. | Sequence | | | |
| d1 | Alpha-actin-2 | | | | | | | | | |
| | 923.6 | 923.6 | -0.014 | -15 | 331 | 338 | IIAPPERK | | | |
| | 998.5 | 998.5 | 0.043 | 43 | 186 | 193 | DLTDYLMK | | | |
| | 1014 | 1015 | 0.041 | 40 | 186 | 193 | DLTDYLMK | | | M |
| | 1131 | 1131 | 0.043 | 38 | 199 | 208 | GYSFVTTAER | 62 | 99.97 | |
| | 1162 | 1162 | 0.03 | 26 | 318 | 328 | EITALAPSTMK | | | |
| | 1501 | 1501 | 0.041 | 27 | 362 | 374 | QEYDEAGPSIVHR | 59 | 99.95 | |
| | 1791 | 1791 | 0.057 | 32 | 241 | 256 | SYELPDGQVITIGNER | 146 | 100 | |
| | 2228 | 2228 | 0.076 | 34 | 294 | 314 | DLYANNVLSGGTTMYPGIADR | 92 | 100 | |
| | 2244 | 2244 | 0.061 | 27 | 294 | 314 | DLYANNVLSGGTTMYPGIADR | | | M |
| | 2372 | 2372 | 0.064 | 27 | 293 | 314 | KDLYANNVLSGGTTMYPGIADR | | | M |
| d2 | beta-lactoglobulin | | | | | | | | | |
| | 837.5 | 837.5 | 0.021 | 25 | 131 | 137 | ALPMHIR | | | |
| | 853.5 | 853.5 | 0.017 | 20 | 131 | 137 | ALPMHIR | | | M |
| | 903.6 | 903.6 | 0.011 | 13 | 65 | 72 | TKIPAVFK | | | |

| | | | | | | | | | | |
|----|--------------------|-------|--------|-----|-----|-----|-------------------------|-----|-------|------|
| | 916.5 | 916.5 | 0.013 | 14 | 73 | 80 | IDALNENK | | | |
| | 1066 | 1066 | 0.011 | 11 | 81 | 89 | VLVLDTDYK | | | |
| | 1179 | 1179 | 0.015 | 13 | 50 | 58 | WENDECAQK | 69 | 99.99 | C |
| | 1194 | 1194 | 0.009 | 7 | 81 | 90 | VLVLDTDYKK | 56 | 99.89 | |
| | 1246 | 1246 | 0.009 | 7 | 114 | 124 | TPEVDDEALEK | 63 | 99.98 | |
| | 1308 | 1308 | 0.018 | 13 | 50 | 59 | WENDECAQKK | | | C |
| | 1636 | 1636 | 9E-04 | 1 | 114 | 127 | TPEVDDEALEKFDK | | | |
| | 1716 | 1716 | 0.003 | 2 | 138 | 151 | LSFNPTQLEEQCHI | 123 | 100 | C |
| | 2313 | 2313 | 0.003 | 1 | 30 | 49 | VYVEELKPTPEGDLEILLQK | 111 | 100 | |
| | 2846 | 2846 | 0.029 | 10 | 91 | 113 | YLLFCMENSAEPEQSLVCQCLVR | 30 | 58.53 | C |
| | 2862 | 2862 | 0.025 | 9 | 91 | 113 | YLLFCMENSAEPEQSLVCQCLVR | 119 | 100 | C, M |
| d3 | lactoglobulin beta | | | | | | | | | |
| | 853.5 | 853.5 | 0.021 | 24 | 142 | 148 | ALPMHIR | | | M |
| | 903.6 | 903.6 | 0.014 | 15 | 76 | 83 | TKIPAVFK | | | |
| | 916.5 | 916.5 | -0.015 | -16 | 84 | 91 | LDAINENK | | | |
| | 1066 | 1066 | 0.014 | 13 | 92 | 100 | VLVLDTDYK | | | |
| | 1194 | 1194 | 0.015 | 13 | 92 | 101 | VLVLDTDYKK | 56 | 99.88 | |
| | 1246 | 1246 | 0.021 | 17 | 125 | 135 | TPEVDDEALEK | | | |
| | 1588 | 1588 | -0.115 | -72 | 1 | 14 | LIVTQTMKGLDIQK | | | |
| | 1636 | 1636 | 0.02 | 12 | 125 | 138 | TPEVDDEALEKFDK | | | |

| | | | | | | | | | | | |
|----|--|-------|--------|-----|-----|-----|-------------------------------|-----|-------|--|---|
| | 1716 | 1716 | 0.021 | 12 | 149 | 162 | LSFNPTLQEEQCHI | | | | C |
| | 2313 | 2313 | 0.022 | 10 | 41 | 60 | VYVEELKPTPEGDLEILLQK | 140 | 100 | | |
| | 2707 | 2707 | -0.157 | -58 | 15 | 40 | VAGTWYSLAMAASDISLLDAQSAPLR | | | | |
| | 2846 | 2846 | 0.037 | 13 | 102 | 124 | YLLFCMENSAEPEQSLVCQCLVR | | | | C |
| d4 | Immunoglobulin light chain, lambda gene cluster | | | | | | | | | | |
| | 820.4 | 820.4 | -0.025 | -31 | 173 | 180 | ADGSTITR | | | | |
| | 1026 | 1025 | -0.028 | -27 | 66 | 74 | TLIYGDTSR | 2 | 0 | | |
| | 1679 | 1679 | -0.06 | -36 | 195 | 209 | YAASSYLSLTSSDWK | 105 | 100 | | |
| | 1708 | 1708 | -0.058 | -34 | 66 | 81 | TLIYGDTSRASGVPDR | | | | |
| | 1742 | 1742 | -0.047 | -27 | 212 | 227 | GSYSCEVTHEGSTVTK | 55 | 99.82 | | C |
| | 1957 | 1957 | -0.053 | -27 | 210 | 227 | SKGSYSCEVTHEGSTVTK | | | | C |
| | 3043 | 3043 | -0.06 | -20 | 37 | 65 | VSITCSGSSSNVGNQYVSWYQLIPGSAPR | | | | C |
| d5 | immunoglobulin gamma 1 heavy chain constant region,partial | | | | | | | | | | |
| | 1170 | 1170 | -0.053 | -45 | 188 | 197 | IQHQDWTGGK | | | | |
| | 1302 | 1302 | -0.036 | -28 | 203 | 214 | VHNEGLPAPIVR | 57 | 99.78 | | |
| | 1827 | 1827 | -0.087 | -48 | 225 | 240 | EPQVYVLAPPQEELSK | | | | |
| | 2153 | 2153 | -0.067 | -31 | 273 | 291 | YGTTPPQLDADSSYFLYSK | | | | |
| | 2782 | 2782 | -0.098 | -35 | 129 | 154 | DTLTISGTPEVTCVVVDVGHDDPEVK | | | | C |
| d6 | serum albumin | | | | | | | | | | |

| | | | | | | | | | | |
|----|------------------------------|-------|--------|-----|-----|-----|-------------------|-----|-------|---|
| | 818.4 | 818.5 | 0.034 | 42 | 431 | 437 | ATEEQLK | | | |
| | 898.5 | 898.5 | 0.039 | 43 | 352 | 358 | LCVLHEK | | | C |
| | 1015 | 1015 | 0.037 | 36 | 418 | 426 | QTALVELLK | | | |
| | 1108 | 1108 | 0.04 | 36 | 457 | 466 | EACFAVEGPK | | | C |
| | 1138 | 1139 | 0.045 | 40 | 368 | 376 | CCTESLVNR | 60 | 99.96 | C |
| | 1143 | 1143 | 0.041 | 35 | 417 | 426 | KQTALVELLK | | | |
| | 1146 | 1146 | -0.048 | -42 | 105 | 114 | AWSVARLSQK | | | |
| | 1166 | 1167 | 0.091 | 78 | 329 | 337 | CCTKPESER | | | C |
| | 1400 | 1400 | 0.042 | 30 | 438 | 449 | TVMENFVAFVDK | 57 | 99.9 | |
| | 1416 | 1416 | 0.042 | 30 | 438 | 449 | TVMENFVAFVDK | 79 | 100 | M |
| | 1881 | 1881 | 0.063 | 33 | 377 | 392 | RPCFSALTPDETYVPK | 119 | 100 | C |
| | 1908 | 1908 | 0.052 | 27 | 398 | 413 | LFTFHADICTLPDTEK | | | C |
| | 1909 | 1909 | -0.006 | -3 | 37 | 52 | SHPQFFAPLLLYYANK | | | |
| | 1928 | 1928 | 0.046 | 24 | 450 | 466 | CCAADDKEACFAVEGPK | 132 | 100 | C |
| | 1942 | 1942 | -0.07 | -36 | 150 | 166 | ADLAKYICDNQDTISSK | | | C |
| d7 | Superoxide dismutase [Cu-Zn] | | | | | | | | | |
| | 1002 | 1002 | 0.03 | 30 | 142 | 151 | LACGVIGIAK | 77 | 100 | C |
| | 1024 | 1025 | 0.049 | 47 | 69 | 77 | HGGPKDEER | | | |
| | 1226 | 1226 | 0.042 | 34 | 78 | 89 | HVGD LGNVTADK | 59 | 99.94 | |

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|----|--------|-------|-------|----|-----|-----|-----------------|----|-------|---|
| | 1456 | 1456 | 0.044 | 30 | 10 | 23 | GDGPVQGTIHFEAK | 80 | 100 | |
| | 1465 | 1465 | 0.116 | 79 | 127 | 141 | GGNEESTKTGNAGSR | | | |
| | 1497 | 1497 | 0.049 | 33 | 114 | 126 | TMVVHEKPDDLGR | 48 | 99.22 | |
| | 1513 | 1513 | 0.039 | 26 | 114 | 126 | TMVVHEKPDDLGR | 40 | 94.2 | M |
| d8 | desmin | | | | | | | | | |
| | 884.5 | 884.5 | 0.029 | 32 | 119 | 125 | FANYIEK | | | |
| | 1002 | 1002 | 0.024 | 24 | 319 | 325 | QEMMEYR | | | M |
| | 1003 | 1003 | 0.024 | 24 | 213 | 222 | ADVDAATLAR | | | |
| | 1017 | 1017 | 0.023 | 22 | 59 | 70 | TSGGAGGLGALR | | | |
| | 1018 | 1018 | 0.031 | 31 | 319 | 325 | QEMMEYR | | | M |
| | 1116 | 1116 | 0.026 | 23 | 110 | 118 | VELQELNDR | 34 | 81.96 | |
| | 1243 | 1243 | 0.025 | 20 | 164 | 173 | RQVEVLTNQR | | | |
| | 1251 | 1251 | 0.027 | 21 | 151 | 160 | VAEIYEEELR | 54 | 99.8 | |
| | 1264 | 1264 | 0.03 | 24 | 202 | 212 | EAAENNLAAFR | | | |
| | 1269 | 1269 | 0.026 | 20 | 288 | 297 | NISEAEEWYK | | | |
| | 1309 | 1309 | 0.075 | 57 | 340 | 350 | GTNDSLMRQMR | | | |
| | 1406 | 1406 | 0.012 | 8 | 229 | 240 | IESLNEEIAFLK | | | |
| | 1484 | 1484 | 0.034 | 23 | 288 | 299 | NISEAEEWYKSK | | | |
| | 1562 | 1562 | 0.027 | 17 | 228 | 240 | RIESLNEEIAFLK | 96 | 100 | |

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|----|---------------|-------|-------|----|-----|-----|-----------------------------------|-----|------|
| | 1588 | 1588 | 0.028 | 18 | 106 | 118 | TNEKVELQELNDR | | |
| | 1606 | 1606 | 0.013 | 8 | 2 | 15 | SQAYSSSQRVSSYR | | |
| | 1674 | 1674 | 0.031 | 18 | 128 | 142 | FLEQQNAALAAEVNR | 135 | 100 |
| | 1700 | 1700 | 0.003 | 2 | 176 | 189 | VDVERDNLLDDLQR | | |
| | 2118 | 2118 | 0.039 | 18 | 17 | 37 | TFGGAPSFPLGSPLSSPVFPR | 117 | 100 |
| | 2245 | 2245 | 0.04 | 18 | 194 | 212 | LQEEIQLKEEAENNLAAFR | 142 | 100 |
| | 2274 | 2274 | 0.027 | 12 | 16 | 37 | RTFGGAPSFPLGSPLSSPVFPR | | |
| | 2900 | 2900 | 0.064 | 22 | 79 | 105 | VPSSYGAGELLDLDFSLADAVNQEFLTT R | 28 | 27.2 |
| | 3116 | 3116 | 0.075 | 24 | 249 | 275 | ELQAQLQEQQVQVEMDMSKPDLTAAALR | | M |
| d9 | alpha-enolase | | | | | | | | |
| | 800.4 | 800.4 | 0.023 | 29 | 257 | 262 | YDLDFK | | |
| | 815.5 | 815.5 | 0.008 | 9 | 222 | 228 | EALELLK | | |
| | 958.5 | 958.5 | 0.004 | 4 | 82 | 89 | LNVVEQEK | | |
| | 1008 | 1008 | 0.011 | 11 | 336 | 343 | SCNCLLLK | | C |
| | 1073 | 1073 | 0.016 | 15 | 254 | 262 | SGKYDLDFK | | |
| | 1144 | 1144 | 0.013 | 11 | 184 | 193 | IGAEVYHNLK | 71 | 100 |
| | 1391 | 1391 | 0.006 | 4 | 16 | 28 | GNPTVEVDLFTAK | | |
| | 1440 | 1440 | 0.007 | 5 | 270 | 281 | YITPDELANLYK | | |

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|----|---------------------------------------|-------|--------|-----|-----|-----|------------------------|-----|-------|---|
| | 1542 | 1542 | 0.012 | 8 | 359 | 372 | LAQSNQWVVMVSHR | | | |
| | 1557 | 1557 | 0.015 | 10 | 240 | 253 | VVIGMDVAASEFYR | 64 | 99.98 | |
| | 1573 | 1573 | 0.004 | 2 | 240 | 253 | VVIGMDVAASEFYR | 86 | 100 | M |
| | 1631 | 1631 | -0.062 | -38 | 180 | 193 | EAMRIGAEVYHNLK | | | |
| | 1634 | 1634 | -0.005 | -3 | 344 | 358 | VNQIGSVTESLQACK | | | C |
| | 1669 | 1669 | 0.018 | 11 | 90 | 103 | IDKLMIEMDGTENK | | | M |
| | 1805 | 1805 | 0.007 | 4 | 33 | 50 | AAVPSGASTGIYEALELR | 178 | 100 | |
| | 1961 | 1961 | -0.001 | -1 | 203 | 221 | DATNVGDEGGFAPNILENK | | | |
| | 1982 | 1982 | 0.004 | 2 | 163 | 179 | LAMQEFMILPVGAENFR | 69 | 99.99 | M |
| | 1998 | 1998 | -0.003 | -1 | 163 | 179 | LAMQEFMILPVGAENFR | 40 | 95.02 | M |
| | 2033 | 2033 | -0.011 | -5 | 307 | 326 | FTASAGIQVVGDDLTVTNPK | | | |
| | 2277 | 2277 | 0.029 | 13 | 33 | 54 | AAVPSGASTGIYEALELRDNDK | | | |
| | 2353 | 2353 | 0.003 | 1 | 373 | 394 | SGETEDTFIADLVVGLCTGQIK | | | C |
| | 2582 | 2582 | -0.009 | -3 | 286 | 306 | DYPVVSIEDPFDQDDWEAWQK | | | |
| k1 | protein disulfide-isomerase precursor | | | | | | | | | |
| | 860.4 | 860.4 | 0.022 | 26 | 312 | 318 | EECPAVR | | | C |
| | 910.4 | 910.5 | 0.015 | 17 | 447 | 454 | FFPASADR | 50 | 99.35 | |
| | 928.5 | 928.5 | 0.01 | 10 | 439 | 446 | VHSFPTLK | 42 | 96.19 | |
| | 962.5 | 962.5 | 0.014 | 14 | 341 | 347 | ITEFCHR | 33 | 67.59 | C |

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|----|---------------------|-------|--------|-----|-----|-----|----------------------|----|-------|---|
| | 966.6 | 966.5 | -0.017 | -18 | 303 | 310 | ILEFFGLK | | | |
| | 970.5 | 970.5 | 0.005 | 5 | 404 | 411 | QLAPIWDK | | | |
| | 988.5 | 988.5 | 0.004 | 4 | 311 | 318 | KEECPAVR | 28 | 0 | C |
| | 1003 | 1003 | -0.036 | -36 | 72 | 80 | LKAEGSEIR | | | |
| | 1207 | 1207 | 5E-04 | 0 | 319 | 328 | LITLEEEMTK | | | |
| | 1212 | 1212 | -0.021 | -17 | 106 | 116 | FFKNGDTASPK | | | |
| | 1223 | 1223 | 0.006 | 5 | 319 | 328 | LITLEEEMTK | | | M |
| | 1228 | 1228 | 0.008 | 6 | 378 | 387 | NFEEVAFDEK | 72 | 100 | |
| | 1310 | 1310 | 0.031 | 24 | 427 | 438 | MDSTANEVEAVK | | | M |
| | 1356 | 1356 | 0.004 | 3 | 378 | 388 | NFEEVAFDEKK | | | |
| | 1410 | 1410 | 0.006 | 4 | 329 | 340 | YKPESDELTAEK | | | |
| | 1425 | 1425 | -0.011 | -7 | 198 | 209 | YQLDKDGVVLFK | | | |
| | 1730 | 1730 | 0 | 0 | 412 | 426 | LGETYKDHENIVIAK | 62 | 99.96 | |
| | 1820 | 1820 | -0.051 | -28 | 439 | 454 | VHSFPTLKFFPASADR | | | |
| | 1834 | 1834 | 0.01 | 5 | 288 | 302 | ILFIFIDSDHTDNQR | | | |
| | 1965 | 1965 | -0.006 | -3 | 233 | 249 | HNQLPLVIEFTEQTAPK | | | |
| | 2420 | 2420 | -0.004 | -2 | 353 | 372 | IKPHLMSQELPDDWDKQPVK | | | M |
| k2 | hemoglobin, gamma 2 | | | | | | | | | |
| | 1102 | 1102 | 0.012 | 11 | 19 | 29 | VDEVGGEALGR | | | |
| | 1127 | 1127 | 0.005 | 4 | 95 | 103 | LHVDPENFR | 76 | 100 | |

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|----|------------------------|-------|--------|-----|-----|-----|---------------------|-----|-------|---|
| | 1168 | 1168 | 0.005 | 4 | 66 | 75 | VLDSFCEGLK | | | C |
| | 1208 | 1208 | 0.006 | 5 | 132 | 143 | VVTGVANALAHR | 86 | 100 | |
| | 1266 | 1266 | 0.009 | 7 | 104 | 115 | LLGNVLVVVLAR | | | |
| | 1275 | 1275 | 0.007 | 6 | 30 | 39 | LLVVYPWTQR | | | |
| | 1296 | 1296 | 0.023 | 18 | 65 | 75 | KVLDSFCEGLK | | | C |
| | 1329 | 1329 | 0.005 | 4 | 17 | 29 | VKVDEVGGEALGR | 112 | 100 | |
| | 1435 | 1435 | 0.013 | 9 | 82 | 94 | GAFASLSELHCDK | | | C |
| | 1702 | 1702 | 0.016 | 9 | 117 | 131 | FGSEFSPELQASFQK | 84 | 100 | |
| | 1858 | 1858 | 6E-04 | 0 | 116 | 131 | RFGSEFSPELQASFQK | 82 | 100 | |
| | 1880 | 1880 | -0.062 | -33 | 66 | 81 | VLDSFCEGLKQLDDLK | | | C |
| | 2015 | 2015 | -0.01 | -5 | 40 | 58 | FFESFGDLSSADAILGNPk | | | |
| k3 | hemoglobin alpha chain | | | | | | | | | |
| | 818.4 | 818.5 | 0.024 | 29 | 94 | 100 | VDPVNFK | | | |
| | 1072 | 1072 | 0.025 | 23 | 33 | 41 | MFLSFPTTK | 60 | 99.96 | |
| | 1088 | 1088 | 0.018 | 16 | 92 | 100 | LRVDPVNFK | 41 | 96.25 | |
| | 1102 | 1102 | -0.014 | -12 | 2 | 12 | VLSAADKGNVK | | | |
| | 1233 | 1233 | -0.035 | -29 | 1 | 12 | MVLSAADKGNVK | | | |
| | 1530 | 1530 | 0.021 | 14 | 18 | 32 | VGGHAAEYGAEALER | 108 | 100 | |
| | 1572 | 1572 | -0.074 | -47 | 129 | 142 | FLASVSTVLTSKYR | | | |

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|----|--------------------|------|--------|-----|-----|-----|------------------------|-----|-------|---|
| | 1834 | 1834 | 0.025 | 13 | 42 | 57 | TYFPFDLSHGSAQVK | 117 | 100 | |
| | 2367 | 2367 | 0.039 | 16 | 70 | 91 | AVEHLDDLPGALSELSDLHAHK | 180 | 100 | |
| k4 | Annexin A2 | | | | | | | | | |
| | 1085 | 1085 | -0.014 | -13 | 149 | 157 | GMYKTDLEK | | | |
| | 1086 | 1087 | 0.021 | 19 | 29 | 37 | AYTNFDAER | 64 | 99.98 | |
| | 1101 | 1101 | -0.001 | -1 | 149 | 157 | GMYKTDLEK | | | M |
| | 1107 | 1107 | -0.049 | -44 | 296 | 304 | SEVDMLKIR | | | M |
| | 1112 | 1112 | 0.016 | 15 | 69 | 77 | QDIAFAYQR | 74 | 100 | |
| | 1212 | 1212 | 0.029 | 24 | 158 | 168 | DIVSDTSGDFR | 99 | 100 | |
| | 1223 | 1223 | 0.025 | 21 | 105 | 115 | TPAQYDASELK | | | |
| | 1245 | 1245 | 0.021 | 17 | 136 | 145 | TNQELQEINR | 85 | 100 | |
| | 1340 | 1340 | 0.028 | 21 | 158 | 169 | DIVSDTSGDFRK | | | |
| | 1543 | 1543 | 0.03 | 19 | 50 | 63 | GVDEVTIVNILTNR | 125 | 100 | |
| | 1772 | 1772 | 0.004 | 2 | 48 | 63 | TKGVDEVTIVNILTNR | | | |
| | 1778 | 1778 | 0.023 | 13 | 120 | 135 | GLGTDEDSLIEIICSR | 124 | 100 | C |
| | 1798 | 1798 | 0.032 | 18 | 153 | 168 | TDLEKDIVSDTSGDFR | | | |
| | 1845 | 1845 | 0.013 | 7 | 11 | 28 | LSLEGDHSTPPSAYGSVK | 119 | 100 | |
| | 2155 | 2155 | 0.044 | 20 | 29 | 47 | AYTNFDAERDALNIETAIK | | | |
| k5 | lactoglobulin beta | | | | | | | | | |

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|----|---------------------------|-------|--------|-----|-----|-----|------------------------|-----|-------|--|-----|
| | 853.5 | 853.5 | 0.017 | 20 | 142 | 148 | ALPMHIR | | | | M |
| | 903.6 | 903.6 | 0.011 | 13 | 76 | 83 | TKIPAVFK | | | | |
| | 916.5 | 916.5 | 0.013 | 14 | 84 | 91 | LDAINENK | | | | |
| | 949.5 | 949.5 | 0.01 | 10 | 1 | 8 | LIVTQTMK | | | | M |
| | 1179 | 1179 | 0.015 | 13 | 61 | 69 | WENDECAQK | 69 | 99.99 | | C |
| | 1194 | 1194 | 0.009 | 7 | 92 | 101 | VLVLDTDYKK | 56 | 99.89 | | |
| | 1246 | 1246 | 0.009 | 7 | 125 | 135 | TPEVDDEALEK | 63 | 99.98 | | |
| | 1308 | 1308 | 0.018 | 13 | 61 | 70 | WENDECAQKK | | | | C |
| | 1636 | 1636 | 9E-04 | 1 | 125 | 138 | TPEVDDEALEKFDK | | | | |
| | 1716 | 1716 | 0.003 | 2 | 149 | 162 | LSFNPTLQEEQCHI | 98 | 100 | | C |
| | 2313 | 2313 | 0.003 | 1 | 41 | 60 | VYVEELKPTPEGDLEILLQK | 111 | 100 | | |
| | 2862 | 2862 | 0.025 | 9 | 102 | 124 | YLLFCMENSAEPEQSLVCQLVR | 119 | 100 | | C,M |
| k6 | Retinol-binding protein 2 | | | | | | | | | | |
| | 861.4 | 861.4 | 0.013 | 15 | 109 | 115 | QWVEGDK | | | | |
| | 1022 | 1022 | 0.015 | 15 | 23 | 31 | ALDIDFATR | 55 | 99.84 | | |
| | 1025 | 1025 | -0.016 | -15 | 33 | 41 | IALHLTQTK | | | | |
| | 1150 | 1150 | -0.053 | -46 | 23 | 32 | ALDIDFATRK | | | | |
| | 1153 | 1153 | 0.012 | 10 | 32 | 41 | KIALHLTQTK | 70 | 100 | | |
| | 1193 | 1193 | 0.014 | 12 | 42 | 51 | IIEQDGDKFK | 72 | 100 | | |
| | 1233 | 1233 | 0.021 | 17 | 106 | 115 | GWKQWVEGDK | | | | |

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|----|--|-------|-------|----|-----|-----|---------------------|-----|-------|---|
| | 1627 | 1627 | 0.02 | 12 | 116 | 128 | LYLELTCGDQVCR | 100 | 100 | C |
| k7 | fatty acid-binding protein, intestinal | | | | | | | | | |
| | 881.5 | 881.5 | 0.03 | 34 | 31 | 38 | LAAHDNLK | | | |
| | 1010 | 1010 | 0.025 | 25 | 30 | 38 | KLAAHDNLK | | | |
| | 1016 | 1016 | 0.023 | 22 | 39 | 47 | LIITQEGNK | 34 | 80.1 | |
| | 1167 | 1167 | 0.038 | 32 | 9 | 17 | VDRNENYEK | 34 | 80.46 | |
| | 1187 | 1187 | 0.035 | 29 | 97 | 107 | LDNGNALNTR | | | |
| | 1195 | 1195 | 0.047 | 39 | 2 | 11 | AFDGTWKVDR | | | |
| | 1202 | 1202 | 0.046 | 39 | 48 | 57 | FTVKESSTFR | | | |
| | 1296 | 1296 | 0.008 | 6 | 18 | 28 | FMEKMGINVVK | | | |
| | 1326 | 1326 | 0.1 | 76 | 1 | 11 | MAFDGTWKVDR | | | |
| | 1343 | 1343 | 0.031 | 23 | 96 | 107 | RLDNGNALNTR | | | |
| | 2117 | 2117 | 0.024 | 11 | 108 | 126 | EIIGGEMVQTYTYEGVEAK | | | |
| k8 | Superoxide dismutase [Cu-Zn] | | | | | | | | | |
| | 1002 | 1002 | 0.03 | 30 | 142 | 151 | LACGVIGIAK | 77 | 100 | C |
| | 1024 | 1025 | 0.049 | 47 | 69 | 77 | HGGPKDEER | | | |
| | 1226 | 1226 | 0.042 | 34 | 78 | 89 | HVGDLGNVTADK | 59 | 99.94 | |
| | 1456 | 1456 | 0.044 | 30 | 10 | 23 | GDGPVQGTIHFEAK | 80 | 100 | |
| | 1465 | 1465 | 0.116 | 79 | 127 | 141 | GGNEESTKTGNAGSR | | | |

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|-----|--|-------|--------|-----|-----|-----|---------------------|----|-------|---|
| | 1497 | 1497 | 0.049 | 33 | 114 | 126 | TMVVHEKPDDLGR | 48 | 99.22 | |
| | 1513 | 1513 | 0.039 | 26 | 114 | 126 | TMVVHEKPDDLGR | 40 | 94.2 | M |
| k9 | Immunoglobulin light chain, lambda gene cluster | | | | | | | | | |
| | 820.4 | 820.4 | -0.02 | -25 | 172 | 179 | ADGSTITR | | | |
| | 1521 | 1521 | -0.073 | -48 | 172 | 185 | ADGSTITRNVETTR | | | |
| | 1679 | 1679 | -0.061 | -36 | 194 | 208 | YAASSYLSLTSSDWK | 77 | 100 | |
| | 1742 | 1742 | -0.053 | -30 | 211 | 226 | GSYSCEVTHEGSTVTK | 96 | 100 | C |
| | 1957 | 1957 | -0.048 | -25 | 209 | 226 | SKGSYSCEVTHEGSTVTK | 33 | 77.62 | C |
| | 2014 | 2014 | -0.075 | -37 | 133 | 151 | SPPSVTLFPPSTEELNGNK | | | |
| k10 | Immunoglobulin light chain, lambda gene cluster | | | | | | | | | |
| | 1236 | 1236 | -0.054 | -44 | 75 | 86 | ASGVPDRFSGSR | | | |
| | 1521 | 1521 | -0.073 | -48 | 173 | 186 | ADGSTITRNVETTR | | | |
| | 1679 | 1679 | -0.061 | -36 | 195 | 209 | YAASSYLSLTSSDWK | 77 | 100 | |
| | 1742 | 1742 | -0.053 | -30 | 212 | 227 | GSYSCEVTHEGSTVTK | 96 | 100 | C |
| | 1957 | 1957 | -0.048 | -25 | 210 | 227 | SKGSYSCEVTHEGSTVTK | 33 | 77.62 | C |
| | 2014 | 2014 | -0.075 | -37 | 134 | 152 | SPPSVTLFPPSTEELNGNK | | | |
| k11 | Ig heavy chain precursor | | | | | | | | | |
| | 1170 | 1170 | -0.053 | -45 | 329 | 338 | IQHQDWTGGK | | | |
| | 1302 | 1302 | -0.036 | -28 | 344 | 355 | VHNEGLPAPIVR | 57 | 99.78 | |

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|-----|----------------------------------|-------|--------|-----|-----|-----|----------------------------|----|-------|------|
| | 1827 | 1827 | -0.087 | -48 | 366 | 381 | EPQVYVLAPPQEELSK | | | |
| | 2112 | 2112 | -0.076 | -36 | 296 | 313 | FSWFVDDVEVNTATTKPR | 46 | 97.08 | |
| | 2153 | 2153 | -0.067 | -31 | 414 | 432 | YGTTPPQLDADSSYFLYSK | | | |
| | 2782 | 2782 | -0.098 | -35 | 270 | 295 | DTLTISGTPEVTCVVVDVGHDDPEVK | | | C |
| k12 | IgG1 heavy chain constant region | | | | | | | | | |
| | 1170 | 1170 | -0.038 | -32 | 188 | 197 | IQHQDWTGGK | 74 | 100 | |
| | 1174 | 1174 | 0.023 | 19 | 173 | 181 | EEQFNSTYR | | | |
| | 1286 | 1286 | -0.022 | -17 | 8 | 18 | VYPLSSCCGDK | | | C |
| | 1302 | 1302 | -0.039 | -30 | 203 | 214 | VHNEGLPAPIVR | 46 | 98.74 | |
| | 1590 | 1590 | -0.1 | -63 | 201 | 214 | CKVHNEGLPAPIVR | | | C |
| | 2112 | 2112 | -0.063 | -30 | 155 | 172 | FSWFVDDVEVNTATTKPR | 51 | 99.62 | |
| | 2782 | 2782 | -0.114 | -41 | 129 | 154 | DTLTISGTPEVTCVVVDVGHDDPEVK | | | C |
| | 3064 | 3064 | -0.104 | -34 | 297 | 321 | NSWQEGDTYTCVVMHEALHNHYTQK | | | C, M |
| h1 | Tropomyosin-3 | | | | | | | | | |
| | 832.4 | 832.4 | -0.066 | -80 | 98 | 104 | ALKDEEK | | | |
| | 861.4 | 861.5 | 0.04 | 46 | 163 | 169 | LMDQNLK | | | |
| | 874.4 | 874.5 | 0.045 | 52 | 34 | 40 | EVEGERR | | | |
| | 894.5 | 894.5 | 0.044 | 49 | 126 | 132 | YEEVARK | | | |
| | 936.4 | 936.5 | 0.045 | 48 | 156 | 162 | EMDEQIR | | | M |
| | 940.4 | 940.5 | 0.04 | 43 | 117 | 124 | HIAEEADR | | | |

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|-------|-------|--------|----|-----|-----|----------------|----|-------|------|
| 962.5 | 962.5 | -0.008 | -8 | 90 | 97 | GMKVIENR | | | M |
| 1069 | 1069 | 0.045 | 42 | 117 | 125 | HIAEEADRK | | | |
| 1072 | 1073 | 0.048 | 45 | 229 | 236 | EEHLCTQR | | | C |
| 1093 | 1094 | 0.074 | 68 | 83 | 92 | AADESERGMK | | | |
| 1116 | 1116 | 0.034 | 31 | 31 | 39 | LQREVEGER | | | |
| 1132 | 1132 | 0.009 | 8 | 105 | 113 | MELQEIQLK | | | |
| 1150 | 1150 | -0.005 | -4 | 1 | 11 | MAGITTIEAVK | | | M |
| 1157 | 1157 | 0.046 | 40 | 133 | 142 | LVIIEGDLER | 43 | 98.03 | |
| 1183 | 1183 | 0.049 | 42 | 182 | 190 | EDKYEEEIK | | | |
| 1190 | 1190 | 0.046 | 39 | 216 | 225 | TIDDLEDKLK | | | |
| 1244 | 1244 | 0.049 | 39 | 56 | 65 | IQLVEEELDR | 68 | 99.99 | |
| 1253 | 1253 | 0.047 | 37 | 154 | 162 | CREMDEQIR | | | C, M |
| 1269 | 1269 | 0.02 | 16 | 114 | 124 | EAKHIAEEADR | | | |
| 1285 | 1285 | 0.048 | 37 | 132 | 142 | KLVIIEGDLER | 97 | 100 | |
| 1317 | 1317 | 0.054 | 41 | 43 | 54 | EQAEAEVASLNR | 64 | 99.98 | |
| 1400 | 1400 | 0.05 | 36 | 55 | 65 | RIQLVEEELDR | 43 | 97.68 | |
| 1462 | 1462 | 0.069 | 47 | 226 | 236 | CTKEEHLCTQR | | | C |
| 1476 | 1476 | 0.064 | 43 | 105 | 116 | MELQEIQLKEAK | | | M |
| 1544 | 1544 | 0.057 | 37 | 41 | 54 | AREQAEAEVASLNR | | | |
| 1643 | 1643 | 0.061 | 37 | 14 | 27 | IQVLQQQADDAEER | 93 | 100 | |

| | | | | | | | | | | |
|----|------------------------------------|-------|--------|-----|-----|-----|--------------------|-----|-------|---|
| | 1672 | 1672 | 0.001 | 1 | 133 | 146 | LVIIEGDLERTEER | | | |
| | 1771 | 1771 | 0.062 | 35 | 13 | 27 | KIQVLQQQADDAEER | 134 | 100 | |
| h2 | actin, gamma-enteric smooth muscle | | | | | | | | | |
| | 800.5 | 800.6 | 0.038 | 48 | 63 | 69 | RGILTLK | | | |
| | 976.4 | 976.5 | 0.04 | 41 | 20 | 29 | AGFAGDDAPR | 66 | 99.99 | |
| | 1131 | 1131 | 0.043 | 38 | 198 | 207 | GYSFVTTAER | | | |
| | 1188 | 1188 | 0.043 | 36 | 41 | 51 | HQGVVMVGMGQK | | | M |
| | 1199 | 1199 | 0.047 | 39 | 30 | 40 | AVFPSIVGRPR | 28 | 22.18 | |
| | 1204 | 1204 | 0.044 | 36 | 41 | 51 | HQGVVMVGMGQK | | | M |
| | 1355 | 1355 | 0.044 | 32 | 52 | 63 | DSYVGDEAQSKR | | | |
| | 1502 | 1502 | 0.058 | 39 | 86 | 96 | IWHHSFYNELR | 67 | 99.99 | |
| | 1956 | 1956 | 0.062 | 31 | 97 | 114 | VAPEEHPTLLTEAPLNPK | 101 | 100 | |
| | 1977 | 1977 | 0.077 | 39 | 70 | 85 | YPIEHGIITNWDDMEK | | | M |
| h3 | transgelin | | | | | | | | | |
| | 870.4 | 870.4 | 0.041 | 47 | 5 | 12 | GPSYGMSR | | | M |
| | 953.5 | 953.5 | 0.034 | 36 | 100 | 108 | AAEDYGVTK | | | |
| | 994.4 | 994.5 | 0.036 | 36 | 147 | 154 | GDPNWFMK | 35 | 84.53 | |
| | 1010 | 1010 | 0.034 | 33 | 147 | 154 | GDPNWFMK | 40 | 95.04 | M |
| | 1082 | 1083 | 0.042 | 39 | 22 | 29 | YDEELEER | | | |
| | 1204 | 1204 | -0.038 | -31 | 48 | 57 | GRLGFQVWLK | | | |

| | | | | | | | | | | |
|----|------------|------|--------|-----|-----|-----|--------------------|----|-------|---|
| | 1205 | 1205 | -0.05 | -42 | 129 | 140 | TLMALGSLAVTK | | | |
| | 1211 | 1211 | 0.048 | 39 | 21 | 29 | KYDEELEER | 51 | 99.57 | |
| | 1221 | 1221 | -0.048 | -39 | 129 | 140 | TLMALGSLAVTK | | | M |
| | 1238 | 1238 | 0.033 | 26 | 90 | 99 | QMEQVAQFLK | | | M |
| | 1238 | 1238 | 0.033 | 26 | 90 | 99 | QMEQVAQFLK | 40 | 95.13 | M |
| | 1245 | 1245 | 0.037 | 30 | 79 | 89 | VPENPPSMVFK | 38 | 90.44 | |
| | 1261 | 1261 | 0.034 | 27 | 79 | 89 | VPENPPSMVFK | 52 | 99.67 | M |
| | 1517 | 1517 | 0.046 | 30 | 65 | 78 | LVNSLYPDGSKPVK | 88 | 100 | |
| | 1547 | 1547 | 0.039 | 25 | 109 | 121 | TDMFQTVDLFEGK | 85 | 100 | M |
| | 2127 | 2127 | 0.088 | 41 | 30 | 47 | LVEWIVMQCGPDVGRPDR | | | C |
| h4 | Annexin A2 | | | | | | | | | |
| | 1085 | 1085 | -0.014 | -13 | 149 | 157 | GMYKTDLEK | | | |
| | 1086 | 1087 | 0.021 | 19 | 29 | 37 | AYTNFDAER | 64 | 99.98 | |
| | 1101 | 1101 | -0.001 | -1 | 149 | 157 | GMYKTDLEK | | | M |
| | 1107 | 1107 | -0.049 | -44 | 296 | 304 | SEVDMLKIR | | | M |
| | 1112 | 1112 | 0.016 | 15 | 69 | 77 | QDIAFAYQR | 74 | 100 | |
| | 1212 | 1212 | 0.029 | 24 | 158 | 168 | DIVSDTSGDFR | 99 | 100 | |
| | 1223 | 1223 | 0.025 | 21 | 105 | 115 | TPAQYDASELK | | | |
| | 1245 | 1245 | 0.021 | 17 | 136 | 145 | TNQELQEINR | 85 | 100 | |
| | 1340 | 1340 | 0.028 | 21 | 158 | 169 | DIVSDTSGDFRK | | | |

| | | | | | | | | | | |
|----|------------------------------|-------|-------|----|-----|-----|--------------------------------|-----|-----|---|
| | 1543 | 1543 | 0.03 | 19 | 50 | 63 | GVDEVTIVNILTNR | 125 | 100 | |
| | 1772 | 1772 | 0.004 | 2 | 48 | 63 | TKGVDEVTIVNILTNR | | | |
| | 1778 | 1778 | 0.023 | 13 | 120 | 135 | GLGTDEDSLIEIICSR | 124 | 100 | C |
| | 1798 | 1798 | 0.032 | 18 | 153 | 168 | TDLEKDIVSDTSGDFR | | | |
| | 1845 | 1845 | 0.013 | 7 | 11 | 28 | LSLEGDHSTPPSAYGSV _k | 119 | 100 | |
| | 2155 | 2155 | 0.044 | 20 | 29 | 47 | AYTNFDAERDALNIETAIK | | | |
| h5 | beta-lactoglobulin precursor | | | | | | | | | |
| | 853.5 | 853.5 | 0.03 | 35 | 158 | 164 | ALPMHIR | | | M |
| | 903.6 | 903.6 | 0.029 | 33 | 92 | 99 | TKIPAVFK | | | |
| | 916.5 | 916.5 | 0.03 | 33 | 100 | 107 | IDALNENK | | | |
| | 1066 | 1066 | 0.027 | 25 | 108 | 116 | VLVLDTDYK | | | |
| | 1121 | 1122 | 0.033 | 29 | 77 | 85 | WENGECAQK | | | C |
| | 1194 | 1194 | 0.033 | 28 | 108 | 117 | VLVLDTDYKK | | | |
| | 1246 | 1246 | 0.032 | 25 | 141 | 151 | TPEVDDEALEK | | | |
| | 1636 | 1636 | 0.038 | 23 | 141 | 154 | TPEVDDEALEKFDK | | | |
| | 1716 | 1716 | 0.035 | 20 | 165 | 178 | LSFNPTQLEEQCHI | 117 | 100 | C |
| | 2313 | 2313 | 0.051 | 22 | 57 | 76 | VYVEELKPTPEGDLEILLQK | 148 | 100 | |
| | 2723 | 2723 | 0.091 | 33 | 31 | 56 | VAGTWYSLAMAASDISLLDAQSAPLR | | | M |
| | 2818 | 2818 | 0.094 | 33 | 118 | 140 | YLLFCMENSAEPEQSLACQLVR | 109 | 100 | C |
| h6 | Ig heavy chain precursor | | | | | | | | | |

| | | | | | | | | | | |
|----|---|------|--------|-----|-----|-----|----------------------------|----|-------|------|
| | 1170 | 1170 | -0.053 | -45 | 329 | 338 | IQHQDWTGGK | | | |
| | 1302 | 1302 | -0.036 | -28 | 344 | 355 | VHNEGLPAPIVR | 57 | 99.78 | |
| | 1827 | 1827 | -0.087 | -48 | 366 | 381 | EPQVYVLAPPQEELSK | | | |
| | 2112 | 2112 | -0.076 | -36 | 296 | 313 | FSWFVDDVEVNTATTKPR | 46 | 97.08 | |
| | 2153 | 2153 | -0.067 | -31 | 414 | 432 | YGTTPPQLDADSSYFLYSK | | | |
| | 2782 | 2782 | -0.098 | -35 | 270 | 295 | DTLTISGTPEVTCVVVDVGHDDPEVK | | | C |
| h7 | IgG1 heavy chain constant region, partial | | | | | | | | | |
| | 1170 | 1170 | -0.038 | -32 | 188 | 197 | IQHQDWTGGK | 74 | 100 | |
| | 1174 | 1174 | 0.023 | 19 | 173 | 181 | EEQFNSTYR | | | |
| | 1286 | 1286 | -0.022 | -17 | 8 | 18 | VYPLSSCCGDK | | | C |
| | 1302 | 1302 | -0.039 | -30 | 203 | 214 | VHNEGLPAPIVR | 46 | 98.74 | |
| | 1590 | 1590 | -0.1 | -63 | 201 | 214 | CKVHNEGLPAPIVR | | | C |
| | 2112 | 2112 | -0.063 | -30 | 155 | 172 | FSWFVDDVEVNTATTKPR | 51 | 99.62 | |
| | 2782 | 2782 | -0.114 | -41 | 129 | 154 | DTLTISGTPEVTCVVVDVGHDDPEVK | | | C |
| | 3064 | 3064 | -0.104 | -34 | 297 | 321 | NSWQEGDTYTCVVMHEALHNHYTQK | | | C, M |
| h8 | Immunoglobulin light chain, lambda gene cluster | | | | | | | | | |
| | 1521 | 1521 | -0.073 | -48 | 172 | 185 | ADGSTITRNVETTR | | | |
| | 1679 | 1679 | -0.061 | -36 | 194 | 208 | YAASSYLSLTSSDWK | 77 | 100 | |
| | 1742 | 1742 | -0.053 | -30 | 211 | 226 | GSYSCEVTHEGSTVTK | 96 | 100 | C |

| | | | | | | | | | | |
|----|--|-------|--------|-----|-----|-----|---------------------|----|-------|---|
| | 1957 | 1957 | -0.048 | -25 | 209 | 226 | SKGSYSCEVTHEGSTVTK | 33 | 77.62 | C |
| | 2014 | 2014 | -0.075 | -37 | 133 | 151 | SPPSVTLFPPSTEELNGNK | | | |
| h9 | Immunoglobulin light chain, lambda gene cluster | | | | | | | | | |
| | 820.4 | 820.4 | -0.02 | -25 | 173 | 180 | ADGSTITR | | | |
| | 1236 | 1236 | -0.054 | -44 | 75 | 86 | ASGVPDRFSGSR | | | |
| | 1521 | 1521 | -0.073 | -48 | 173 | 186 | ADGSTITRNVETTR | | | |
| | 1679 | 1679 | -0.061 | -36 | 195 | 209 | YAASSYLSLTSSDWK | 77 | 100 | |
| | 1742 | 1742 | -0.053 | -30 | 212 | 227 | GSYSCEVTHEGSTVTK | 96 | 100 | C |
| | 1957 | 1957 | -0.048 | -25 | 210 | 227 | SKGSYSCEVTHEGSTVTK | 33 | 77.62 | C |
| | 2014 | 2014 | -0.075 | -37 | 134 | 152 | SPPSVTLFPPSTEELNGNK | | | |

*M means oxidation of methionine; C means carbamidomethylation of cysteine.