# Exploring human milk dynamics: Inter-individual variation in milk proteome, peptidome and metabolome

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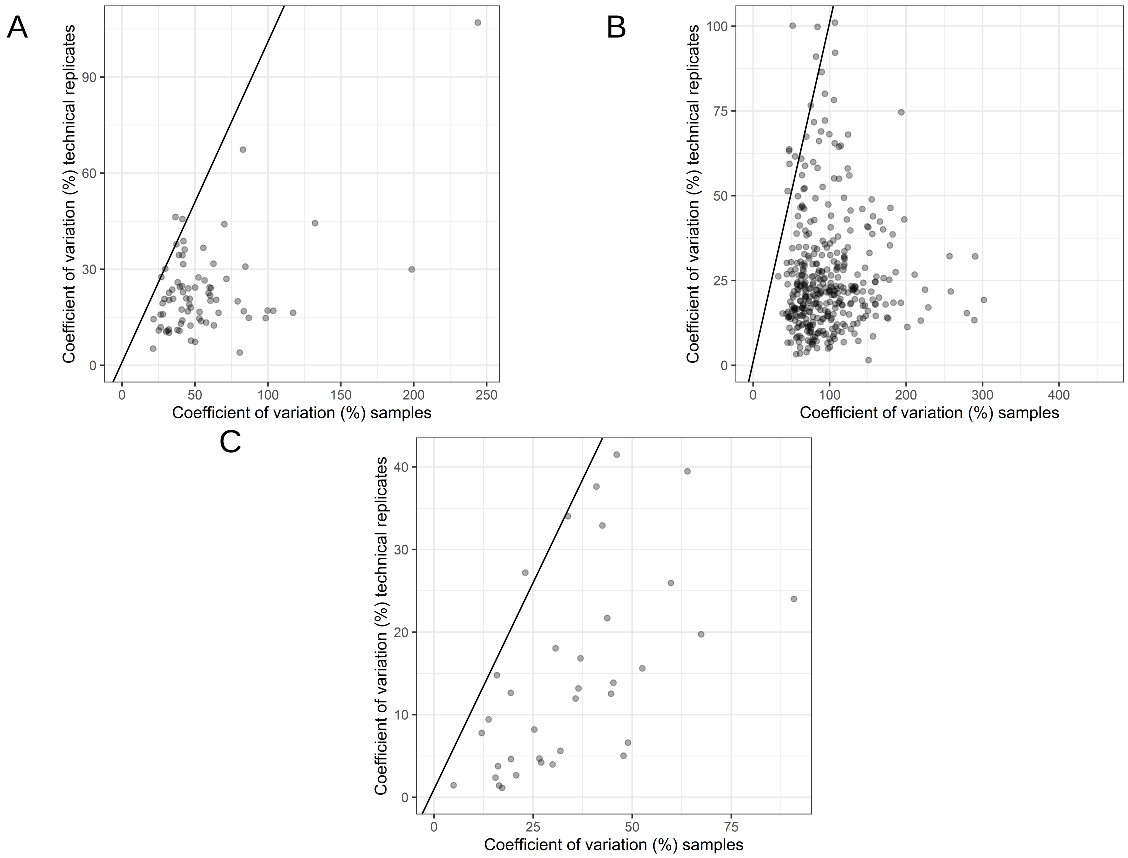
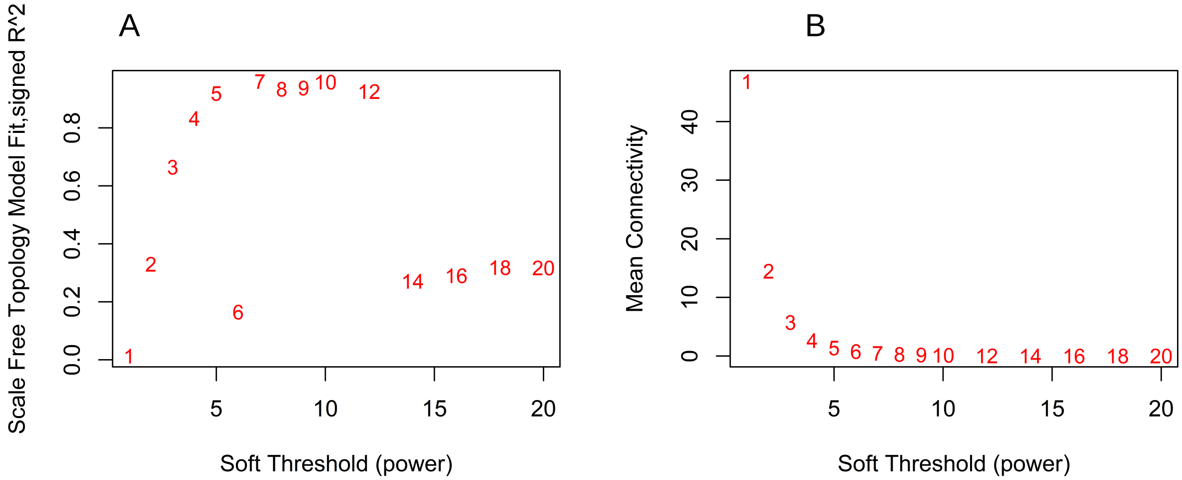
# Overall CV (%) of proteins, peptides, and metabolites plotted against CV (%) of technical replicates



Supplemental Figure S 1: The overall CV (%) plotted against the CV (%) of the technical replicates for the proteins (A), peptides (B) and metabolites (C). The diagonal line is drawn to indicate the features for which technical CV > overall CV.

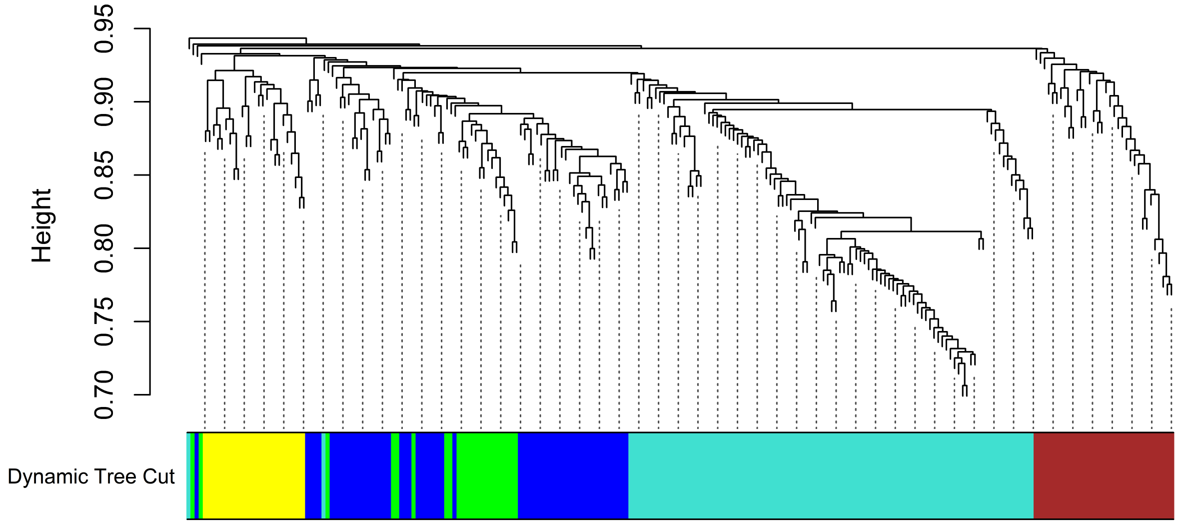
Technical replicates of proteomics data (n = 5) were used from a previous study.[1] Technical replicates of peptidomics data (n = 5) were used from a previous experiment (unpublished work, Wageningen University, 2016-05-10). Technical replicates of metabolomics data (n = 4) were analysed together with the samples used for the current study. Datafiles of all technical replicates were analysed with the same software and settings as described in the materials and methods.

# Visualization of the determination of the WGCNA soft-threshold power for the proteomics data.



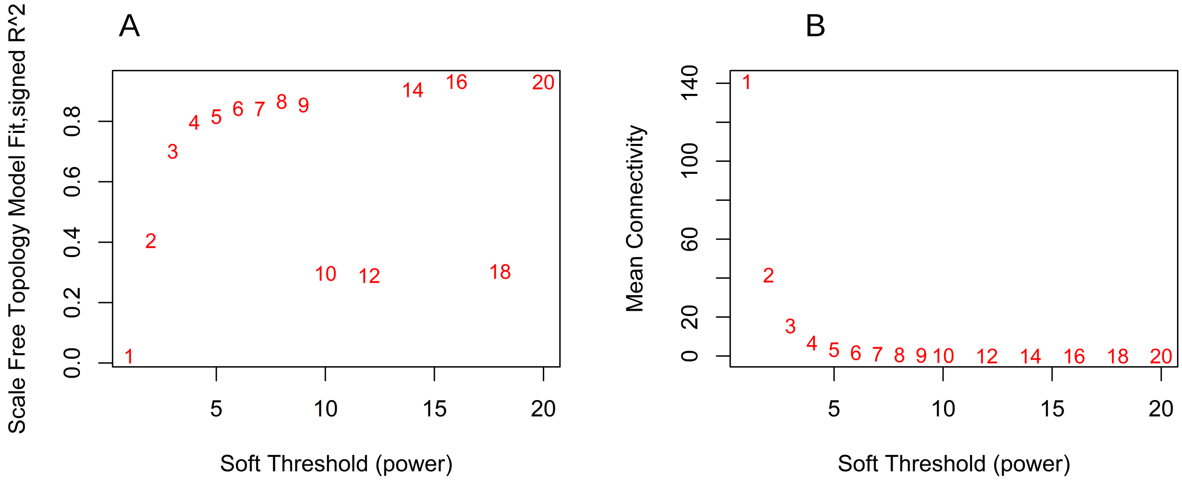
Supplemental Figure S 2: Determination of the soft-threshold power for WGCNA on proteomics data. (A) Scale-free topology fit index (y-axis) for soft-threshold values of 1-20 (x-axis). (B) Mean connectivity analysis with degree (y-axis) and soft-threshold values of 1-20 (x-axis).

## WGCNA cluster dendrogram and overview for the proteomics data.



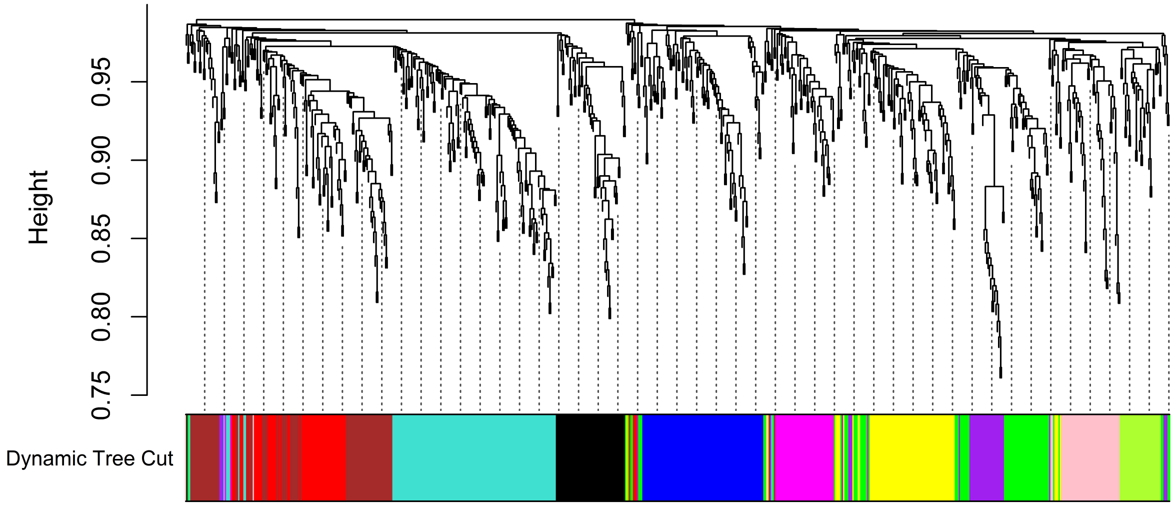
Supplemental Figure S 3: Cluster dendrogram and cluster overview for the proteomics data. Different colors indicate the different clusters, where turquoise = cluster 1, blue = cluster 2, brown = cluster 3, yellow = cluster 4 and green = cluster 5.

# Visualization of the determination of the WGCNA soft-threshold power for the peptidomics data.



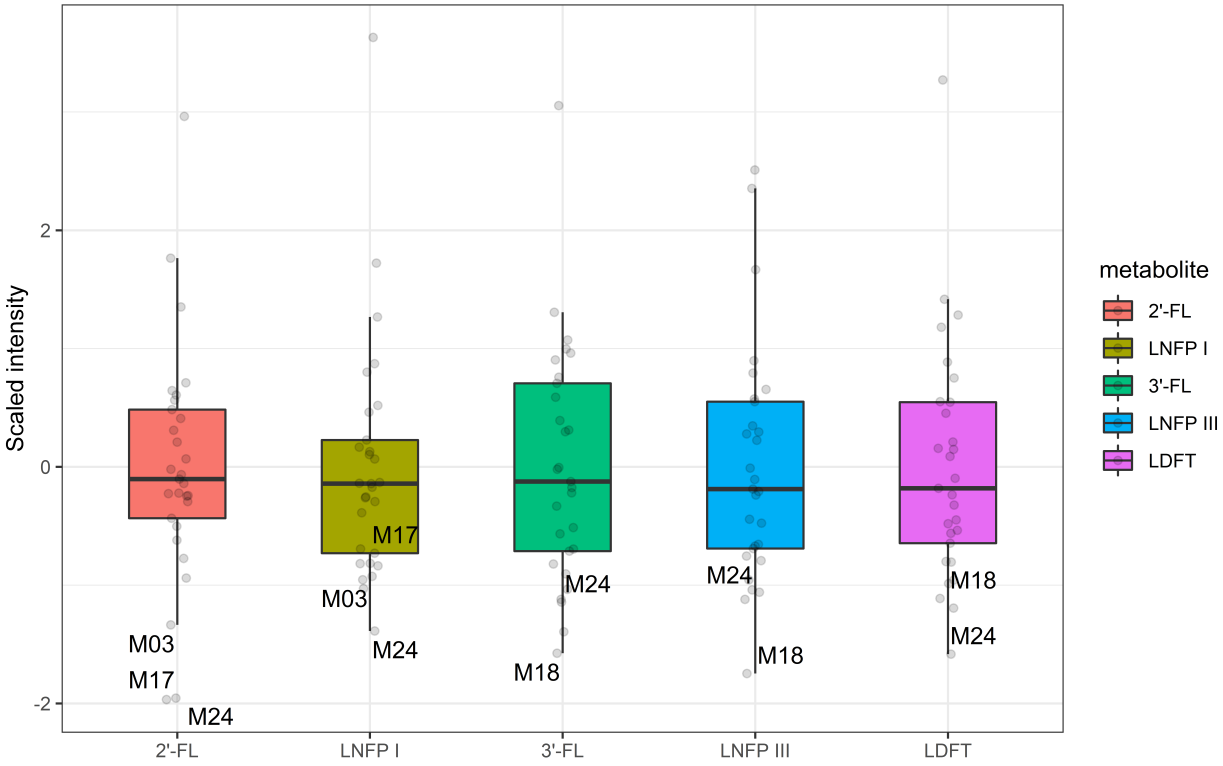
Supplemental Figure S 4: Determination of the soft-threshold power for WGCNA on peptidomics data. (A) Scale-free topology fit index (y-axis) for soft-threshold values of 1-20 (x-axis). (B) Mean connectivity analysis with degree (y-axis) and soft-threshold values of 1-20 (x-axis).

# WGCNA cluster dendrogram and overview for the peptidomics data.



Supplemental Figure S 5: Cluster dendrogram and cluster overview for the peptidomics data. Different colors indicate the different clusters, where turquoise = cluster 1, blue = cluster 2, brown = cluster 3, yellow = cluster 4, green = cluster 5, red = cluster 6, black = cluster 7, pink = cluster 8, magenta = cluster 9, purple = cluster 10 and greenyellow = cluster 11.

# Boxplots showing the proposed non-secretor and Lewis negative mothers.



Supplemental Figure S 6: Scaled intensitites for HMOs. Labels indicate samples from mothers proposed as non-secretor (Se(-)) or Lewis negative (Le(-)).

# Table with all identified proteins.

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score.

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identificat-ion score |
|---|---|---|---|---|---|---|
| A0A193CHR0 | 10E8 heavy chain variable region | 7.8 | 66.2 | 5 | 28.2 | 39.0 |
| P31946 | 14-3-3 protein beta/alpha | 7.2 | 39.9 | 1 | 43.1 | 115.1 |
| P62258 | 14-3-3 protein epsilon | 7.5 | 37.4 | 1 | 54.5 | 181.9 |
| Q04917 | 14-3-3 protein eta | 6.7 | 37.9 | 1 | 29.3 | 18.8 |
| P61981 | 14-3-3 protein gamma | 6.7 | 62.5 | 1 | 36.7 | 133.8 |
| P31947 | 14-3-3 protein sigma | 7.2 | 31.5 | 1 | 29.0 | 6.5 |
| P63104 | 14-3-3 protein zeta/delta | 7.9 | 31.3 | 1 | 63.7 | 323.3 |
| B9EKV4 | 4-trimethylaminobutyraldehyde dehydrogenase | 7.1 | 36.7 | 1 | 11.4 | 8.9 |
| Q9BRK5 | 45 kDa calcium-binding protein | 7.5 | 36.4 | 1 | 29.8 | 36.2 |
| P60709 | Actin | 8.9 | 21.7 | 1 | 63.5 | 323.3 |
| P07108 | Acyl-CoA-binding protein | 7.6 | 44.9 | 1 | 18.4 | 28.8 |
| P02768 | Albumin | 10.8 | 21.4 | 2 | 93.9 | 323.3 |
| P35747 | Albumin | 6.9 | 43.5 | 2 | 15.0 | 4.0 |
| P14550 | Aldo-keto reductase family 1 member A1] | 7.2 | 34.8 | 1 | 33.8 | 56.4 |
| P02763 | Alpha-1-acid glycoprotein 1 | 8.1 | 41.3 | 1 | 44.8 | 220.0 |
| P19652 | Alpha-1-acid glycoprotein 2 | 6.8 | 60.6 | 2 | 24.4 | 11.4 |
| P01011 | Alpha-1-antichymotrypsin | 8.9 | 86.9 | 4 | 47.5 | 323.3 |
| P01009 | Alpha-1-antitrypsin | 9.2 | 26.4 | 2 | 67.7 | 323.3 |
| P04217 | Alpha-1B-glycoprotein | 7.8 | 35.0 | 3 | 33.1 | 77.6 |
| P08697 | Alpha-2-antiplasmin | 7.8 | 29.6 | 1 | 17.5 | 41.9 |
| P02765 | Alpha-2-HS-glycoprotein | 7.8 | 36.6 | 1 | 25.9 | 58.0 |
| P01023 | Alpha-2-macroglobulin | 7.5 | 40.3 | 2 | 11.1 | 30.4 |
| O43707 | Alpha-actinin-4 | 7.0 | 43.0 | 1 | 12.1 | 27.3 |
| P04745 | Alpha-amylase 1B | 8.4 | 62.9 | 3 | 39.7 | 249.8 |
| P06733 | Alpha-enolase | 8.6 | 28.0 | 1 | 73.0 | 323.3 |
| P00709 | Alpha-lactalbumin | 10.8 | 41.9 | 5 | 54.2 | 323.3 |
| P47710 | Alpha-S1-casein | 9.9 | 71.6 | 4 | 80.0 | 5.9 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identification score |
|---|---|---|---|---|---|---|
| P05067 | Amyloid-beta precursor protein | 6.8 | 57.2 | 5 | 10.8 | 19.7 |
| P01019 | Angiotensinogen | 6.9 | 42.8 | 2 | 7.7 | 7.3 |
| A2KBC6 | Anti-FactorVIII scFv | 8.1 | 46.0 | 3 | 45.4 | 323.3 |
| P01008 | Antithrombin-III | 7.5 | 38.1 | 3 | 23.3 | 26.1 |
| P02647 | Apolipoprotein A-I | 8.4 | 41.1 | 1 | 74.2 | 227.3 |
| P02652 | Apolipoprotein A-II | 7.8 | 56.6 | 1 | 40.4 | 28.1 |
| P06727 | Apolipoprotein A-IV | 7.1 | 49.5 | 2 | 35.6 | 37.0 |
| P04114 | Apolipoprotein B-100 | 8.2 | 80.7 | 2 | 4.4 | 33.0 |
| P05090 | Apolipoprotein D | 7.3 | 58.4 | 2 | 33.0 | 16.6 |
| P02649 | Apolipoprotein E | 7.2 | 39.4 | 3 | 40.8 | 29.6 |
| P15289 | Arylsulfatase A | 6.5 | 100.6 | 2 | 20.9 | 9.5 |
| P15291 | Beta-1,4-galactosyltransferase 1 | 7.3 | 44.1 | 2 | 38.4 | 102.1 |
| P02749 | Beta-2-glycoprotein 1GPI | 7.5 | 47.4 | 2 | 43.1 | 61.0 |
| P61769 | Beta-2-microglobulin | 8.8 | 37.3 | 2 | 58.8 | 89.2 |
| P05814 | Beta-casein | 9.6 | 41.4 | 4 | 35.8 | 323.3 |
| Q13410 | Butyrophilin subfamily 1 member A1 | 8.6 | 47.2 | 4 | 46.4 | 323.3 |
| B4E1Z4 | C3/C5 convertase | 7.8 | 61.1 | 2 | 16.0 | 159.1 |
| P0DP25 | Calmodulin-3 | 7.6 | 42.0 | 1 | 56.4 | 32.0 |
| Q9NZT1 | Calmodulin-like protein 5 | 7.0 | 77.9 | 1 | 53.4 | 39.2 |
| P27797 | Calreticulin | 7.3 | 37.5 | 1 | 25.6 | 12.8 |
| P22676 | Calretinin | 7.0 | 25.0 | 2 | 15.1 | 83.1 |
| P00918 | Carbonic anhydrase 2 | 6.6 | 41.8 | 2 | 8.1 | 4.6 |
| P23280 | Carbonic anhydrase 6 | 8.0 | 62.0 | 3 | 22.4 | 134.3 |
| O75612 | Carboxylic ester hydrolase | 9.6 | 40.9 | 3 | 58.0 | 323.3 |
| P07858 | Cathepsin B | 6.7 | 53.2 | 2 | 21.2 | 7.2 |
| P07339 | Cathepsin D | 7.2 | 53.4 | 4 | 14.8 | 61.6 |
| Q9UBR2 | Cathepsin Z | 6.4 | 20.5 | 2 | 7.3 | 7.4 |
| E9PR17 | CD59 glycoprotein | 7.3 | 83.5 | 4 | 30.6 | 13.5 |
| Q96K68 | cDNA FLJ14473 fis | 10.2 | 47.1 | 3 | 53.8 | 323.3 |
| B3KU96 | cDNA FLJ39433 fis | 6.9 | 31.2 | 1 | 22.4 | 14.2 |
| Q6ZW64 | cDNA FLJ41552 fis | 8.1 | 117.2 | 3 | 52.0 | 58.2 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identification score |
|---|---|---|---|---|---|---|
| Q6ZVX0 | cDNA FLJ41981 fis | 8.5 | 62.5 | 3 | 53.2 | 164.8 |
| B4DPP8 | cDNA FLJ53075 | 7.7 | 39.6 | 3 | 22.2 | 68.6 |
| P29373 | Cellular retinoic acid-binding protein 2 | 6.8 | 38.9 | 1 | 39.9 | 7.1 |
| P00450 | Ceruloplasmin | 7.8 | 27.6 | 2 | 25.8 | 55.2 |
| A0A2P9AAP7 | Chaperone protein DnaK | 7.1 | 35.5 | 2 | 4.9 | 2.6 |
| P36222 | Chitinase-3-like protein 1 | 6.8 | 122.8 | 2 | 21.4 | 15.3 |
| O00299 | Chloride intracellular channel protein 1 | 6.8 | 31.0 | 1 | 33.6 | 14.6 |
| Q6WN34 | Chordin-like protein 2 | 8.3 | 50.1 | 3 | 25.1 | 86.8 |
| H0YCU0 | Chordin-like protein 2 | 7.5 | 42.4 | 3 | 30.8 | 11.7 |
| P10909 | Clusterin | 9.3 | 62.6 | 4 | 52.6 | 323.3 |
| P23528 | Cofilin-1 | 7.2 | 40.4 | 2 | 62.5 | 42.3 |
| A2NB45 | Cold agglutinin FS-1 L-chain | 7.3 | 81.5 | 2 | 38.9 | 6.1 |
| P01024 | Complement C3 | 9.0 | 41.3 | 4 | 56.6 | 323.3 |
| P0C0L5 | Complement C4-B | 8.4 | 64.6 | 4 | 44.3 | 323.3 |
| P02748 | Complement component C9 | 6.7 | 56.1 | 1 | 9.7 | 13.5 |
| P08603 | Complement factor H | 6.5 | 46.5 | 2 | 4.5 | 12.8 |
| P08185 | Corticosteroid-binding globulin | 7.0 | 33.0 | 2 | 5.7 | 3.3 |
| P04080 | Cystatin-B | 7.1 | 42.0 | 1 | 55.1 | 22.4 |
| P01034 | Cystatin-C | 8.2 | 50.5 | 5 | 37.0 | 35.6 |
| P00171 | Cytochrome b5 | 6.4 | 49.1 | 2 | 25.4 | 4.1 |
| P21399 | Cytoplasmic aconitate hydratase | 7.0 | 43.5 | 1 | 8.8 | 16.1 |
| P28838 | Cytosol aminopeptidase | 6.7 | 40.2 | 1 | 11.9 | 12.2 |
| Q96KP4 | Cytosolic non-specific dipeptidase | 8.0 | 38.0 | 1 | 38.7 | 54.7 |
| E1B7J1 | Deleted. | 6.8 | 35.1 | 2 | 5.9 | 4.6 |
| P81605 | Dermcidin | 6.8 | 70.1 | 1 | 22.7 | 6.1 |
| Q02487 | Desmocollin-2 | 7.6 | 57.4 | 2 | 2.6 | 6.9 |
| Q16555 | Dihydropyrimidinase-related protein 2 | 6.6 | 44.2 | 5 | 10.5 | 82.4 |
| Q14118 | Dystroglycan | 7.3 | 47.7 | 1 | 5.0 | 14.5 |
| P13639 | Elongation factor 2 | 6.9 | 42.6 | 1 | 6.2 | 10.0 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identification score |
|---|---|---|---|---|---|---|
| P11021 | Endoplasmic reticulum chaperone BiP | 7.9 | 28.2 | 1 | 33.8 | 124.0 |
| P14625 | Endoplasmin | 7.5 | 51.1 | 1 | 23.1 | 40.3 |
| Q15375 | Ephrin type-A receptor 7 | 6.5 | 52.2 | 2 | 3.8 | 7.5 |
| V9HW68 | Epididymis luminal protein 214 | 8.7 | 42.9 | 5 | 41.5 | 166.4 |
| V9HWJ7 | Epididymis secretory protein Li 37 | 6.8 | 39.5 | 1 | 13.7 | 9.0 |
| Q08345 | Epithelial discoidin domain-containing receptor 1 | 7.1 | 40.2 | 2 | 7.4 | 48.7 |
| P15311 | Ezrin | 7.8 | 34.4 | 1 | 30.4 | 103.9 |
| P05413 | Fatty acid-binding protein | 9.3 | 45.1 | 1 | 95.5 | 323.3 |
| P49327 | Fatty acid synthase S-acetyltransferase | 8.4 | 63.0 | 1 | 33.9 | 323.3 |
| P02671 | Fibrinogen alpha chain | 7.3 | 57.8 | 2 | 10.4 | 51.2 |
| P02675 | Fibrinogen beta chain | 6.9 | 35.4 | 2 | 20.9 | 26.1 |
| Q5D862 | Filaggrin-2 | 6.9 | 27.9 | 2 | 3.0 | 67.6 |
| P15328 | Folate receptor alpha | 7.0 | 49.2 | 5 | 12.6 | 22.3 |
| Q12841 | Follistatin-related protein 1 | 8.0 | 80.6 | 1 | 47.4 | 323.3 |
| P04075 | Fructose-bisphosphate aldolase A | 8.3 | 38.0 | 1 | 45.1 | 225.7 |
| Q08380 | Galectin-3-binding protein | 8.4 | 32.3 | 3 | 26.5 | 323.3 |
| V9HWI6 | Gc-globulin | 8.5 | 32.3 | 1 | 53.8 | 281.1 |
| A0A0X9T7V9 | GCT-A4 light chain variable region | 7.7 | 71.7 | 5 | 39.4 | 9.1 |
| A0A0X9T0H6 | GCT-A5 heavy chain variable region | 8.0 | 66.7 | 4 | 17.5 | 57.0 |
| A0A0X9UWL5 | GCT-A5 light chain variable region | 7.4 | 71.3 | 5 | 46.9 | 95.6 |
| A0A125QYY5 | GCT-A9 light chain variable region | 7.2 | 59.8 | 5 | 31.8 | 153.0 |
| P06396 | Gelsolin | 8.0 | 34.4 | 3 | 27.0 | 68.1 |
| P06744 | Glucose-6-phosphate isomerase | 6.8 | 27.1 | 1 | 7.9 | 7.3 |
| P14314 | Glucosidase 2 subunit beta | 7.7 | 37.4 | 1 | 12.9 | 44.8 |
| P48637 | Glutathione synthetase | 7.2 | 34.1 | 1 | 16.4 | 28.3 |
| P04406 | Glyceraldehyde-3-phosphate dehydrogenase | 7.8 | 43.3 | 1 | 31.9 | 20.2 |
| Q8NBJ4 | Golgi membrane protein 1 | 7.1 | 44.0 | 5 | 20.4 | 17.1 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identificat-ion score |
|---|---|---|---|---|---|---|
| Q9HAV0 | Guanine nucleotide-binding protein subunit beta-4 | 6.6 | 70.2 | 1 | 10.0 | 8.8 |
| P00738 | Haptoglobin | 9.2 | 52.4 | 2 | 52.5 | 261.7 |
| P17066 | Heat shock 70 kDa protein 6 | 7.2 | 33.3 | 1 | 14.6 | 13.7 |
| P11142 | Heat shock cognate 71 kDa protein | 7.8 | 32.3 | 1 | 28.5 | 117.9 |
| P40292 | Heat shock protein 90 | 7.2 | 49.1 | 2 | 5.9 | 84.9 |
| P04792 | Heat shock protein beta-1 | 7.0 | 43.9 | 1 | 41.5 | 10.2 |
| P07900 | Heat shock protein HSP 90-alpha | 8.0 | 46.9 | 1 | 24.6 | 224.0 |
| P08238 | Heat shock protein HSP 90-beta | 7.2 | 39.8 | 1 | 25.4 | 23.5 |
| Q6LAM1 | Heavy chain of factor I | 6.9 | 70.7 | 2 | 18.4 | 23.4 |
| Q9NRV9 | Heme-binding protein 1 | 6.6 | 39.9 | 1 | 23.3 | 4.9 |
| P02790 | Hemopexin | 7.3 | 34.0 | 2 | 20.6 | 32.8 |
| Q86YZ3 | Hornerin | 7.9 | 243.9 | 1 | 13.9 | 208.2 |
| A0A125QYY9 | IBM-B2 heavy chain variable region | 7.5 | 87.8 | 1 | 30.9 | 25.8 |
| S6B291 | IgG H chain | 6.7 | 67.8 | 5 | 35.6 | 16.5 |
| S6AWF4 | IgG L chain | 7.8 | 35.0 | 3 | 31.1 | 5.1 |
| Q6PIL8 | IGK@ protein | 9.5 | 43.6 | 3 | 65.3 | 323.3 |
| Q6IN99 | IGL@ protein | 8.7 | 47.4 | 3 | 52.6 | 5.3 |
| Q0KKI6 | Immunoblobulin light chain | 7.5 | 60.6 | 5 | 63.6 | 91.5 |
| P0DOX2 | Immunoglobulin alpha-2 heavy chain | 7.5 | 87.3 | 4 | 47.0 | 31.1 |
| Q9NPP6 | Immunoglobulin heavy chain variant | 7.0 | 98.5 | 5 | 59.6 | 13.6 |
| P01861 | Immunoglobulin heavy constant gamma 4 | 7.6 | 76.5 | 4 | 24.7 | 62.2 |
| P01871 | Immunoglobulin heavy constant mu | 8.1 | 198.6 | 3 | 37.8 | 107.2 |
| P01591 | Immunoglobulin J chain | 9.4 | 55.8 | 3 | 81.1 | 148.8 |
| P0DOX8 | Immunoglobulin lambda-1 light chain | 8.0 | 53.2 | 3 | 47.7 | 183.0 |
| Q15181 | Inorganic pyrophosphatase | 6.7 | 25.8 | 2 | 22.1 | 11.1 |
| P18065 | Insulin-like growth factor-binding protein 2 | 7.8 | 32.3 | 3 | 39.4 | 149.6 |
| P19827 | Inter-alpha-trypsin inhibitor heavy chain H1 | 7.3 | 120.2 | 2 | 11.3 | 20.3 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identificat-ion score |
|---|---|---|---|---|---|---|
| P19823 | Inter-alpha-trypsin inhibitor heavy chain H2 | 7.3 | 36.2 | 2 | 9.3 | 26.5 |
| Q14624 | Inter-alpha-trypsin inhibitor heavy chain H4 | 8.2 | 37.4 | 1 | 16.1 | 38.5 |
| O75874 | Isocitrate dehydrogenase cytoplasmic-specific ICDH | 7.4 | 37.5 | 1 | 22.9 | 26.5 |
| Q92876 | Kallikrein-6 | 7.8 | 57.6 | 5 | 29.9 | 41.6 |
| P07498 | Kappa-casein | 8.5 | 82.9 | 4 | 53.3 | 57.2 |
| O43278 | Kunitz-type protease inhibitor 1 | 7.0 | 41.5 | 2 | 15.3 | 7.1 |
| P07195 | L-lactate dehydrogenase B chain | 8.1 | 44.0 | 1 | 36.5 | 78.3 |
| Q08431 | Lactadherin | 7.8 | 60.4 | 4 | 44.6 | 51.7 |
| P22079 | Lactoperoxidase | 7.8 | 84.5 | 1 | 25.0 | 42.0 |
| P02788 | Lactotransferrin | 10.9 | 45.4 | 3 | 89.8 | 57.1 |
| Q99538 | Legumain | 6.9 | 42.8 | 1 | 17.5 | 9.7 |
| P02750 | Leucine-rich alpha-2-glycoprotein | 8.4 | 26.9 | 3 | 38.2 | 59.3 |
| Q86X29 | Lipolysis-stimulated lipoprotein receptor | 6.5 | 21.3 | 2 | 4.3 | 7.3 |
| P06858 | Lipoprotein lipase | 7.4 | 99.8 | 4 | 24.3 | 61.7 |
| P61626 | Lysozyme C | 8.4 | 132.3 | 4 | 70.9 | 63.9 |
| P22897 | Macrophage mannose receptor 1 | 9.3 | 30.2 | 2 | 42.9 | 323.3 |
| P40925 | Malate dehydrogenase | 7.5 | 30.8 | 1 | 37.6 | 95.5 |
| P49006 | MARCKS-related protein | 7.0 | 67.4 | 3 | 14.1 | 31.2 |
| P01033 | Metalloproteinase inhibitor 1 | 6.9 | 29.8 | 3 | 32.2 | 7.1 |
| Q13228 | Methanethiol oxidase | 7.0 | 39.7 | 1 | 22.5 | 38.4 |
| P26038 | Moesin | 7.1 | 22.2 | 1 | 21.3 | 13.0 |
| P08571 | Monocyte differentiation antigen CD14 | 9.2 | 29.1 | 3 | 47.2 | 323.3 |
| P15941 | Mucin-1 | 7.5 | 56.5 | 4 | 36.2 | 18.9 |
| A0A0G2JQJ2 | Mucin-4 | 7.3 | 74.7 | 4 | 9.6 | 40.3 |
| Q9UL85 | Myosin-reactive immunoglobulin kappa chain variable region | 7.3 | 64.9 | 2 | 24.8 | 218.0 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identificat-ion score |
|---|---|---|---|---|---|---|
| Q9UL78 | Myosin-reactive immunoglobulin light chain variable region | 8.1 | 41.9 | 5 | 65.1 | 323.3 |
| Q9UL82 | Myosin-reactive immunoglobulin light chain variable region | 7.2 | 49.0 | 5 | 28.0 | 4.4 |
| P29966 | Myristoylated alanine-rich C-kinase substrate | 7.9 | 51.3 | 1 | 14.8 | 25.7 |
| Q7Z3X3 | N-acetylglucosamine-6-sulfatase | 7.3 | 57.6 | 1 | 14.3 | 18.7 |
| O94760 | N,N-dimethylarginine dimethylaminohydrolase 1 | 6.9 | 28.8 | 1 | 11.2 | 35.9 |
| O14745 | Na/H exchange regulatory cofactor NHE-RF1/H exchanger | 7.5 | 34.3 | 1 | 38.8 | 41.8 |
| P43490 | Nicotinamide phosphoribosyltransferase | 6.9 | 44.9 | 2 | 16.7 | 8.7 |
| P61916 | NPC intracellular cholesterol transporter 2 | 7.4 | 53.0 | 1 | 39.3 | 61.0 |
| Q02818 | Nucleobindin-1 | 8.1 | 41.8 | 1 | 56.0 | 121.1 |
| P80303 | Nucleobindin-2 | 8.4 | 39.0 | 1 | 56.2 | 302.0 |
| Q9H173 | Nucleotide exchange factor SIL1 | 6.5 | 26.4 | 1 | 10.3 | 7.8 |
| P10451 | Osteopontin | 9.8 | 42.1 | 1 | 66.4 | 323.3 |
| Q99497 | Parkinson disease protein 7 | 7.6 | 30.8 | 1 | 43.2 | 19.8 |
| P62937 | Peptidyl-prolyl cis-trans isomerase A | 7.9 | 33.7 | 2 | 43.6 | 49.1 |
| P23284 | Peptidyl-prolyl cis-trans isomerase B | 7.5 | 32.1 | 5 | 29.3 | 17.8 |
| Q99541 | Perilipin-2 | 7.7 | 61.0 | 4 | 43.9 | 51.7 |
| O60664 | Perilipin-3 | 7.5 | 36.8 | 1 | 36.7 | 141.9 |
| Q06830 | Peroxiredoxin-1 | 7.7 | 32.3 | 1 | 49.7 | 25.4 |
| P32119 | Peroxiredoxin-2 | 7.2 | 36.8 | 1 | 39.9 | 10.5 |
| P30041 | Peroxiredoxin-6 | 6.6 | 39.7 | 1 | 21.9 | 9.9 |
| P13696 | Phosphatidylethanolamine-binding protein 1 | 7.3 | 39.2 | 1 | 34.2 | 12.6 |
| P36871 | Phosphoglucomutase-1 | 7.7 | 43.7 | 1 | 31.5 | 109.1 |
| P00558 | Phosphoglycerate kinase 1 | 7.5 | 41.3 | 1 | 30.0 | 53.8 |
| P36955 | Pigment epithelium-derived factor | 6.9 | 30.1 | 1 | 17.2 | 16.9 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identification score |
|---|---|---|---|---|---|---|
| P05155 | Plasma protease C1 inhibitor | 7.5 | 35.1 | 2 | 11.7 | 19.4 |
| P16671 | Platelet glycoprotein 4 | 7.2 | 56.8 | 4 | 13.8 | 9.8 |
| O00592 | Podocalyxin | 7.2 | 79.3 | 4 | 6.6 | 259.5 |
| P01833 | Polymeric immunoglobulin receptor | 10.3 | 25.1 | 3 | 61.9 | 323.3 |
| P01133 | Pro-epidermal growth factor | 7.5 | 34.3 | 3 | 9.8 | 54.9 |
| P07737 | Profilin-1 | 6.8 | 36.8 | 2 | 38.6 | 56.6 |
| P07602 | Prosaposin | 8.1 | 60.0 | 4 | 33.8 | 87.5 |
| P02760 | Protein AMBP | 6.9 | 38.3 | 2 | 7.4 | 6.6 |
| P07237 | Protein disulfide-isomerase | 7.9 | 35.2 | 1 | 39.8 | 144.9 |
| P30101 | Protein disulfide-isomerase A3 | 7.1 | 48.4 | 1 | 31.7 | 38.2 |
| P13667 | Protein disulfide-isomerase A4 | 7.0 | 42.8 | 1 | 12.4 | 12.5 |
| P23297 | Protein S100-A1 | 7.0 | 80.8 | 1 | 26.6 | 67.2 |
| P00734 | Prothrombin | 6.9 | 19.6 | 2 | 12.7 | 11.5 |
| P50395 | Rab GDP dissociation inhibitor beta | 7.6 | 30.0 | 1 | 32.1 | 121.5 |
| P62491 | Ras-related protein Rab-11A | 6.6 | 30.7 | 1 | 28.4 | 6.2 |
| Q9NP72 | Ras-related protein Rab-18 | 6.7 | 35.2 | 2 | 16.0 | 14.8 |
| P62820 | Ras-related protein Rab-1A | 7.0 | 34.5 | 1 | 32.4 | 97.7 |
| P51149 | Ras-related protein Rab-7a | 6.8 | 39.4 | 1 | 26.9 | 87.2 |
| A0N5G5 | Rheumatoid factor D5 light chain | 7.7 | 56.4 | 5 | 28.0 | 79.1 |
| A2J1M8 | Rheumatoid factor RF-IP12 | 7.7 | 59.3 | 3 | 21.1 | 22.6 |
| P52565 | Rho GDP-dissociation inhibitor 1 | 7.6 | 41.5 | 1 | 43.1 | 33.8 |
| P02787 | Serotransferrin | 8.5 | 35.0 | 2 | 56.4 | 323.3 |
| P55854 | Small ubiquitin-related modifier 3 | 6.6 | 55.4 | 2 | 17.0 | 9.5 |
| P27105 | Stomatin | 6.7 | 205.5 | 4 | 31.6 | 31.0 |
| O00391 | Sulfhydryl oxidase 1 | 7.7 | 46.5 | 3 | 23.6 | 200.9 |
| Q99536 | Synaptic vesicle membrane protein VAT-1 homolog | 6.8 | 36.9 | 2 | 10.7 | 7.1 |
| P31431 | Syndecan-4 | 7.7 | 41.9 | 3 | 5.6 | 14.2 |
| P24821 | Tenascin | 7.7 | 246.8 | 5 | 19.9 | 323.3 |
| P10599 | Thioredoxin | 6.9 | 67.5 | 2 | 31.4 | 9.7 |
| P04066 | Tissue alpha-L-fucosidase | 7.0 | 83.0 | 4 | 7.5 | 25.6 |

Supplemental Table S 1: List with all identified proteins, including their mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, sequence coverage, and identification score. *(continued)*

| Uniprot ID | Leading protein name | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Sequence coverage (%) | Identificat-ion score |
|---|---|---|---|---|---|---|
| Q8WZ42 | Titin | 9.3 | 56.7 | 1 | 0.8 | 18.8 |
| O43493 | Trans-Golgi network integral membrane protein 2 | 7.0 | 32.0 | 1 | 10.6 | 94.4 |
| P20061 | Transcobalamin-1 | 7.8 | 103.7 | 4 | 20.8 | 92.2 |
| P55072 | Transitional endoplasmic reticulum ATPase-ATPase p97 subunit | 7.7 | 69.0 | 5 | 5.8 | 4.8 |
| Q53EM5 | Transketolase variant | 7.9 | 59.4 | 1 | 29.4 | 30.8 |
| P60174 | Triosephosphate isomerase | 7.7 | 27.2 | 1 | 66.7 | 99.4 |
| Q1ZYL5 | Tropomyosin 1 alpha variant 6 | 6.5 | 46.6 | 1 | 33.1 | 40.3 |
| Q5VU61 | Tropomyosin alpha-3 chain | 7.3 | 57.3 | 1 | 54.3 | 20.9 |
| O75347 | Tubulin-specific chaperone A | 6.8 | 28.0 | 2 | 35.7 | 4.9 |
| P62987 | Ubiquitin-60S ribosomal protein L40 | 6.8 | 16.2 | 2 | 67.2 | 13.7 |
| P22314 | Ubiquitin-like modifier-activating enzyme 1 | 7.0 | 38.8 | 1 | 11.2 | 162.7 |
| Q8NEJ1 | Uncharacterized protein | 10.0 | 50.1 | 3 | 52.1 | 323.3 |
| Q16851 | UTP–glucose-1-phosphate uridylyltransferase | 8.5 | 40.4 | 1 | 54.5 | 155.9 |
| P02774 | Vitamin D-binding protein | 7.6 | 47.3 | 1 | 48.5 | 5.7 |
| P04004 | Vitronectin | 7.9 | 27.9 | 3 | 21.5 | 38.6 |
| P47989 | Xanthine dehydrogenase/oxidase | 9.4 | 26.4 | 1 | 57.5 | 323.3 |
| P25311 | Zinc-alpha-2-glycoprotein | 8.2 | 54.2 | 1 | 50.7 | 63.6 |

# Table with all identified peptides.

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score.

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| KVPQLEIVPN | P02662 | Alpha-S1-casein | 120-129 | 6.3 | 57.4 | 8 | 96.3 |
| RPKLPLRYPE | P47710 | Alpha-S1-casein | 16-25 | 7.3 | 133.2 | 3 | 115.6 |
| RPKLPLRYPER | P47710 | Alpha-S1-casein | 16-26 | 5.6 | 156.4 | 3 | 67.2 |
| RPKLPLRYPERL | P47710 | Alpha-S1-casein | 16-27 | 6.2 | 91.0 | 1 | 72.3 |
| RPKLPLRYPERLQ | P47710 | Alpha-S1-casein | 16-28 | 6.7 | 73.0 | 3 | 135.0 |
| RPKLPLRYPERLQNP | P47710 | Alpha-S1-casein | 16-30 | 6.4 | 75.5 | 6 | 72.9 |
| RPKLPLRYPERLQNPS | P47710 | Alpha-S1-casein | 16-31 | 6.1 | 60.1 | 3 | 84.9 |
| RPKLPLRYPERLQNPSE | P47710 | Alpha-S1-casein | 16-32 | 7.5 | 63.2 | 3 | 179.1 |
| RPKLPLRYPERLQNPSESSEPIP | P47710 | Alpha-S1-casein | 16-38 | 6.5 | 99.3 | 3 | 76.0 |
| RPKLPLRYPERLQNPSESSEPIPLE | P47710 | Alpha-S1-casein | 16-40 | 6.5 | 68.0 | 7 | 131.6 |
| SDISNPTAHENYEKNNVMLQW | P47710 | Alpha-S1-casein | 165-185 | 6.1 | 290.3 | 2 | 148.4 |
| DISNPTAHENYEKNN | P47710 | Alpha-S1-casein | 166-180 | 5.5 | 45.1 | 2 | 77.1 |
| DISNPTAHENYEKNNV | P47710 | Alpha-S1-casein | 166-181 | 5.4 | 92.4 | 2 | 73.2 |
| DISNPTAHENYEKNNVMLQW | P47710 | Alpha-S1-casein | 166-185 | 5.8 | 63.2 | 4 | 103.8 |
| SNPTAHENYEKNNV | P47710 | Alpha-S1-casein | 168-181 | 6.0 | 182.5 | 2 | 191.8 |
| NPTAHENYEKNNV | P47710 | Alpha-S1-casein | 169-181 | 5.8 | 146.4 | 10 | 136.5 |
| NPTAHENYEKNNVML | P47710 | Alpha-S1-casein | 169-183 | 5.8 | 156.8 | 2 | 51.8 |
| HENYEKNNVML | P47710 | Alpha-S1-casein | 173-183 | 6.2 | 78.6 | 2 | 140.1 |
| ENYEKNNVML | P47710 | Alpha-S1-casein | 174-183 | 5.5 | 77.5 | 4 | 78.1 |
| NYEKNNVML | P47710 | Alpha-S1-casein | 175-183 | 6.2 | 52.1 | 2 | 96.3 |
| KLPLRYPERLQNPSE | P47710 | Alpha-S1-casein | 18-32 | 5.9 | 75.4 | 3 | 68.8 |
| TDAPSFSDIPNPI | P02662 | Alpha-S1-casein | 189-201 | 6.0 | 55.6 | 8 | 155.2 |
| LPLRYPERLQNPSE | P47710 | Alpha-S1-casein | 19-32 | 6.6 | 68.3 | 6 | 139.0 |
| YPERLQNPSESSEPIP | P47710 | Alpha-S1-casein | 23-38 | 6.4 | 45.7 | 1 | 116.0 |
| RLQNPSESSEPIP | P47710 | Alpha-S1-casein | 26-38 | 6.7 | 59.2 | 7 | 140.1 |
| RLQNPSESSEPIPL | P47710 | Alpha-S1-casein | 26-39 | 6.2 | 146.3 | 2 | 108.7 |
| RLQNPSESSEPIPLE | P47710 | Alpha-S1-casein | 26-40 | 6.8 | 70.7 | 7 | 168.9 |
| RLQNPSESSEPIPLESREE | P47710 | Alpha-S1-casein | 26-44 | 5.7 | 32.9 | 3 | 83.3 |
| RLQNPSESSEPIPLESREEYMNGMN | P47710 | Alpha-S1-casein | 26-50 | 8.1 | 63.7 | 7 | 258.5 |
| LQNPSESSEPIPLESREEYMNGMN | P47710 | Alpha-S1-casein | 27-50 | 7.1 | 67.9 | 7 | 224.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| NPSESSEPIPLESRE | P47710 | Alpha-S1-casein | 29-43 | 5.5 | 58.7 | 9 | 80.5 |
| NPSESSEPIPLESREE | P47710 | Alpha-S1-casein | 29-44 | 5.9 | 88.9 | 1 | 204.1 |
| NPSESSEPIPLESREEYMNGMN | P47710 | Alpha-S1-casein | 29-50 | 6.6 | 183.5 | 1 | 295.0 |
| NPSESSEPIPLESREEYMNGMNR | P47710 | Alpha-S1-casein | 29-51 | 6.2 | 157.5 | 7 | 97.5 |
| ESSEPIPLESREEYMNGMNR | P47710 | Alpha-S1-casein | 32-51 | 5.9 | 58.5 | 7 | 56.9 |
| SSEPIPLESREEYMNGMN | P47710 | Alpha-S1-casein | 33-50 | 6.7 | 68.5 | 7 | 220.2 |
| SSEPIPLESREEYMNGMNR | P47710 | Alpha-S1-casein | 33-51 | 6.3 | 95.0 | 7 | 64.5 |
| SEPIPLESREE | P47710 | Alpha-S1-casein | 34-44 | 5.7 | 53.3 | 7 | 76.8 |
| SEPIPLESREEYMNGMN | P47710 | Alpha-S1-casein | 34-50 | 6.1 | 84.0 | 1 | 160.2 |
| EPIPLESREEYMNGMN | P47710 | Alpha-S1-casein | 35-50 | 6.3 | 154.5 | 1 | 213.4 |
| FVAPFPEVFGK | P02662 | Alpha-S1-casein | 39-49 | 5.4 | 68.6 | 6 | 61.0 |
| ESREEYMNGMNR | P47710 | Alpha-S1-casein | 40-51 | 5.4 | 143.9 | 3 | 65.5 |
| SREEYMNGMNR | P47710 | Alpha-S1-casein | 41-51 | 4.9 | 109.1 | 2 | 86.0 |
| QRNILREKQTDEIKDT | P47710 | Alpha-S1-casein | 52-67 | 5.7 | 76.6 | 6 | 111.0 |
| QRNILREKQTDEIKDTR | P47710 | Alpha-S1-casein | 52-68 | 6.8 | 170.0 | 6 | 89.5 |
| NILREKQTDEIK | P47710 | Alpha-S1-casein | 54-65 | 5.8 | 170.6 | 1 | 136.3 |
| NILREKQTDEIKDT | P47710 | Alpha-S1-casein | 54-67 | 6.1 | 65.9 | 6 | 204.3 |
| NILREKQTDEIKDTR | P47710 | Alpha-S1-casein | 54-68 | 7.3 | 63.9 | 3 | 186.8 |
| REKQTDEIKDT | P47710 | Alpha-S1-casein | 57-67 | 5.1 | 107.9 | 3 | 114.8 |
| EKQTDEIKDT | P47710 | Alpha-S1-casein | 58-67 | 5.6 | 71.0 | 6 | 232.4 |
| EKQTDEIKDTR | P47710 | Alpha-S1-casein | 58-68 | 7.1 | 106.7 | 3 | 252.3 |
| KQTDEIKDTR | P47710 | Alpha-S1-casein | 59-68 | 5.2 | 175.4 | 3 | 82.4 |
| HIQKEDVPSER | P02662 | Alpha-S1-casein | 95-105 | 5.8 | 101.0 | 8 | 122.7 |
| EVPKAKDTVYT | P05814 | Beta-casein | 100-110 | 7.3 | 47.1 | 3 | 188.9 |
| EVPKAKDTVYTK | P05814 | Beta-casein | 100-111 | 6.3 | 61.9 | 3 | 104.0 |
| EVPKAKDTVYTKG | P05814 | Beta-casein | 100-112 | 6.3 | 100.5 | 2 | 103.8 |
| EVPKAKDTVYTKGR | P05814 | Beta-casein | 100-113 | 5.7 | 84.1 | 2 | 96.6 |
| EVPKAKDTVYTKGRVMP | P05814 | Beta-casein | 100-116 | 5.7 | 81.1 | 2 | 54.3 |
| VPKAKDTVYT | P05814 | Beta-casein | 101-110 | 6.8 | 107.5 | 10 | 186.7 |
| VPKAKDTVYTK | P05814 | Beta-casein | 101-111 | 5.7 | 99.6 | 3 | 124.4 |
| VPKAKDTVYTKG | P05814 | Beta-casein | 101-112 | 5.7 | 122.5 | 2 | 132.8 |
| VPKAKDTVYTKGRVM | P05814 | Beta-casein | 101-115 | 5.4 | 85.5 | 4 | 65.1 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| AKDTVYTKGR | P05814 | Beta-casein | 104-113 | 6.4 | 114.5 | 3 | 256.9 |
| AKDTVYTKGRV | P05814 | Beta-casein | 104-114 | 5.6 | 79.5 | 3 | 127.2 |
| AKDTVYTKGRVMP | P05814 | Beta-casein | 104-116 | 6.8 | 120.2 | 3 | 182.0 |
| AKDTVYTKGRVMPV | P05814 | Beta-casein | 104-117 | 5.8 | 201.7 | 2 | 142.8 |
| AKDTVYTKGRVMPVL | P05814 | Beta-casein | 104-118 | 7.1 | 104.7 | 3 | 227.6 |
| AKDTVYTKGRVMPVLK | P05814 | Beta-casein | 104-119 | 7.9 | 83.6 | 3 | 217.1 |
| AKDTVYTKGRVMPVLKSPTIP | P05814 | Beta-casein | 104-124 | 6.9 | 219.3 | 2 | 99.9 |
| KDTVYTKGRVMP | P05814 | Beta-casein | 105-116 | 6.1 | 131.2 | 6 | 122.4 |
| KDTVYTKGRVMPV | P05814 | Beta-casein | 105-117 | 5.5 | 95.1 | 3 | 73.0 |
| KDTVYTKGRVMPVL | P05814 | Beta-casein | 105-118 | 6.9 | 73.0 | 3 | 122.3 |
| KDTVYTKGRVMPVLK | P05814 | Beta-casein | 105-119 | 6.9 | 119.3 | 3 | 156.2 |
| DTVYTKGR | P05814 | Beta-casein | 106-113 | 6.9 | 127.9 | 3 | 183.7 |
| DTVYTKGRV | P05814 | Beta-casein | 106-114 | 6.4 | 93.6 | 1 | 205.7 |
| DTVYTKGRVMP | P05814 | Beta-casein | 106-116 | 6.5 | 78.6 | 3 | 140.8 |
| DTVYTKGRVMPVL | P05814 | Beta-casein | 106-118 | 7.7 | 59.9 | 6 | 199.7 |
| DTVYTKGRVMPVLK | P05814 | Beta-casein | 106-119 | 8.3 | 77.5 | 3 | 204.5 |
| DTVYTKGRVMPVLKSPTIP | P05814 | Beta-casein | 106-124 | 6.7 | 160.4 | 6 | 107.6 |
| DTVYTKGRVMPVLKSPTIPF | P05814 | Beta-casein | 106-125 | 6.1 | 258.4 | 3 | 126.2 |
| TVYTKGRVMPVL | P05814 | Beta-casein | 107-118 | 6.5 | 98.9 | 6 | 131.0 |
| TVYTKGRVMPVLK | P05814 | Beta-casein | 107-119 | 6.1 | 203.4 | 6 | 76.5 |
| VYTKGRVMPVLK | P05814 | Beta-casein | 108-119 | 5.6 | 130.6 | 3 | 72.7 |
| YTKGRVMPVL | P05814 | Beta-casein | 109-118 | 5.5 | 63.7 | 3 | 85.1 |
| YTKGRVMPVLK | P05814 | Beta-casein | 109-119 | 6.3 | 106.0 | 3 | 96.2 |
| TKGRVMPVLKSPTIP | P05814 | Beta-casein | 110-124 | 5.8 | 176.7 | 2 | 55.7 |
| GRVMPVLK | P05814 | Beta-casein | 112-119 | 7.9 | 102.1 | 3 | 175.8 |
| GRVMPVLKSPTIP | P05814 | Beta-casein | 112-124 | 8.3 | 127.2 | 2 | 89.3 |
| GRVMPVLKSPTIPF | P05814 | Beta-casein | 112-125 | 7.2 | 289.3 | 2 | 121.9 |
| GRVMPVLKSPTIPFFD | P05814 | Beta-casein | 112-127 | 6.7 | 140.7 | 6 | 170.0 |
| GRVMPVLKSPTIPFFDPQIP | P05814 | Beta-casein | 112-131 | 6.6 | 188.6 | 6 | 69.1 |
| GRVMPVLKSPTIPFFDPQIPK | P05814 | Beta-casein | 112-132 | 7.2 | 100.5 | 6 | 135.7 |
| GRVMPVLKSPTIPFFDPQIPKLTD | P05814 | Beta-casein | 112-135 | 6.2 | 130.8 | 1 | 110.2 |
| RVMPVLKSPT | P05814 | Beta-casein | 113-122 | 5.7 | 155.8 | 3 | 85.7 |
| RVMPVLKSPTIP | P05814 | Beta-casein | 113-124 | 6.0 | 127.8 | 1 | 67.2 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| VMPVLKSPTIP | P05814 | Beta-casein | 114-124 | 7.0 | 183.6 | 2 | 120.1 |
| VMPVLKSPTIPF | P05814 | Beta-casein | 114-125 | 5.9 | 301.8 | 5 | 87.9 |
| VMPVLKSPTIPFFD | P05814 | Beta-casein | 114-127 | 5.8 | 195.1 | 2 | 120.1 |
| VMPVLKSPTIPFFDPQIPK | P05814 | Beta-casein | 114-132 | 6.3 | 89.7 | 6 | 94.0 |
| MPVLKSPT | P05814 | Beta-casein | 115-122 | 6.0 | 101.4 | 3 | 127.1 |
| MPVLKSPTIP | P05814 | Beta-casein | 115-124 | 7.3 | 74.0 | 1 | 103.8 |
| MPVLKSPTIPFFD | P05814 | Beta-casein | 115-127 | 5.9 | 108.5 | 6 | 154.2 |
| MPVLKSPTIPFFDPQIP | P05814 | Beta-casein | 115-131 | 7.3 | 108.0 | 6 | 156.2 |
| MPVLKSPTIPFFDPQIPK | P05814 | Beta-casein | 115-132 | 6.7 | 126.2 | 1 | 159.8 |
| PVLKSPTIPFFDPQIP | P05814 | Beta-casein | 116-131 | 5.7 | 126.3 | 6 | 94.1 |
| VLKSPTIPFFDPQIP | P05814 | Beta-casein | 117-131 | 5.7 | 114.9 | 6 | 88.2 |
| VLKSPTIPFFDPQIPK | P05814 | Beta-casein | 117-132 | 5.6 | 78.1 | 6 | 123.0 |
| KSPTIPFFDPQIP | P05814 | Beta-casein | 119-131 | 5.6 | 97.6 | 6 | 71.0 |
| SPTIPFFDPQ | P05814 | Beta-casein | 120-129 | 5.3 | 40.6 | 6 | 69.4 |
| SPTIPFFDPQIP | P05814 | Beta-casein | 120-131 | 6.5 | 140.8 | 6 | 90.6 |
| SPTIPFFDPQIPK | P05814 | Beta-casein | 120-132 | 6.7 | 118.5 | 6 | 148.3 |
| SPTIPFFDPQIPKL | P05814 | Beta-casein | 120-133 | 5.6 | 312.3 | 1 | 123.6 |
| SPTIPFFDPQIPKLT | P05814 | Beta-casein | 120-134 | 5.7 | 106.5 | 1 | 89.8 |
| SPTIPFFDPQIPKLTD | P05814 | Beta-casein | 120-135 | 6.3 | 142.4 | 1 | 169.9 |
| SPTIPFFDPQIPKLTDLEN | P05814 | Beta-casein | 120-138 | 5.7 | 86.7 | 1 | 111.1 |
| PTIPFFDPQIPKL | P05814 | Beta-casein | 121-133 | 5.6 | 55.9 | 1 | 96.3 |
| PTIPFFDPQIPKLTD | P05814 | Beta-casein | 121-135 | 6.0 | 53.4 | 4 | 122.7 |
| FDPQIPKLTDLENL | P05814 | Beta-casein | 126-139 | 5.7 | 106.0 | 2 | 112.1 |
| DPQIPKLTDLENL | P05814 | Beta-casein | 127-139 | 5.9 | 109.5 | 1 | 107.8 |
| DPQIPKLTDLENLH | P05814 | Beta-casein | 127-140 | 5.8 | 117.7 | 1 | 132.9 |
| DPQIPKLTDLENLHLP | P05814 | Beta-casein | 127-142 | 5.9 | 105.7 | 1 | 132.4 |
| DPQIPKLTDLENLHLPLP | P05814 | Beta-casein | 127-144 | 6.1 | 111.3 | 1 | 82.0 |
| TDLENLHLP | P05814 | Beta-casein | 134-142 | 5.8 | 73.9 | 1 | 226.7 |
| TDLENLHLPLP | P05814 | Beta-casein | 134-144 | 5.3 | 147.3 | 1 | 147.2 |
| DLENLHLP | P05814 | Beta-casein | 135-142 | 5.9 | 89.0 | 1 | 124.9 |
| LENLHLPLPLLQ | P05814 | Beta-casein | 136-147 | 5.1 | 109.1 | 10 | 65.3 |
| ENLHLPLPLL | P05814 | Beta-casein | 137-146 | 5.3 | 114.5 | 1 | 87.0 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| ENLHLPLPLLQ | P05814 | Beta-casein | 137-147 | 5.3 | 81.8 | 1 | 95.1 |
| LLQPLMQQVPQPIP | P05814 | Beta-casein | 145-158 | 5.4 | 98.3 | 1 | 111.7 |
| LLQPLMQQVPQPIPQT | P05814 | Beta-casein | 145-160 | 7.2 | 93.8 | 1 | 161.9 |
| LLQPLMQQVPQPIPQTL | P05814 | Beta-casein | 145-161 | 6.0 | 224.8 | 2 | 186.9 |
| LLQPLMQQVPQPIPQTLALPPQP | P05814 | Beta-casein | 145-167 | 6.2 | 193.8 | 1 | 89.5 |
| LQPLMQQVPQPIPQT | P05814 | Beta-casein | 146-160 | 5.7 | 83.1 | 1 | 123.8 |
| QPLMQQVPQPIPQT | P05814 | Beta-casein | 147-160 | 6.5 | 132.9 | 1 | 120.1 |
| QPLMQQVPQPIPQTL | P05814 | Beta-casein | 147-161 | 5.5 | 75.9 | 1 | 86.0 |
| QPLMQQVPQPIPQTLALPPQP | P05814 | Beta-casein | 147-167 | 5.8 | 128.6 | 1 | 89.0 |
| PLMQQVPQPIPQTL | P05814 | Beta-casein | 148-161 | 5.8 | 90.2 | 4 | 83.0 |
| LMQQVPQPIPQT | P05814 | Beta-casein | 149-160 | 6.5 | 132.5 | 1 | 109.0 |
| LMQQVPQPIPQTLALPPQP | P05814 | Beta-casein | 149-167 | 5.8 | 114.2 | 1 | 71.7 |
| MQQVPQPIPQT | P05814 | Beta-casein | 150-160 | 5.9 | 100.8 | 1 | 58.7 |
| QQVPQPIPQTL | P05814 | Beta-casein | 151-161 | 6.2 | 60.7 | 4 | 159.1 |
| QQVPQPIPQTLALPPQPLWSVPQP | P05814 | Beta-casein | 151-174 | 5.7 | 110.6 | 1 | 47.8 |
| QVPQPIPQTL | P05814 | Beta-casein | 152-161 | 5.9 | 61.8 | 4 | 91.3 |
| VPQPIPQTLALPPQP | P05814 | Beta-casein | 153-167 | 6.0 | 156.8 | 1 | 68.1 |
| RETIESLSSSEE | P05814 | Beta-casein | 16-27 | 5.9 | 95.2 | 7 | 195.5 |
| RETIESLSSSEESITEY | P05814 | Beta-casein | 16-32 | 6.7 | 65.7 | 7 | 213.8 |
| RETIESLSSSEESITEYK | P05814 | Beta-casein | 16-33 | 7.9 | 76.8 | 7 | 410.6 |
| RETIESLSSSEESITEYKQ | P05814 | Beta-casein | 16-34 | 6.0 | 114.5 | 3 | 116.3 |
| RETIESLSSSEESITEYKQK | P05814 | Beta-casein | 16-35 | 6.8 | 87.3 | 7 | 270.5 |
| RETIESLSSSEESITEYKQKVE | P05814 | Beta-casein | 16-37 | 6.7 | 93.9 | 7 | 168.7 |
| RETIESLSSSEESITEYKQKVEK | P05814 | Beta-casein | 16-38 | 6.9 | 117.9 | 7 | 239.3 |
| LALPPQPLWSVPQP | P05814 | Beta-casein | 161-174 | 5.6 | 125.0 | 1 | 116.8 |
| LALPPQPLWSVPQPK | P05814 | Beta-casein | 161-175 | 5.5 | 142.8 | 6 | 100.7 |
| ALPPQPLWSVPQP | P05814 | Beta-casein | 162-174 | 6.0 | 59.8 | 6 | 91.6 |
| ETIESLSSSEE | P05814 | Beta-casein | 17-27 | 5.4 | 60.9 | 7 | 84.5 |
| ETIESLSSSEESITE | P05814 | Beta-casein | 17-31 | 7.0 | 105.7 | 11 | 189.7 |
| ETIESLSSSEESITEY | P05814 | Beta-casein | 17-32 | 6.8 | 55.3 | 7 | 267.6 |
| ETIESLSSSEESITEYK | P05814 | Beta-casein | 17-33 | 8.3 | 55.6 | 7 | 384.8 |
| ETIESLSSSEESITEYKQ | P05814 | Beta-casein | 17-34 | 6.4 | 125.4 | 7 | 279.6 |
| ETIESLSSSEESITEYKQK | P05814 | Beta-casein | 17-35 | 7.1 | 83.3 | 7 | 169.8 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| ETIESLSSSEESITEYKQKV | P05814 | Beta-casein | 17-36 | 5.9 | 97.5 | 2 | 45.3 |
| ETIESLSSSEESITEYKQKVE | P05814 | Beta-casein | 17-37 | 6.6 | 159.7 | 1 | 197.7 |
| ETIESLSSSEESITEYKQKVEK | P05814 | Beta-casein | 17-38 | 7.5 | 112.1 | 1 | 179.6 |
| SVPQPKVLPIPQQVVPYP | P05814 | Beta-casein | 170-187 | 6.1 | 144.0 | 1 | 104.9 |
| SVPQPKVLPIPQQVVPYPQ | P05814 | Beta-casein | 170-188 | 6.4 | 290.6 | 1 | 96.7 |
| SVPQPKVLPIPQQVVPYPQR | P05814 | Beta-casein | 170-189 | 6.9 | 461.9 | 1 | 107.4 |
| VPQPKVLPIPQQ | P05814 | Beta-casein | 171-182 | 6.0 | 154.2 | 4 | 93.6 |
| VPQPKVLPIPQQV | P05814 | Beta-casein | 171-183 | 6.0 | 51.9 | 2 | 132.0 |
| VPQPKVLPIPQQVVP | P05814 | Beta-casein | 171-185 | 6.5 | 80.6 | 1 | 85.4 |
| VPQPKVLPIPQQVVPYP | P05814 | Beta-casein | 171-187 | 6.8 | 96.4 | 1 | 128.0 |
| QPKVLPIPQQVVP | P05814 | Beta-casein | 173-185 | 5.7 | 69.7 | 1 | 59.4 |
| QPKVLPIPQQVVPYP | P05814 | Beta-casein | 173-187 | 5.9 | 115.8 | 1 | 131.4 |
| VLPIPQQV | P05814 | Beta-casein | 176-183 | 6.2 | 97.7 | 6 | 130.0 |
| VLPIPQQVVP | P05814 | Beta-casein | 176-185 | 6.5 | 68.3 | 1 | 89.6 |
| VLPIPQQVVPYP | P05814 | Beta-casein | 176-187 | 6.9 | 85.3 | 6 | 133.6 |
| VLPIPQQVVPYPQ | P05814 | Beta-casein | 176-188 | 5.7 | 175.0 | 6 | 131.0 |
| VLPIPQQVVPYPQR | P05814 | Beta-casein | 176-189 | 7.2 | 229.2 | 6 | 175.7 |
| VLPIPQQVVPYPQRAVP | P05814 | Beta-casein | 176-192 | 5.9 | 71.9 | 1 | 79.7 |
| VLPIPQQVVPYPQRAVPV | P05814 | Beta-casein | 176-193 | 5.9 | 179.5 | 2 | 100.7 |
| VLPIPQQVVPYPQRAVPVQ | P05814 | Beta-casein | 176-194 | 6.6 | 133.1 | 1 | 108.3 |
| VLPIPQQVVPYPQRAVPVQA | P05814 | Beta-casein | 176-195 | 7.5 | 72.1 | 1 | 168.4 |
| VLPIPQQVVPYPQRAVPVQAL | P05814 | Beta-casein | 176-196 | 6.6 | 68.3 | 1 | 153.4 |
| LPIPQQVVPYP | P05814 | Beta-casein | 177-187 | 6.1 | 107.7 | 1 | 89.3 |
| LPIPQQVVPYPQRA | P05814 | Beta-casein | 177-190 | 6.3 | 75.7 | 1 | 145.9 |
| LPIPQQVVPYPQRAV | P05814 | Beta-casein | 177-191 | 5.6 | 110.9 | 1 | 81.3 |
| LPIPQQVVPYPQRAVP | P05814 | Beta-casein | 177-192 | 6.6 | 64.6 | 1 | 138.2 |
| LPIPQQVVPYPQRAVPV | P05814 | Beta-casein | 177-193 | 5.7 | 111.8 | 1 | 58.7 |
| LPIPQQVVPYPQRAVPVQ | P05814 | Beta-casein | 177-194 | 6.8 | 77.9 | 1 | 122.4 |
| LPIPQQVVPYPQRAVPVQA | P05814 | Beta-casein | 177-195 | 7.4 | 88.9 | 1 | 162.7 |
| PIPQQVVPYPQRAVPVQ | P05814 | Beta-casein | 178-194 | 6.0 | 74.1 | 2 | 84.7 |
| PIPQQVVPYPQRAVPVQA | P05814 | Beta-casein | 178-195 | 6.2 | 93.0 | 2 | 115.8 |
| IPQQVVPYPQRAVPVQA | P05814 | Beta-casein | 179-195 | 6.9 | 112.2 | 1 | 122.5 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| TIESLSSSEESITEY | P05814 | Beta-casein | 18-32 | 6.1 | 68.6 | 7 | 110.4 |
| TIESLSSSEESITEYK | P05814 | Beta-casein | 18-33 | 7.6 | 73.4 | 7 | 347.7 |
| TIESLSSSEESITEYKQK | P05814 | Beta-casein | 18-35 | 5.9 | 82.4 | 7 | 52.5 |
| TIESLSSSEESITEYKQKVEK | P05814 | Beta-casein | 18-38 | 6.2 | 118.8 | 7 | 59.5 |
| VVPYPQRAVPVQ | P05814 | Beta-casein | 183-194 | 6.5 | 128.4 | 4 | 107.2 |
| VPYPQRAVPVQ | P05814 | Beta-casein | 184-194 | 5.8 | 75.1 | 1 | 98.4 |
| VPYPQRAVPVQA | P05814 | Beta-casein | 184-195 | 6.3 | 57.4 | 2 | 130.8 |
| IESLSSSEESITEYK | P05814 | Beta-casein | 19-33 | 7.2 | 83.8 | 7 | 386.6 |
| NQELLLNPTHQIYP | P05814 | Beta-casein | 199-212 | 5.9 | 143.6 | 2 | 47.3 |
| NQELLLNPTHQIYPVT | P05814 | Beta-casein | 199-214 | 6.5 | 71.9 | 4 | 108.4 |
| NQELLLNPTHQIYPVTQ | P05814 | Beta-casein | 199-215 | 6.1 | 58.2 | 4 | 116.0 |
| NQELLLNPTHQIYPVTQPLAPV | P05814 | Beta-casein | 199-220 | 5.7 | 101.4 | 1 | 120.1 |
| NQELLLNPTHQIYPVTQPLAPVH | P05814 | Beta-casein | 199-221 | 6.1 | 95.0 | 1 | 53.2 |
| ESLSSSEESITE | P05814 | Beta-casein | 20-31 | 6.3 | 77.7 | 7 | 174.0 |
| ESLSSSEESITEYK | P05814 | Beta-casein | 20-33 | 7.0 | 88.2 | 7 | 278.5 |
| ESLSSSEESITEYKQKVEK | P05814 | Beta-casein | 20-38 | 6.2 | 155.8 | 1 | 59.0 |
| ELLLNPTHQIYP | P05814 | Beta-casein | 201-212 | 5.6 | 123.8 | 1 | 55.6 |
| ELLLNPTHQIYPVTQ | P05814 | Beta-casein | 201-215 | 5.8 | 68.2 | 1 | 70.5 |
| ELLLNPTHQIYPVTQPLAPVHNPIS | P05814 | Beta-casein | 201-225 | 5.9 | 105.6 | 1 | 118.2 |
| LLLNPTHQIYPVT | P05814 | Beta-casein | 202-214 | 6.3 | 52.5 | 4 | 73.1 |
| LLLNPTHQIYPVTQ | P05814 | Beta-casein | 202-215 | 5.8 | 59.6 | 4 | 82.4 |
| LLLNPTHQIYPVTQPLAPVHNPIS | P05814 | Beta-casein | 202-225 | 6.1 | 75.5 | 1 | 117.6 |
| LLLNPTHQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 202-226 | 7.8 | 67.3 | 4 | 228.8 |
| LLNPTHQIYPVTQ | P05814 | Beta-casein | 203-215 | 5.9 | 34.0 | 1 | 70.0 |
| LLNPTHQIYPVTQPLAPVHNPIS | P05814 | Beta-casein | 203-225 | 6.5 | 103.7 | 2 | 129.3 |
| LLNPTHQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 203-226 | 8.2 | 85.2 | 2 | 316.4 |
| LNPTHQIYPVT | P05814 | Beta-casein | 204-214 | 5.5 | 44.4 | 5 | 78.9 |
| LNPTHQIYPVTQ | P05814 | Beta-casein | 204-215 | 5.7 | 44.8 | 2 | 71.0 |
| LNPTHQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 204-226 | 7.6 | 88.0 | 2 | 263.6 |
| NPTHQIYPVTQ | P05814 | Beta-casein | 205-215 | 6.3 | 54.4 | 1 | 103.7 |
| NPTHQIYPVTQPLAPVH | P05814 | Beta-casein | 205-221 | 6.5 | 166.2 | 1 | 228.1 |
| NPTHQIYPVTQPLAPVHNP | P05814 | Beta-casein | 205-223 | 6.2 | 159.4 | 6 | 80.0 |
| NPTHQIYPVTQPLAPVHNPIS | P05814 | Beta-casein | 205-225 | 7.0 | 136.6 | 10 | 190.1 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| NPTHQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 205-226 | 7.8 | 64.0 | 1 | 281.1 |
| PTHQIYPVTQPLAPVHNPIS | P05814 | Beta-casein | 206-225 | 6.0 | 106.3 | 1 | 113.5 |
| PTHQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 206-226 | 7.5 | 53.9 | 5 | 214.2 |
| THQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 207-226 | 6.8 | 61.7 | 9 | 138.1 |
| YQEPVLGPVRGPFPIIV | P02666 | Beta-casein | 208-224 | 5.7 | 107.8 | 8 | 127.4 |
| HQIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 208-226 | 6.8 | 143.4 | 4 | 244.7 |
| QIYPVTQPLAPVHNPISV | P05814 | Beta-casein | 209-226 | 7.3 | 178.9 | 4 | 258.0 |
| SLSSSEESITE | P05814 | Beta-casein | 21-31 | 6.3 | 72.5 | 7 | 127.6 |
| SLSSSEESITEY | P05814 | Beta-casein | 21-32 | 6.0 | 58.7 | 7 | 105.8 |
| SLSSSEESITEYK | P05814 | Beta-casein | 21-33 | 7.2 | 59.6 | 7 | 250.7 |
| SLSSSEESITEYKQKV | P05814 | Beta-casein | 21-36 | 6.3 | 117.9 | 7 | 147.2 |
| SLSSSEESITEYKQKVE | P05814 | Beta-casein | 21-37 | 5.7 | 104.7 | 1 | 45.7 |
| SLSSSEESITEYKQKVEK | P05814 | Beta-casein | 21-38 | 6.7 | 89.0 | 7 | 101.0 |
| IYPVTQPLAPVHNPISV | P05814 | Beta-casein | 210-226 | 6.5 | 193.3 | 8 | 192.9 |
| YPVTQPLAPVH | P05814 | Beta-casein | 211-221 | 5.6 | 173.2 | 1 | 176.8 |
| YPVTQPLAPVHNPISV | P05814 | Beta-casein | 211-226 | 7.4 | 64.2 | 1 | 235.3 |
| PVTQPLAPVH | P05814 | Beta-casein | 212-221 | 5.3 | 122.3 | 5 | 172.2 |
| PVTQPLAPVHNPISV | P05814 | Beta-casein | 212-226 | 7.7 | 81.0 | 2 | 254.2 |
| VTQPLAPVHNPISV | P05814 | Beta-casein | 213-226 | 7.2 | 159.4 | 2 | 162.2 |
| TQPLAPVHNPI | P05814 | Beta-casein | 214-224 | 6.0 | 130.1 | 2 | 68.8 |
| TQPLAPVHNPISV | P05814 | Beta-casein | 214-226 | 8.4 | 97.1 | 2 | 156.0 |
| QPLAPVHNPISV | P05814 | Beta-casein | 215-226 | 8.4 | 67.1 | 2 | 123.6 |
| PLAPVHNPISV | P05814 | Beta-casein | 216-226 | 8.3 | 45.2 | 4 | 193.1 |
| LAPVHNPISV | P05814 | Beta-casein | 217-226 | 6.8 | 279.6 | 3 | 97.6 |
| LSSSEESITEYK | P05814 | Beta-casein | 22-33 | 7.0 | 86.8 | 7 | 263.1 |
| LSSSEESITEYKQKV | P05814 | Beta-casein | 22-36 | 5.8 | 78.0 | 7 | 57.1 |
| LSSSEESITEYKQKVEK | P05814 | Beta-casein | 22-38 | 6.1 | 97.7 | 7 | 60.9 |
| SSSEESITEYK | P05814 | Beta-casein | 23-33 | 7.2 | 66.0 | 7 | 255.1 |
| SSSEESITEYKQK | P05814 | Beta-casein | 23-35 | 5.2 | 102.6 | 1 | 51.0 |
| SSSEESITEYKQKV | P05814 | Beta-casein | 23-36 | 6.3 | 119.8 | 6 | 210.3 |
| SSSEESITEYKQKVE | P05814 | Beta-casein | 23-37 | 5.7 | 86.3 | 7 | 79.6 |
| SSSEESITEYKQKVEK | P05814 | Beta-casein | 23-38 | 6.0 | 119.3 | 6 | 86.6 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| SSEESITEYK | P05814 | Beta-casein | 24-33 | 6.8 | 57.7 | 7 | 258.5 |
| SEESITEYK | P05814 | Beta-casein | 25-33 | 7.0 | 58.0 | 7 | 218.8 |
| SEESITEYKQKV | P05814 | Beta-casein | 25-36 | 6.4 | 90.7 | 7 | 222.3 |
| EESITEYKQKV | P05814 | Beta-casein | 26-36 | 6.7 | 117.8 | 7 | 250.1 |
| EESITEYKQKVEK | P05814 | Beta-casein | 26-38 | 5.4 | 85.9 | 6 | 53.3 |
| ESITEYKQKVEK | P05814 | Beta-casein | 27-38 | 5.9 | 66.8 | 3 | 83.6 |
| SITEYKQKVEK | P05814 | Beta-casein | 28-38 | 6.0 | 110.8 | 3 | 86.0 |
| TEYKQKVE | P05814 | Beta-casein | 30-37 | 6.2 | 82.0 | 4 | 173.7 |
| TEYKQKVEKV | P05814 | Beta-casein | 30-39 | 6.8 | 63.1 | 4 | 165.0 |
| TEYKQKVEKVKHED | P05814 | Beta-casein | 30-43 | 5.9 | 61.1 | 4 | 204.8 |
| TEYKQKVEKVKHEDQQQ | P05814 | Beta-casein | 30-46 | 5.8 | 86.8 | 4 | 126.8 |
| TEYKQKVEKVKHEDQQQGEDE | P05814 | Beta-casein | 30-50 | 5.3 | 125.7 | 10 | 98.1 |
| KQKVEKVKHEDQQQG | P05814 | Beta-casein | 33-47 | 5.2 | 161.1 | 2 | 84.5 |
| QKVEKVKHEDQQQG | P05814 | Beta-casein | 34-47 | 6.2 | 80.5 | 3 | 92.9 |
| QKVEKVKHEDQQQGEDEHQD | P05814 | Beta-casein | 34-53 | 7.0 | 93.9 | 3 | 265.5 |
| QKVEKVKHEDQQQGEDEHQDK | P05814 | Beta-casein | 34-54 | 7.1 | 118.8 | 6 | 384.1 |
| KVEKVKHEDQQQGEDEHQDK | P05814 | Beta-casein | 35-54 | 6.4 | 123.8 | 6 | 360.0 |
| VEKVKHEDQQQGEDEHQD | P05814 | Beta-casein | 36-53 | 6.6 | 78.6 | 6 | 311.0 |
| VEKVKHEDQQQGEDEHQDK | P05814 | Beta-casein | 36-54 | 7.0 | 142.4 | 6 | 386.5 |
| EKVKHEDQQQGEDEHQD | P05814 | Beta-casein | 37-53 | 6.3 | 150.7 | 1 | 341.7 |
| EKVKHEDQQQGEDEHQDK | P05814 | Beta-casein | 37-54 | 6.4 | 179.4 | 6 | 317.5 |
| KVKHEDQQQGEDEHQDK | P05814 | Beta-casein | 38-54 | 5.7 | 405.8 | 2 | 280.2 |
| VKHEDQQQGEDEHQ | P05814 | Beta-casein | 39-52 | 5.5 | 168.5 | 3 | 208.8 |
| VKHEDQQQGEDEHQD | P05814 | Beta-casein | 39-53 | 7.5 | 134.0 | 3 | 397.5 |
| VKHEDQQQGEDEHQDK | P05814 | Beta-casein | 39-54 | 7.8 | 152.1 | 3 | 411.3 |
| VKHEDQQQGEDEHQDKIYP | P05814 | Beta-casein | 39-57 | 6.1 | 74.3 | 3 | 74.1 |
| VKHEDQQQGEDEHQDKIYPS | P05814 | Beta-casein | 39-58 | 6.4 | 82.2 | 6 | 198.2 |
| VKHEDQQQGEDEHQDKIYPSFQPQP | P05814 | Beta-casein | 39-63 | 6.9 | 110.7 | 1 | 169.4 |
| HEDQQQGEDEHQD | P05814 | Beta-casein | 41-53 | 6.3 | 82.9 | 3 | 370.2 |
| HEDQQQGEDEHQDK | P05814 | Beta-casein | 41-54 | 6.7 | 84.2 | 3 | 353.8 |
| HEDQQQGEDEHQDKIYP | P05814 | Beta-casein | 41-57 | 6.3 | 87.2 | 2 | 125.5 |
| HEDQQQGEDEHQDKIYPS | P05814 | Beta-casein | 41-58 | 6.1 | 64.3 | 6 | 175.5 |
| HEDQQQGEDEHQDKIYPSFQPQP | P05814 | Beta-casein | 41-63 | 6.0 | 75.6 | 1 | 73.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| EDQQQGEDEHQD | P05814 | Beta-casein | 42-53 | 5.3 | 81.5 | 3 | 120.1 |
| EDQQQGEDEHQDK | P05814 | Beta-casein | 42-54 | 5.3 | 127.4 | 3 | 62.1 |
| EDQQQGEDEHQDKIYP | P05814 | Beta-casein | 42-57 | 5.7 | 58.1 | 2 | 45.9 |
| EDQQQGEDEHQDKIYPS | P05814 | Beta-casein | 42-58 | 5.6 | 92.0 | 4 | 94.5 |
| DQQQGEDEHQDKIYP | P05814 | Beta-casein | 43-57 | 6.2 | 49.2 | 2 | 125.3 |
| DQQQGEDEHQDKIYPS | P05814 | Beta-casein | 43-58 | 6.4 | 65.3 | 6 | 202.6 |
| GEDEHQDK | P05814 | Beta-casein | 47-54 | 5.2 | 77.3 | 7 | 241.5 |
| GEDEHQDKIYPS | P05814 | Beta-casein | 47-58 | 5.4 | 108.3 | 2 | 64.6 |
| FQSEEQQQTEDELQDK | P02666 | Beta-casein | 48-63 | 5.4 | 43.5 | 6 | 111.4 |
| VYPFPGPIPN | P02666 | Beta-casein | 74-83 | 6.0 | 67.9 | 8 | 108.2 |
| GFLPQNILPLAQPA | P05814 | Beta-casein | 75-88 | 5.9 | 197.7 | 2 | 129.4 |
| QNILPLAQPAVVLPVPQPEIMEVPK | P05814 | Beta-casein | 79-103 | 5.6 | 93.3 | 1 | 83.0 |
| ILPLAQPAVVLPVPQPEIMEVPK | P05814 | Beta-casein | 81-103 | 6.3 | 326.2 | 1 | 104.0 |
| PLAQPAVVLPVPQPEI | P05814 | Beta-casein | 83-98 | 6.2 | 74.9 | 4 | 110.9 |
| LAQPAVVLPVPQPEIMEVPK | P05814 | Beta-casein | 84-103 | 6.5 | 107.2 | 6 | 93.8 |
| LAQPAVVLPVPQPEIMEVPKA | P05814 | Beta-casein | 84-104 | 5.8 | 167.4 | 1 | 114.7 |
| LAQPAVVLPVPQPEIMEVPKAKDT | P05814 | Beta-casein | 84-107 | 5.7 | 74.8 | 6 | 85.3 |
| AQPAVVLPVPQPEIMEVPK | P05814 | Beta-casein | 85-103 | 6.6 | 73.0 | 6 | 138.9 |
| AQPAVVLPVPQPEIMEVPKA | P05814 | Beta-casein | 85-104 | 6.0 | 101.8 | 1 | 132.1 |
| AQPAVVLPVPQPEIMEVPKAKDT | P05814 | Beta-casein | 85-107 | 6.0 | 80.0 | 1 | 63.2 |
| AQPAVVLPVPQPEIMEVPKAKDTVY | P05814 | Beta-casein | 85-109 | 6.0 | 149.2 | 1 | 52.5 |
| QPAVVLPVPQPEIMEVP | P05814 | Beta-casein | 86-102 | 5.5 | 158.7 | 1 | 75.7 |
| QPAVVLPVPQPEIMEVPK | P05814 | Beta-casein | 86-103 | 7.1 | 102.1 | 1 | 155.1 |
| QPAVVLPVPQPEIMEVPKA | P05814 | Beta-casein | 86-104 | 6.4 | 127.3 | 1 | 156.6 |
| QPAVVLPVPQPEIMEVPKAKDTVYT | P05814 | Beta-casein | 86-110 | 6.1 | 105.4 | 3 | 80.2 |
| QPAVVLPVPQPEI | P05814 | Beta-casein | 86-98 | 5.6 | 73.8 | 1 | 74.2 |
| PAVVLPVPQPEI | P05814 | Beta-casein | 87-98 | 5.8 | 62.0 | 4 | 90.6 |
| AVVLPVPQPEIMEVPKAKDTVYT | P05814 | Beta-casein | 88-110 | 6.4 | 78.8 | 1 | 55.8 |
| VVLPVPQPEIMEVPK | P05814 | Beta-casein | 89-103 | 7.0 | 143.9 | 2 | 112.4 |
| VVLPVPQPEIMEVPKA | P05814 | Beta-casein | 89-104 | 6.4 | 159.9 | 2 | 151.9 |
| VVLPVPQPEIMEVPKAKDTVYT | P05814 | Beta-casein | 89-110 | 7.3 | 137.6 | 10 | 87.6 |
| VLPVPQPEIMEVPK | P05814 | Beta-casein | 90-103 | 6.3 | 139.6 | 2 | 101.9 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| LPVPQPEIME | P05814 | Beta-casein | 91-100 | 5.7 | 104.9 | 1 | 79.9 |
| LPVPQPEIMEVP | P05814 | Beta-casein | 91-102 | 5.8 | 93.0 | 3 | 54.6 |
| LPVPQPEIMEVPK | P05814 | Beta-casein | 91-103 | 7.5 | 74.6 | 1 | 142.1 |
| LPVPQPEIMEVPKA | P05814 | Beta-casein | 91-104 | 6.7 | 92.6 | 1 | 137.2 |
| LPVPQPEIMEVPKAKDT | P05814 | Beta-casein | 91-107 | 6.9 | 69.9 | 1 | 179.5 |
| LPVPQPEIMEVPKAKDTV | P05814 | Beta-casein | 91-108 | 6.4 | 71.1 | 1 | 137.4 |
| LPVPQPEIMEVPKAKDTVYT | P05814 | Beta-casein | 91-110 | 7.1 | 75.1 | 1 | 120.3 |
| VPQPEIMEVPK | P05814 | Beta-casein | 93-103 | 6.4 | 109.5 | 1 | 143.5 |
| TQTPVVVPPFLQPEV | P02666 | Beta-casein | 93-107 | 5.9 | 67.8 | 8 | 70.0 |
| VPQPEIMEVPKAKDT | P05814 | Beta-casein | 93-107 | 6.3 | 91.4 | 1 | 130.2 |
| VPQPEIMEVPKAKDTVYT | P05814 | Beta-casein | 93-110 | 6.6 | 82.7 | 1 | 147.2 |
| QPEIMEVPKAKDT | P05814 | Beta-casein | 95-107 | 5.5 | 106.1 | 1 | 50.6 |
| TPVVVPPFLQPEV | P02666 | Beta-casein | 95-107 | 5.6 | 64.5 | 8 | 70.1 |
| QPEIMEVPKAKDTVYT | P05814 | Beta-casein | 95-110 | 6.4 | 73.0 | 1 | 45.7 |
| EIMEVPKAKDTVYT | P05814 | Beta-casein | 97-110 | 6.7 | 69.3 | 1 | 149.3 |
| EIMEVPKAKDTVYTK | P05814 | Beta-casein | 97-111 | 6.1 | 106.9 | 6 | 80.5 |
| IMEVPKAKDTVYT | P05814 | Beta-casein | 98-110 | 5.7 | 91.0 | 1 | 75.8 |
| MEVPKAKDTVYT | P05814 | Beta-casein | 99-110 | 6.2 | 54.9 | 3 | 99.6 |
| MEVPKAKDTVYTK | P05814 | Beta-casein | 99-111 | 5.4 | 79.7 | 3 | 70.6 |
| MEVPKAKDTVYTKG | P05814 | Beta-casein | 99-112 | 5.6 | 104.9 | 4 | 96.7 |
| AKLGAVYTEGGFVEGVNK | P19835 | Bile salt-activated lipase | 21-38 | 6.3 | 88.4 | 3 | 229.6 |
| AKLGAVYTEGGFVEGVNKK | P19835 | Bile salt-activated lipase | 21-39 | 6.5 | 100.4 | 3 | 145.1 |
| KLGAVYTEGGFVEGVNK | P19835 | Bile salt-activated lipase | 22-38 | 6.3 | 62.7 | 3 | 205.3 |
| KLGAVYTEGGFVEGVNKK | P19835 | Bile salt-activated lipase | 22-39 | 6.3 | 69.2 | 3 | 214.5 |
| GAVYTEGGFVEGVNK | P19835 | Bile salt-activated lipase | 24-38 | 6.2 | 56.3 | 3 | 210.9 |
| GAVYTEGGFVEGVNKK | P19835 | Bile salt-activated lipase | 24-39 | 6.2 | 105.4 | 3 | 78.4 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| TEGGFVEGVNK | P19835 | Bile salt-activated lipase | 28-38 | 6.1 | 57.1 | 3 | 207.8 |
| TEGGFVEGVNKK | P19835 | Bile salt-activated lipase | 28-39 | 6.1 | 73.8 | 3 | 134.6 |
| EGGFVEGVNK | P19835 | Bile salt-activated lipase | 29-38 | 6.6 | 69.4 | 3 | 114.5 |
| GNKKVTEEDFYK | P19835 | Bile salt-activated lipase | 355-366 | 5.7 | 107.1 | 3 | 110.9 |
| TTENSGYLEITK | P19835 | Bile salt-activated lipase | 512-523 | 5.5 | 100.6 | 2 | 131.8 |
| GIPFAAPTKALENPQPHPGWQGTL | P19835 | Bile salt-activated lipase | 52-75 | 6.6 | 61.5 | 6 | 120.5 |
| GIPFAAPTKALENPQPHPGWQGTLK | P19835 | Bile salt-activated lipase | 52-76 | 6.2 | 119.1 | 3 | 60.7 |
| APTKALENPQPHPGWQGTL | P19835 | Bile salt-activated lipase | 57-75 | 5.8 | 54.7 | 6 | 63.3 |
| ALENPQPHPGWQGTLK | P19835 | Bile salt-activated lipase | 61-76 | 5.4 | 108.8 | 3 | 67.4 |
| IPASSLPRLTPWI | Q13410 | Butyrophilin subfamily 1 member A1 | 235-247 | 5.3 | 80.0 | 1 | 152.1 |
| IPASSLPRLTPWIV | Q13410 | Butyrophilin subfamily 1 member A1 | 235-248 | 5.5 | 68.6 | 1 | 129.9 |
| IPASSLPRLTPWIVA | Q13410 | Butyrophilin subfamily 1 member A1 | 235-249 | 5.8 | 91.3 | 7 | 122.7 |
| IPASSLPRLTPWIVAVA | Q13410 | Butyrophilin subfamily 1 member A1 | 235-251 | 5.4 | 78.9 | 1 | 116.5 |
| APFDVIGPPEPI | Q13410 | Butyrophilin subfamily 1 member A1 | 27-38 | 5.6 | 119.4 | 2 | 70.0 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| APFDVIGPPEPILA | Q13410 | Butyrophilin subfamily 1 member A1 | 27-40 | 5.4 | 80.8 | 4 | 101.1 |
| YEDSKSVRLE | Q13410 | Butyrophilin subfamily 1 member A1 | 319-328 | 5.3 | 92.0 | 3 | 78.7 |
| DGPERVTVIANAQDLS | Q13410 | Butyrophilin subfamily 1 member A1 | 477-492 | 6.3 | 65.9 | 4 | 124.3 |
| KEIPLSPMGED | Q13410 | Butyrophilin subfamily 1 member A1 | 493-503 | 5.6 | 63.8 | 9 | 91.9 |
| KEIPLSPMGEDS | Q13410 | Butyrophilin subfamily 1 member A1 | 493-504 | 5.9 | 113.4 | 10 | 105.9 |
| KEIPLSPMGEDSAPR | Q13410 | Butyrophilin subfamily 1 member A1 | 493-507 | 6.2 | 78.2 | 10 | 150.4 |
| KEIPLSPMGEDSAPRD | Q13410 | Butyrophilin subfamily 1 member A1 | 493-508 | 5.8 | 88.6 | 10 | 86.6 |
| KEIPLSPMGEDSAPRDADTLH | Q13410 | Butyrophilin subfamily 1 member A1 | 493-513 | 7.3 | 73.4 | 10 | 196.6 |
| KEIPLSPMGEDSAPRDADTLHS | Q13410 | Butyrophilin subfamily 1 member A1 | 493-514 | 6.4 | 92.2 | 10 | 191.8 |
| EIPLSPMGEDSAPR | Q13410 | Butyrophilin subfamily 1 member A1 | 494-507 | 6.3 | 91.2 | 10 | 84.7 |
| EIPLSPMGEDSAPRDADTLH | Q13410 | Butyrophilin subfamily 1 member A1 | 494-513 | 6.8 | 82.3 | 10 | 60.6 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| IPLSPMGEDSAPR | Q13410 | Butyrophilin subfamily 1 member A1 | 495-507 | 6.7 | 74.2 | 10 | 215.6 |
| IPLSPMGEDSAPRD | Q13410 | Butyrophilin subfamily 1 member A1 | 495-508 | 5.9 | 86.5 | 10 | 99.5 |
| IPLSPMGEDSAPRDADTLH | Q13410 | Butyrophilin subfamily 1 member A1 | 495-513 | 6.9 | 60.7 | 10 | 170.9 |
| PLSPMGEDSAPRD | Q13410 | Butyrophilin subfamily 1 member A1 | 496-508 | 5.8 | 81.0 | 10 | 111.1 |
| SPMGEDSAPR | Q13410 | Butyrophilin subfamily 1 member A1 | 498-507 | 5.5 | 75.6 | 10 | 94.7 |
| SPMGEDSAPRD | Q13410 | Butyrophilin subfamily 1 member A1 | 498-508 | 5.8 | 96.9 | 10 | 146.1 |
| SPMGEDSAPRDADTLH | Q13410 | Butyrophilin subfamily 1 member A1 | 498-513 | 6.1 | 80.0 | 10 | 113.4 |
| GEDSAPRDADTLH | Q13410 | Butyrophilin subfamily 1 member A1 | 501-513 | 5.8 | 74.3 | 10 | 58.7 |
| GEDSAPRDADTLHS | Q13410 | Butyrophilin subfamily 1 member A1 | 501-514 | 5.1 | 73.3 | 10 | 68.8 |
| SAPRDADTLHSKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 504-526 | 6.1 | 64.5 | 5 | 60.7 |
| APRDADTLH | Q13410 | Butyrophilin subfamily 1 member A1 | 505-513 | 6.3 | 103.8 | 7 | 98.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| APRDADTLHSKLIP | Q13410 | Butyrophilin subfamily 1 member A1 | 505-518 | 5.9 | 69.9 | 5 | 71.6 |
| APRDADTLHSKLIPT | Q13410 | Butyrophilin subfamily 1 member A1 | 505-519 | 5.6 | 65.2 | 6 | 55.9 |
| APRDADTLHSKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 505-526 | 6.7 | 66.6 | 6 | 67.3 |
| DADTLHSKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 508-526 | 6.9 | 54.8 | 4 | 77.9 |
| ADTLHSKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 509-526 | 6.6 | 108.7 | 5 | 161.8 |
| DTLHSKLI | Q13410 | Butyrophilin subfamily 1 member A1 | 510-517 | 5.4 | 68.2 | 8 | 122.0 |
| DTLHSKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 510-526 | 5.5 | 53.8 | 10 | 54.0 |
| HSKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 513-526 | 5.5 | 101.9 | 11 | 71.0 |
| SKLIPTQPSQG | Q13410 | Butyrophilin subfamily 1 member A1 | 514-524 | 6.6 | 75.0 | 5 | 130.0 |
| SKLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 514-526 | 6.9 | 64.6 | 4 | 126.0 |
| KLIPTQPSQG | Q13410 | Butyrophilin subfamily 1 member A1 | 515-524 | 6.0 | 65.9 | 5 | 66.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| KLIPTQPSQGAP | Q13410 | Butyrophilin subfamily 1 member A1 | 515-526 | 6.2 | 150.9 | 2 | 61.3 |
| KVSPAVLVHRDG | Q13410 | Butyrophilin subfamily 1 member A1 | 69-80 | 5.6 | 110.5 | 4 | 68.0 |
| SPAVLVHRDGREQE | Q13410 | Butyrophilin subfamily 1 member A1 | 71-84 | 5.9 | 38.5 | 9 | 173.7 |
| SPAVLVHRDGREQEAEQMPEY | Q13410 | Butyrophilin subfamily 1 member A1 | 71-91 | 6.6 | 107.9 | 1 | 167.4 |
| DGREQEAEQMPE | Q13410 | Butyrophilin subfamily 1 member A1 | 79-90 | 6.1 | 47.4 | 11 | 112.8 |
| DGREQEAEQMPEY | Q13410 | Butyrophilin subfamily 1 member A1 | 79-91 | 7.2 | 49.3 | 9 | 172.1 |
| DGREQEAEQMPEYR | Q13410 | Butyrophilin subfamily 1 member A1 | 79-92 | 7.5 | 61.2 | 11 | 329.7 |
| DGREQEAEQMPEYRG | Q13410 | Butyrophilin subfamily 1 member A1 | 79-93 | 6.8 | 101.8 | 9 | 203.9 |
| DGREQEAEQMPEYRGR | Q13410 | Butyrophilin subfamily 1 member A1 | 79-94 | 7.2 | 67.0 | 11 | 180.6 |
| GREQEAEQMPEY | Q13410 | Butyrophilin subfamily 1 member A1 | 80-91 | 6.0 | 87.7 | 9 | 139.9 |
| GREQEAEQMPEYR | Q13410 | Butyrophilin subfamily 1 member A1 | 80-92 | 6.1 | 86.9 | 11 | 115.1 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| GREQEAEQMPEYRGR | Q13410 | Butyrophilin subfamily 1 member A1 | 80-94 | 5.6 | 79.7 | 11 | 147.1 |
| GRATLVQDGIA | Q13410 | Butyrophilin subfamily 1 member A1 | 93-103 | 6.3 | 85.2 | 5 | 73.8 |
| GRATLVQDGIAK | Q13410 | Butyrophilin subfamily 1 member A1 | 93-104 | 6.5 | 68.3 | 11 | 132.3 |
| GRATLVQDGIAKGRVA | Q13410 | Butyrophilin subfamily 1 member A1 | 93-108 | 6.1 | 63.9 | 5 | 115.3 |
| GRATLVQDGIAKGRVAL | Q13410 | Butyrophilin subfamily 1 member A1 | 93-109 | 5.8 | 52.1 | 10 | 78.2 |
| TLVQDGIAKGRVA | Q13410 | Butyrophilin subfamily 1 member A1 | 96-108 | 5.8 | 112.8 | 5 | 73.8 |
| APLSFIPR | Q6WN34 | Chordin-like protein 2 | 221-228 | 5.8 | 91.2 | 9 | 127.8 |
| HFRPKGAGSTTV | Q6WN34 | Chordin-like protein 2 | 229-240 | 5.7 | 84.0 | 5 | 60.4 |
| HFRPKGAGSTTVK | Q6WN34 | Chordin-like protein 2 | 229-241 | 5.6 | 94.8 | 11 | 87.0 |
| RPKGAGSTTVKIV | Q6WN34 | Chordin-like protein 2 | 231-243 | 5.6 | 91.0 | 8 | 82.4 |
| RPKGAGSTTVKIVL | Q6WN34 | Chordin-like protein 2 | 231-244 | 5.9 | 78.8 | 6 | 75.7 |
| GAGSTTVKIVLK | Q6WN34 | Chordin-like protein 2 | 234-245 | 5.6 | 64.5 | 3 | 94.6 |
| APGRVLVHTSVSPSPDNL | Q6WN34 | Chordin-like protein 2 | 334-351 | 5.6 | 58.0 | 7 | 74.8 |
| ELKVTASPDKVTKT | Q6WN34 | Chordin-like protein 2 | 416-429 | 5.8 | 76.8 | 2 | 65.5 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| KVTASPDKVTKT | Q6WN34 | Chordin-like protein 2 | 418-429 | 6.1 | 66.1 | 10 | 150.3 |
| SLERLPSPDPGAEGHGQS | H0YCU0 | Chordin-like protein 2 | 64-81 | 5.6 | 103.7 | 2 | 94.6 |
| PGAEGHGQSRQSDQDITKT | H0YCU0 | Chordin-like protein 2 | 73-91 | 5.6 | 82.8 | 8 | 132.8 |
| QSDQDITKT | H0YCU0 | Chordin-like protein 2 | 83-91 | 6.1 | 104.0 | 4 | 214.8 |
| NGFKSHALQLNNRQ | P0C0L5 | Complement C4-B | 1337-1350 | 5.4 | 142.1 | 1 | 101.5 |
| NGFKSHALQLNNRQI | P0C0L5 | Complement C4-B | 1337-1351 | 6.4 | 256.8 | 9 | 270.2 |
| NGFKSHALQLNNRQIR | P0C0L5 | Complement C4-B | 1337-1352 | 5.4 | 138.0 | 1 | 56.9 |
| DDPDAPLQPVTPLQ | P0C0L5 | Complement C4-B | 1429-1442 | 5.9 | 100.2 | 1 | 71.6 |
| DDPDAPLQPVTPLQL | P0C0L5 | Complement C4-B | 1429-1443 | 5.9 | 90.0 | 1 | 97.2 |
| DDPDAPLQPVTPLQLFEG | P0C0L5 | Complement C4-B | 1429-1446 | 6.1 | 97.4 | 9 | 125.6 |
| DDPDAPLQPVTPLQLFEGR | P0C0L5 | Complement C4-B | 1429-1447 | 6.3 | 77.1 | 1 | 121.8 |
| DDPDAPLQPVTPLQLFEGRRN | P0C0L5 | Complement C4-B | 1429-1449 | 7.2 | 83.2 | 1 | 122.0 |
| PDAPLQPVTPLQLFEGRRN | P0C0L5 | Complement C4-B | 1431-1449 | 5.5 | 109.5 | 7 | 71.0 |
| DSGEGDFLAEGGGVR | P02671 | Fibrinogen alpha chain | 21-35 | 7.2 | 65.2 | 11 | 326.4 |
| KPVPDLVPGNF | P02671 | Fibrinogen alpha chain | 227-237 | 5.7 | 123.5 | 9 | 85.7 |
| EGDFLAEGGGVR | P02671 | Fibrinogen alpha chain | 24-35 | 6.0 | 118.5 | 4 | 211.3 |
| SSSYSKQFTSSTSYNRGDSTFES | P02671 | Fibrinogen alpha chain | 576-598 | 5.7 | 59.1 | 1 | 112.0 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| DEAGSEADHEGTHS | P02671 | Fibrinogen alpha chain | 605-618 | 5.8 | 74.7 | 11 | 205.1 |
| DEAGSEADHEGTHST | P02671 | Fibrinogen alpha chain | 605-619 | 5.4 | 71.7 | 9 | 60.2 |
| DEAGSEADHEGTHSTK | P02671 | Fibrinogen alpha chain | 605-620 | 5.5 | 82.5 | 5 | 74.7 |
| DEAGSEADHEGTHSTKRG | P02671 | Fibrinogen alpha chain | 605-622 | 6.1 | 85.3 | 5 | 117.4 |
| DEAGSEADHEGTHSTKRGHA | P02671 | Fibrinogen alpha chain | 605-624 | 6.0 | 84.3 | 9 | 199.8 |
| GPEAAKSDETAAK | P04792 | Heat shock protein beta-1 | 193-205 | 5.6 | 87.3 | 4 | 99.8 |
| RPNLHPSFIAIPPKKIQD | P07498 | Kappa-casein | 110-127 | 5.8 | 125.7 | 1 | 39.2 |
| IAIPPKKIQDK | P07498 | Kappa-casein | 118-128 | 5.8 | 90.4 | 3 | 88.7 |
| RPAIAINNPYVP | P07498 | Kappa-casein | 66-77 | 5.8 | 139.0 | 1 | 72.5 |
| RPAIAINNPYVPR | P07498 | Kappa-casein | 66-78 | 5.9 | 122.1 | 2 | 77.6 |
| TYYANPAVVRPHAQIP | P07498 | Kappa-casein | 79-94 | 6.3 | 163.4 | 9 | 65.1 |
| TYYANPAVVRPHAQIPQ | P07498 | Kappa-casein | 79-95 | 6.3 | 107.4 | 9 | 122.4 |
| TYYANPAVVRPHAQIPQR | P07498 | Kappa-casein | 79-96 | 6.6 | 67.2 | 9 | 141.8 |
| YANPAVVRPHAQIPQR | P07498 | Kappa-casein | 81-96 | 5.6 | 109.7 | 9 | 88.1 |
| ANPAVVRPHAQIPQ | P07498 | Kappa-casein | 82-95 | 5.6 | 89.9 | 1 | 49.4 |
| NPAVVRPHAQIPQR | P07498 | Kappa-casein | 83-96 | 5.6 | 154.6 | 9 | 96.7 |
| VVRPHAQIPQRQYLPNSHPPTVV | P07498 | Kappa-casein | 86-108 | 6.1 | 178.0 | 1 | 92.5 |
| IPQRQYLPNSHPPTVV | P07498 | Kappa-casein | 93-108 | 5.9 | 119.1 | 1 | 86.0 |
| IPQRQYLPNSHPPTVVR | P07498 | Kappa-casein | 93-109 | 6.5 | 164.4 | 9 | 27.5 |
| RQYLPNSHPPTVVR | P07498 | Kappa-casein | 96-109 | 5.3 | 127.2 | 6 | 51.5 |
| LPNSHPPTVVR | P07498 | Kappa-casein | 99-109 | 6.6 | 255.3 | 9 | 93.3 |
| DPSKPSSNVA | P22897 | Macrophage mannose receptor 1 | 1380-1389 | 5.0 | 143.9 | 2 | 100.0 |
| DPSKPSSNVAG | P22897 | Macrophage mannose receptor 1 | 1380-1390 | 6.2 | 89.8 | 4 | 101.4 |
| DPSKPSSNVAGVVI | P22897 | Macrophage mannose receptor 1 | 1380-1393 | 6.4 | 52.0 | 8 | 39.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| DPSKPSSNVAGVVII | P22897 | Macrophage mannose receptor 1 | 1380-1394 | 7.1 | 45.0 | 11 | 128.2 |
| DPSKPSSNVAGVVIIV | P22897 | Macrophage mannose receptor 1 | 1380-1395 | 7.3 | 45.6 | 11 | 122.4 |
| DPSKPSSNVAGVVIIVI | P22897 | Macrophage mannose receptor 1 | 1380-1396 | 6.7 | 43.6 | 11 | 106.5 |
| KPSSNVAGVVII | P22897 | Macrophage mannose receptor 1 | 1383-1394 | 5.7 | 77.3 | 10 | 54.4 |
| KPSSNVAGVVIIV | P22897 | Macrophage mannose receptor 1 | 1383-1395 | 5.8 | 67.0 | 10 | 75.3 |
| EYPTYHTHGRYVPPS | P15941 | Mucin-1 | 1208-1222 | 5.9 | 59.4 | 7 | 66.2 |
| EYPTYHTHGRYVPPSS | P15941 | Mucin-1 | 1208-1223 | 6.3 | 77.0 | 5 | 51.8 |
| EYPTYHTHGRYVPPSSTD | P15941 | Mucin-1 | 1208-1225 | 5.6 | 77.4 | 3 | 43.4 |
| YPTYHTHGRYVPP | P15941 | Mucin-1 | 1209-1221 | 5.5 | 117.9 | 6 | 74.6 |
| YPTYHTHGRYVPPSS | P15941 | Mucin-1 | 1209-1223 | 5.8 | 52.9 | 5 | 46.4 |
| HTHGRYVPPSS | P15941 | Mucin-1 | 1213-1223 | 5.7 | 93.9 | 5 | 84.7 |
| HTHGRYVPPSSTD | P15941 | Mucin-1 | 1213-1225 | 5.1 | 100.4 | 1 | 53.3 |
| PPSSTDRSPYE | P15941 | Mucin-1 | 1220-1230 | 5.3 | 65.2 | 5 | 63.3 |
| STDRSPYEKVSAGNGGSSLS | P15941 | Mucin-1 | 1223-1242 | 6.3 | 52.4 | 5 | 92.3 |
| STDRSPYEKVSAGNGGSSLSY | P15941 | Mucin-1 | 1223-1243 | 6.3 | 65.2 | 5 | 164.6 |
| TDRSPYEKVSAGNGGSSL | P15941 | Mucin-1 | 1224-1241 | 5.9 | 94.3 | 5 | 65.7 |
| TDRSPYEKVSAGNGGSSLS | P15941 | Mucin-1 | 1224-1242 | 6.9 | 51.6 | 5 | 153.2 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| TDRSPYEKVSAGNGGSSLSY | P15941 | Mucin-1 | 1224-1243 | 6.9 | 61.9 | 5 | 158.0 |
| DRSPYEKVSAGNGGSSL | P15941 | Mucin-1 | 1225-1241 | 5.9 | 79.9 | 5 | 64.5 |
| DRSPYEKVSAGNGGSSLS | P15941 | Mucin-1 | 1225-1242 | 6.6 | 62.0 | 5 | 116.3 |
| DRSPYEKVSAGNGGSSLSY | P15941 | Mucin-1 | 1225-1243 | 6.7 | 64.8 | 10 | 191.2 |
| SPYEKVSAGNGGS | P15941 | Mucin-1 | 1227-1239 | 5.6 | 62.0 | 5 | 152.0 |
| SPYEKVSAGNGGSS | P15941 | Mucin-1 | 1227-1240 | 6.0 | 55.7 | 5 | 196.4 |
| SPYEKVSAGNGGSSL | P15941 | Mucin-1 | 1227-1241 | 6.5 | 88.0 | 5 | 285.5 |
| SPYEKVSAGNGGSSLS | P15941 | Mucin-1 | 1227-1242 | 6.8 | 49.3 | 5 | 302.6 |
| SPYEKVSAGNGGSSLSY | P15941 | Mucin-1 | 1227-1243 | 6.8 | 46.8 | 5 | 299.6 |
| YEKVSAGNGGSS | P15941 | Mucin-1 | 1229-1240 | 4.9 | 108.2 | 7 | 107.1 |
| YEKVSAGNGGSSL | P15941 | Mucin-1 | 1229-1241 | 5.8 | 96.9 | 5 | 206.1 |
| YEKVSAGNGGSSLS | P15941 | Mucin-1 | 1229-1242 | 5.5 | 56.3 | 2 | 82.2 |
| YEKVSAGNGGSSLSY | P15941 | Mucin-1 | 1229-1243 | 5.5 | 67.1 | 5 | 121.0 |
| EKVSAGNGGSSL | P15941 | Mucin-1 | 1230-1241 | 5.7 | 95.7 | 5 | 150.1 |
| EKVSAGNGGSSLS | P15941 | Mucin-1 | 1230-1242 | 5.9 | 50.8 | 4 | 152.5 |
| TNPAVAATSANL | P15941 | Mucin-1 | 1244-1255 | 6.7 | 68.9 | 3 | 83.4 |
| NPAVAATSANL | P15941 | Mucin-1 | 1245-1255 | 6.9 | 47.3 | 11 | 220.0 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| TYDGRGDSVVYGLR | P10451 | Osteopontin | 155-168 | 6.9 | 82.7 | 8 | 163.8 |
| TYDGRGDSVVYGLRSK | P10451 | Osteopontin | 155-170 | 5.5 | 81.6 | 3 | 67.7 |
| YDGRGDSVVYGLR | P10451 | Osteopontin | 156-168 | 6.1 | 83.8 | 6 | 112.4 |
| DGRGDSVVYGLR | P10451 | Osteopontin | 157-168 | 6.3 | 118.7 | 8 | 141.1 |
| DGRGDSVVYGLRSKSKKF | P10451 | Osteopontin | 157-174 | 5.6 | 99.3 | 2 | 31.8 |
| GRGDSVVYGLR | P10451 | Osteopontin | 158-168 | 6.5 | 82.3 | 8 | 204.3 |
| GRGDSVVYGLRSK | P10451 | Osteopontin | 158-170 | 5.8 | 70.6 | 3 | 63.7 |
| GRGDSVVYGLRSKSKKF | P10451 | Osteopontin | 158-174 | 5.9 | 62.2 | 8 | 41.6 |
| RGDSVVYGLR | P10451 | Osteopontin | 159-168 | 6.7 | 85.9 | 8 | 255.1 |
| RGDSVVYGLRSK | P10451 | Osteopontin | 159-170 | 5.8 | 70.3 | 3 | 86.9 |
| RGDSVVYGLRSKS | P10451 | Osteopontin | 159-171 | 5.4 | 95.4 | 8 | 52.5 |
| DSVVYGLR | P10451 | Osteopontin | 161-168 | 7.0 | 107.8 | 8 | 174.2 |
| DSVVYGLRSK | P10451 | Osteopontin | 161-170 | 5.7 | 116.8 | 3 | 91.6 |
| DSVVYGLRSKSKK | P10451 | Osteopontin | 161-173 | 5.0 | 85.0 | 3 | 85.3 |
| DSVVYGLRSKSKKF | P10451 | Osteopontin | 161-174 | 5.9 | 96.8 | 8 | 111.1 |
| SVVYGLRSKSKKF | P10451 | Osteopontin | 162-174 | 5.7 | 97.7 | 8 | 95.4 |
| VYGLRSKSKKF | P10451 | Osteopontin | 164-174 | 5.6 | 186.3 | 2 | 75.0 |
| YGLRSKSKKF | P10451 | Osteopontin | 165-174 | 5.5 | 211.2 | 2 | 80.0 |
| SKSKKFRRPD | P10451 | Osteopontin | 169-178 | 5.6 | 113.1 | 10 | 78.7 |
| SKSKKFRRPDIQYPD | P10451 | Osteopontin | 169-183 | 5.4 | 90.6 | 2 | 63.7 |
| SKSKKFRRPDIQYPDATD | P10451 | Osteopontin | 169-186 | 6.9 | 114.7 | 11 | 111.2 |
| SKSKKFRRPDIQYPDATDEDITSH | P10451 | Osteopontin | 169-192 | 6.8 | 165.9 | 11 | 189.5 |
| IPVKQADSG | P10451 | Osteopontin | 17-25 | 6.0 | 101.5 | 8 | 93.4 |
| SKKFRRPDIQYPDATD | P10451 | Osteopontin | 171-186 | 6.2 | 59.3 | 7 | 112.7 |
| KFRRPDIQYPDATD | P10451 | Osteopontin | 173-186 | 5.8 | 101.6 | 4 | 88.1 |
| FRRPDIQYPDATD | P10451 | Osteopontin | 174-186 | 6.2 | 89.4 | 2 | 106.0 |
| RRPDIQYPDATD | P10451 | Osteopontin | 175-186 | 5.6 | 48.9 | 5 | 140.1 |
| RRPDIQYPDATDEDITSH | P10451 | Osteopontin | 175-192 | 5.9 | 150.1 | 2 | 211.1 |
| RPDIQYPDATD | P10451 | Osteopontin | 176-186 | 6.6 | 66.9 | 2 | 182.7 |
| RPDIQYPDATDED | P10451 | Osteopontin | 176-188 | 5.6 | 50.2 | 3 | 87.4 |
| RPDIQYPDATDEDIT | P10451 | Osteopontin | 176-190 | 6.5 | 101.9 | 2 | 77.6 |
| RPDIQYPDATDEDITSH | P10451 | Osteopontin | 176-192 | 7.1 | 99.4 | 2 | 278.5 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| DIQYPDATDEDIT | P10451 | Osteopontin | 178-190 | 6.2 | 100.0 | 5 | 96.8 |
| DIQYPDATDEDITSH | P10451 | Osteopontin | 178-192 | 7.0 | 81.6 | 2 | 164.0 |
| DIQYPDATDEDITSHMESEELNGAY | P10451 | Osteopontin | 178-202 | 6.4 | 110.3 | 1 | 114.9 |
| YPDATDEDITSH | P10451 | Osteopontin | 181-192 | 6.1 | 116.7 | 2 | 290.9 |
| DATDEDITSH | P10451 | Osteopontin | 183-192 | 6.0 | 97.2 | 1 | 258.2 |
| ATDEDITSH | P10451 | Osteopontin | 184-192 | 5.1 | 93.7 | 4 | 225.8 |
| TDEDITSH | P10451 | Osteopontin | 185-192 | 5.5 | 120.8 | 6 | 130.1 |
| EDITSHME | P10451 | Osteopontin | 187-194 | 5.7 | 88.3 | 8 | 126.2 |
| EDITSHMESEELNGAYK | P10451 | Osteopontin | 187-203 | 5.7 | 76.3 | 4 | 87.9 |
| NGAYKAIPVAQD | P10451 | Osteopontin | 199-210 | 5.4 | 60.9 | 3 | 96.9 |
| GAYKAIPVAQDLNAPSD | P10451 | Osteopontin | 200-216 | 6.2 | 61.3 | 8 | 89.4 |
| AIPVAQDLNAPS | P10451 | Osteopontin | 204-215 | 6.4 | 86.8 | 8 | 141.9 |
| AIPVAQDLNAPSD | P10451 | Osteopontin | 204-216 | 6.8 | 59.2 | 3 | 199.1 |
| AIPVAQDLNAPSDWD | P10451 | Osteopontin | 204-218 | 5.9 | 110.8 | 3 | 128.0 |
| IPVAQDLNAPS | P10451 | Osteopontin | 205-215 | 7.0 | 135.5 | 2 | 216.1 |
| PVAQDLNAPSD | P10451 | Osteopontin | 206-216 | 6.0 | 70.2 | 2 | 78.9 |
| DLNAPSDWDSRGK | P10451 | Osteopontin | 210-222 | 5.4 | 130.7 | 1 | 52.6 |
| ETSQLDDQSAETHSHKQS | P10451 | Osteopontin | 226-243 | 5.6 | 101.9 | 1 | 57.5 |
| ETSQLDDQSAETHSHKQSRLY | P10451 | Osteopontin | 226-246 | 5.4 | 113.5 | 1 | 135.7 |
| DSGSSEEKQLYNKYPDAVAT | P10451 | Osteopontin | 23-42 | 6.1 | 163.9 | 1 | 207.3 |
| DDQSAETHSHKQSRLY | P10451 | Osteopontin | 231-246 | 6.0 | 111.3 | 2 | 179.5 |
| DQSAETHSHKQSRLY | P10451 | Osteopontin | 232-246 | 5.6 | 76.7 | 6 | 133.5 |
| SKEEDKHLKF | P10451 | Osteopontin | 291-300 | 5.3 | 56.8 | 7 | 116.8 |
| SKEEDKHLKFRIS | P10451 | Osteopontin | 291-303 | 5.7 | 170.4 | 11 | 106.6 |
| FRISHELDSASSEVN | P10451 | Osteopontin | 300-314 | 6.0 | 100.9 | 3 | 51.5 |
| RISHELDSASSEVN | P10451 | Osteopontin | 301-314 | 5.5 | 107.6 | 8 | 109.2 |
| ISHELDSASSEVN | P10451 | Osteopontin | 302-314 | 6.3 | 71.5 | 6 | 199.7 |
| SHELDSASSEVN | P10451 | Osteopontin | 303-314 | 6.5 | 72.1 | 6 | 225.7 |
| HELDSASSEVN | P10451 | Osteopontin | 304-314 | 5.9 | 57.6 | 6 | 155.4 |
| NKYPDAVAT | P10451 | Osteopontin | 34-42 | 5.9 | 136.2 | 2 | 85.2 |
| PSQKQNLLAPQN | P10451 | Osteopontin | 48-59 | 5.5 | 98.0 | 7 | 68.9 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| YLTQETNKVE | P12272 | Parathyroid hormone-related protein | 103-112 | 5.4 | 135.0 | 2 | 112.1 |
| KEQPLKTPGKK | P12272 | Parathyroid hormone-related protein | 115-125 | 5.5 | 104.7 | 2 | 78.7 |
| EHQLLHDKGKSIQD | P12272 | Parathyroid hormone-related protein | 40-53 | 5.4 | 82.2 | 8 | 73.9 |
| ATSEVSPNSKPSPNTK | P12272 | Parathyroid hormone-related protein | 74-89 | 5.5 | 81.8 | 8 | 72.9 |
| TSEVSPNSKPSPNTK | P12272 | Parathyroid hormone-related protein | 75-89 | 4.9 | 66.8 | 2 | 71.0 |
| NAKGAVTGAKDAVTTTVT | Q99541 | Perilipin-2 | 107-124 | 5.9 | 79.4 | 5 | 164.0 |
| GAVTGAKDAVTTTVT | Q99541 | Perilipin-2 | 110-124 | 5.5 | 81.3 | 10 | 24.9 |
| GAKDAVTTTVT | Q99541 | Perilipin-2 | 114-124 | 5.5 | 103.6 | 8 | 116.3 |
| GAKDSVASTITGVMD | Q99541 | Perilipin-2 | 125-139 | 5.4 | 71.9 | 10 | 110.7 |
| KTKGAVTGSVEKTKSVVSG | Q99541 | Perilipin-2 | 140-158 | 5.6 | 123.6 | 1 | 137.9 |
| SVEKTKSVVSG | Q99541 | Perilipin-2 | 148-158 | 5.8 | 76.2 | 5 | 138.2 |
| SGVENALTKSELL | Q99541 | Perilipin-2 | 174-186 | 6.1 | 64.4 | 5 | 181.7 |
| SGVENALTKSELLVEQ | Q99541 | Perilipin-2 | 174-189 | 6.3 | 62.1 | 5 | 212.2 |
| SGVENALTKSELLVEQY | Q99541 | Perilipin-2 | 174-190 | 5.8 | 79.9 | 5 | 210.1 |
| GVENALTKSELL | Q99541 | Perilipin-2 | 175-186 | 5.8 | 78.7 | 5 | 121.4 |
| GVENALTKSELLVEQ | Q99541 | Perilipin-2 | 175-189 | 5.6 | 62.8 | 10 | 86.3 |
| LPLTEEELEKEAKKVEGFDLV | Q99541 | Perilipin-2 | 191-211 | 5.6 | 97.1 | 5 | 59.3 |
| EELEKEAKKVE | Q99541 | Perilipin-2 | 196-206 | 5.7 | 73.7 | 5 | 100.6 |
| EELEKEAKKVEGFDLV | Q99541 | Perilipin-2 | 196-211 | 6.7 | 99.6 | 5 | 108.6 |
| ASVAVDPQPSVV | Q99541 | Perilipin-2 | 2-13 | 6.1 | 116.4 | 2 | 163.9 |
| ASVAVDPQPSVVT | Q99541 | Perilipin-2 | 2-14 | 6.3 | 49.7 | 5 | 185.1 |
| ASVAVDPQPSVVTR | Q99541 | Perilipin-2 | 2-15 | 6.8 | 42.5 | 5 | 113.5 |
| ASVAVDPQPSVVTRVV | Q99541 | Perilipin-2 | 2-17 | 6.0 | 102.7 | 2 | 262.4 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| ASVAVDPQPSVVTRVVNLPLV | Q99541 | Perilipin-2 | 2-22 | 6.2 | 62.3 | 5 | 106.9 |
| ASVAVDPQPSVVTRVVNLPLVS | Q99541 | Perilipin-2 | 2-23 | 7.1 | 49.1 | 5 | 110.4 |
| SLSTKLHSRAYQQALS | Q99541 | Perilipin-2 | 222-237 | 6.6 | 120.0 | 10 | 124.3 |
| RVKEAKQKSQQTIS | Q99541 | Perilipin-2 | 238-251 | 5.9 | 120.2 | 5 | 151.5 |
| RVKEAKQKSQQTISQ | Q99541 | Perilipin-2 | 238-252 | 4.9 | 120.4 | 10 | 45.9 |
| RVKEAKQKSQQTISQLH | Q99541 | Perilipin-2 | 238-254 | 6.6 | 130.2 | 5 | 230.3 |
| LVGPFYPQLTESQNAQD | Q99541 | Perilipin-2 | 401-417 | 6.3 | 105.1 | 6 | 59.9 |
| LVGPFYPQLTESQNAQDQ | Q99541 | Perilipin-2 | 401-418 | 5.9 | 157.8 | 7 | 42.8 |
| DQGAEMDKSSQETQR | Q99541 | Perilipin-2 | 417-431 | 5.0 | 100.1 | 10 | 45.9 |
| DQGAEMDKSSQETQRSEHKTH | Q99541 | Perilipin-2 | 417-437 | 5.7 | 109.8 | 4 | 100.7 |
| AEMDKSSQETQRSEHKTH | Q99541 | Perilipin-2 | 420-437 | 6.5 | 146.4 | 5 | 176.9 |
| EMDKSSQETQRSEHKTH | Q99541 | Perilipin-2 | 421-437 | 5.7 | 109.0 | 5 | 90.6 |
| AENGVKTITS | Q99541 | Perilipin-2 | 50-59 | 5.4 | 99.9 | 5 | 103.7 |
| VDPQPSVVTRVVN | Q99541 | Perilipin-2 | 6-18 | 5.7 | 85.4 | 10 | 93.3 |
| ALPIIQKLEPQIA | Q99541 | Perilipin-2 | 65-77 | 6.3 | 44.1 | 5 | 139.9 |
| ALPIIQKLEPQIAVANTY | Q99541 | Perilipin-2 | 65-82 | 5.7 | 84.5 | 5 | 143.9 |
| LPIIQKLEPQIA | Q99541 | Perilipin-2 | 66-77 | 6.4 | 57.5 | 5 | 199.4 |
| NQPSTQIVANAKGAVT | Q99541 | Perilipin-2 | 98-113 | 6.0 | 59.4 | 10 | 159.5 |
| QPSTQIVANAKGAVT | Q99541 | Perilipin-2 | 99-113 | 6.0 | 51.6 | 5 | 66.5 |
| ADTKELVSSKVSGAQEMVS | O60664 | Perilipin-3 | 119-137 | 5.5 | 85.0 | 5 | 55.0 |
| DTKELVSSKVSGAQ | O60664 | Perilipin-3 | 120-133 | 5.1 | 103.7 | 2 | 56.5 |
| GVDKTKSVVTG | O60664 | Perilipin-3 | 161-171 | 5.3 | 76.0 | 5 | 74.8 |
| VGPFAPGITEKAPEEK | O60664 | Perilipin-3 | 418-433 | 6.1 | 85.2 | 10 | 54.0 |
| VGPFAPGITEKAPEEKK | O60664 | Perilipin-3 | 418-434 | 6.1 | 100.5 | 5 | 53.2 |
| GAQPILSKLEPQIA | O60664 | Perilipin-3 | 77-90 | 5.6 | 68.7 | 5 | 101.9 |
| AQPILSKLEPQIA | O60664 | Perilipin-3 | 78-90 | 5.9 | 53.7 | 5 | 119.4 |
| QPILSKLEPQIA | O60664 | Perilipin-3 | 79-90 | 5.9 | 63.2 | 5 | 98.0 |
| GPPEEAEDRFSMPLIIT | O00592 | Podocalyxin | 449-465 | 5.7 | 117.8 | 3 | 116.5 |
| LTKDDLDEEEDTHL | O00592 | Podocalyxin | 545-558 | 5.9 | 84.8 | 4 | 159.1 |
| TKDDLDEEEDTHL | O00592 | Podocalyxin | 546-558 | 6.0 | 86.5 | 4 | 247.3 |
| DDLDEEEDTHL | O00592 | Podocalyxin | 548-558 | 5.6 | 153.4 | 9 | 169.1 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| ADAAPDEKVLDSGFREIENK | P01833 | Polymeric immunoglobulin receptor | 578-597 | 6.3 | 66.8 | 2 | 119.4 |
| DAAPDEKVLDSGFREIEN | P01833 | Polymeric immunoglobulin receptor | 579-596 | 5.7 | 88.6 | 9 | 97.6 |
| DAAPDEKVLDSGFREIENK | P01833 | Polymeric immunoglobulin receptor | 579-597 | 6.7 | 72.2 | 9 | 145.9 |
| EIENKAIQDPRLFAEEK | P01833 | Polymeric immunoglobulin receptor | 593-609 | 6.6 | 53.2 | 4 | 74.0 |
| ENKAIQDPRLFAEEK | P01833 | Polymeric immunoglobulin receptor | 595-609 | 5.7 | 52.7 | 4 | 49.3 |
| AIQDPRLF | P01833 | Polymeric immunoglobulin receptor | 598-605 | 6.1 | 70.0 | 3 | 133.1 |
| AIQDPRLFAEEK | P01833 | Polymeric immunoglobulin receptor | 598-609 | 6.7 | 73.3 | 3 | 79.2 |
| AIQDPRLFAEEKAVADT | P01833 | Polymeric immunoglobulin receptor | 598-614 | 5.8 | 80.9 | 2 | 75.5 |
| AIQDPRLFAEEKAVADTR | P01833 | Polymeric immunoglobulin receptor | 598-615 | 6.7 | 52.6 | 9 | 155.1 |
| AIQDPRLFAEEKAVADTRDQ | P01833 | Polymeric immunoglobulin receptor | 598-617 | 6.2 | 62.9 | 4 | 149.7 |
| AIQDPRLFAEEKAVADTRDQADGS | P01833 | Polymeric immunoglobulin receptor | 598-621 | 7.0 | 56.9 | 9 | 159.7 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| AIQDPRLFAEEKAVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 598-622 | 6.9 | 43.7 | 9 | 74.1 |
| QDPRLFAEEKAVADTR | P01833 | Polymeric immunoglobulin receptor | 600-615 | 6.1 | 78.9 | 2 | 114.6 |
| DPRLFAEEKAVAD | P01833 | Polymeric immunoglobulin receptor | 601-613 | 6.3 | 51.1 | 9 | 117.1 |
| DPRLFAEEKAVADTR | P01833 | Polymeric immunoglobulin receptor | 601-615 | 6.6 | 73.1 | 9 | 101.5 |
| DPRLFAEEKAVADTRDQ | P01833 | Polymeric immunoglobulin receptor | 601-617 | 6.3 | 120.9 | 9 | 64.5 |
| PRLFAEEKAVADTR | P01833 | Polymeric immunoglobulin receptor | 602-615 | 5.5 | 90.3 | 2 | 76.6 |
| LFAEEKAVADTRDQA | P01833 | Polymeric immunoglobulin receptor | 604-618 | 5.8 | 110.8 | 2 | 59.2 |
| LFAEEKAVADTRDQAD | P01833 | Polymeric immunoglobulin receptor | 604-619 | 5.5 | 49.4 | 4 | 58.9 |
| LFAEEKAVADTRDQADG | P01833 | Polymeric immunoglobulin receptor | 604-620 | 5.5 | 56.1 | 2 | 100.1 |
| LFAEEKAVADTRDQADGS | P01833 | Polymeric immunoglobulin receptor | 604-621 | 5.9 | 106.9 | 9 | 88.4 |
| LFAEEKAVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 604-622 | 6.7 | 46.9 | 4 | 160.1 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| FAEEKAVADTRD | P01833 | Polymeric immunoglobulin receptor | 605-616 | 5.7 | 62.1 | 9 | 107.1 |
| FAEEKAVADTRDQA | P01833 | Polymeric immunoglobulin receptor | 605-618 | 6.1 | 61.1 | 9 | 144.3 |
| FAEEKAVADTRDQAD | P01833 | Polymeric immunoglobulin receptor | 605-619 | 5.8 | 87.9 | 5 | 152.9 |
| FAEEKAVADTRDQADG | P01833 | Polymeric immunoglobulin receptor | 605-620 | 5.9 | 66.4 | 10 | 81.3 |
| FAEEKAVADTRDQADGS | P01833 | Polymeric immunoglobulin receptor | 605-621 | 6.0 | 137.9 | 9 | 200.2 |
| FAEEKAVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 605-622 | 6.9 | 73.8 | 4 | 189.6 |
| FAEEKAVADTRDQADGSRASV | P01833 | Polymeric immunoglobulin receptor | 605-625 | 5.5 | 82.6 | 2 | 87.8 |
| FAEEKAVADTRDQADGSRASVD | P01833 | Polymeric immunoglobulin receptor | 605-626 | 5.6 | 61.7 | 5 | 53.6 |
| AEEKAVADTRDQA | P01833 | Polymeric immunoglobulin receptor | 606-618 | 5.8 | 125.9 | 9 | 154.3 |
| AEEKAVADTRDQADGS | P01833 | Polymeric immunoglobulin receptor | 606-621 | 5.6 | 106.6 | 2 | 150.2 |
| AEEKAVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 606-622 | 6.6 | 93.8 | 4 | 157.1 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| EEKAVADTRDQ | P01833 | Polymeric immunoglobulin receptor | 607-617 | 5.0 | 67.8 | 4 | 121.8 |
| EEKAVADTRDQA | P01833 | Polymeric immunoglobulin receptor | 607-618 | 5.8 | 124.1 | 4 | 144.0 |
| EEKAVADTRDQADG | P01833 | Polymeric immunoglobulin receptor | 607-620 | 6.7 | 69.5 | 4 | 225.2 |
| EEKAVADTRDQADGS | P01833 | Polymeric immunoglobulin receptor | 607-621 | 6.0 | 64.1 | 9 | 187.4 |
| EEKAVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 607-622 | 6.7 | 49.1 | 11 | 103.5 |
| EKAVADTRDQADG | P01833 | Polymeric immunoglobulin receptor | 608-620 | 6.6 | 50.8 | 11 | 243.8 |
| EKAVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 608-622 | 5.7 | 72.4 | 11 | 51.6 |
| AVADTRDQAD | P01833 | Polymeric immunoglobulin receptor | 610-619 | 6.0 | 64.6 | 11 | 177.1 |
| AVADTRDQADG | P01833 | Polymeric immunoglobulin receptor | 610-620 | 6.4 | 72.9 | 4 | 204.3 |
| AVADTRDQADGS | P01833 | Polymeric immunoglobulin receptor | 610-621 | 6.2 | 87.7 | 4 | 209.8 |
| AVADTRDQADGSR | P01833 | Polymeric immunoglobulin receptor | 610-622 | 5.7 | 150.2 | 1 | 94.2 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| AVADTRDQADGSRA | P01833 | Polymeric immunoglobulin receptor | 610-623 | 5.9 | 62.0 | 8 | 117.9 |
| AVADTRDQADGSRAS | P01833 | Polymeric immunoglobulin receptor | 610-624 | 6.4 | 84.3 | 10 | 144.7 |
| AVADTRDQADGSRASV | P01833 | Polymeric immunoglobulin receptor | 610-625 | 5.8 | 131.5 | 2 | 120.7 |
| AVADTRDQADGSRASVD | P01833 | Polymeric immunoglobulin receptor | 610-626 | 6.5 | 51.2 | 4 | 177.7 |
| AVADTRDQADGSRASVDS | P01833 | Polymeric immunoglobulin receptor | 610-627 | 5.6 | 69.2 | 8 | 104.4 |
| AVADTRDQADGSRASVDSG | P01833 | Polymeric immunoglobulin receptor | 610-628 | 6.7 | 58.7 | 8 | 253.3 |
| AVADTRDQADGSRASVDSGS | P01833 | Polymeric immunoglobulin receptor | 610-629 | 5.4 | 86.3 | 8 | 68.1 |
| AVADTRDQADGSRASVDSGSSE | P01833 | Polymeric immunoglobulin receptor | 610-631 | 5.6 | 58.2 | 8 | 85.1 |
| AVADTRDQADGSRASVDSGSSEE | P01833 | Polymeric immunoglobulin receptor | 610-632 | 6.1 | 57.5 | 9 | 161.7 |
| AVADTRDQADGSRASVDSGSSEEQ | P01833 | Polymeric immunoglobulin receptor | 610-633 | 5.8 | 51.7 | 8 | 138.3 |
| AVADTRDQADGSRASVDSGSSEEQG | P01833 | Polymeric immunoglobulin receptor | 610-634 | 6.2 | 55.1 | 8 | 169.6 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| VADTRDQADGSRA | P01833 | Polymeric immunoglobulin receptor | 611-623 | 5.6 | 160.1 | 5 | 95.0 |
| VADTRDQADGSRAS | P01833 | Polymeric immunoglobulin receptor | 611-624 | 6.1 | 81.8 | 11 | 145.8 |
| VADTRDQADGSRASV | P01833 | Polymeric immunoglobulin receptor | 611-625 | 5.2 | 77.9 | 2 | 92.9 |
| VADTRDQADGSRASVD | P01833 | Polymeric immunoglobulin receptor | 611-626 | 5.7 | 50.9 | 9 | 126.6 |
| VADTRDQADGSRASVDSG | P01833 | Polymeric immunoglobulin receptor | 611-628 | 5.8 | 57.6 | 8 | 103.5 |
| VADTRDQADGSRASVDSGSSEE | P01833 | Polymeric immunoglobulin receptor | 611-632 | 5.7 | 128.8 | 9 | 163.4 |
| VADTRDQADGSRASVDSGSSEEQG | P01833 | Polymeric immunoglobulin receptor | 611-634 | 5.7 | 72.3 | 8 | 95.7 |
| VADTRDQADGSRASVDSGSSEEQGG | P01833 | Polymeric immunoglobulin receptor | 611-635 | 5.7 | 58.4 | 8 | 145.1 |
| ADTRDQADGSRASV | P01833 | Polymeric immunoglobulin receptor | 612-625 | 5.1 | 73.7 | 2 | 69.7 |
| DTRDQADGSRASVDSGSSE | P01833 | Polymeric immunoglobulin receptor | 613-631 | 5.6 | 51.2 | 9 | 136.3 |
| DTRDQADGSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 613-637 | 6.3 | 130.5 | 9 | 259.4 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| TRDQADGSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 614-637 | 5.4 | 123.8 | 1 | 134.8 |
| DQADGSRASVD | P01833 | Polymeric immunoglobulin receptor | 616-626 | 5.8 | 56.6 | 11 | 150.0 |
| DQADGSRASVDSG | P01833 | Polymeric immunoglobulin receptor | 616-628 | 5.9 | 74.1 | 5 | 239.0 |
| DQADGSRASVDSGSSE | P01833 | Polymeric immunoglobulin receptor | 616-631 | 5.4 | 54.0 | 5 | 141.5 |
| DQADGSRASVDSGSSEE | P01833 | Polymeric immunoglobulin receptor | 616-632 | 5.7 | 68.9 | 9 | 297.2 |
| DQADGSRASVDSGSSEEQ | P01833 | Polymeric immunoglobulin receptor | 616-633 | 5.4 | 39.2 | 8 | 68.8 |
| DQADGSRASVDSGSSEEQG | P01833 | Polymeric immunoglobulin receptor | 616-634 | 5.8 | 50.4 | 8 | 187.9 |
| DQADGSRASVDSGSSEEQGG | P01833 | Polymeric immunoglobulin receptor | 616-635 | 5.8 | 48.5 | 8 | 244.4 |
| DQADGSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 616-637 | 6.9 | 88.4 | 9 | 409.7 |
| DQADGSRASVDSGSSEEQGGSSR | P01833 | Polymeric immunoglobulin receptor | 616-638 | 6.7 | 59.9 | 11 | 384.8 |
| DQADGSRASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 616-639 | 7.5 | 57.9 | 8 | 374.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| DQADGSRASVDSGSSEEQGGSSRAL | P01833 | Polymeric immunoglobulin receptor | 616-640 | 5.9 | 44.1 | 4 | 235.6 |
| QADGSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 617-637 | 5.4 | 110.8 | 9 | 240.2 |
| QADGSRASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 617-639 | 5.9 | 51.2 | 4 | 213.7 |
| ADGSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 618-637 | 5.6 | 96.8 | 4 | 280.7 |
| ADGSRASVDSGSSEEQGGSSR | P01833 | Polymeric immunoglobulin receptor | 618-638 | 5.2 | 125.3 | 4 | 56.1 |
| ADGSRASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 618-639 | 5.7 | 69.2 | 4 | 176.8 |
| DGSRASVDSGSSEE | P01833 | Polymeric immunoglobulin receptor | 619-632 | 4.8 | 106.9 | 4 | 142.1 |
| DGSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 619-637 | 6.1 | 86.1 | 9 | 323.0 |
| DGSRASVDSGSSEEQGGSSR | P01833 | Polymeric immunoglobulin receptor | 619-638 | 5.6 | 112.4 | 5 | 147.9 |
| DGSRASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 619-639 | 6.5 | 79.9 | 9 | 226.7 |
| DGSRASVDSGSSEEQGGSSRALVST | P01833 | Polymeric immunoglobulin receptor | 619-643 | 5.8 | 81.1 | 9 | 53.7 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| GSRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 620-637 | 5.1 | 78.7 | 3 | 124.4 |
| GSRASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 620-639 | 5.9 | 48.6 | 11 | 156.9 |
| SRASVDSGSSEEQGGSS | P01833 | Polymeric immunoglobulin receptor | 621-637 | 5.4 | 111.6 | 4 | 185.6 |
| SRASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 621-639 | 5.7 | 53.5 | 8 | 131.1 |
| ASVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 623-639 | 6.1 | 65.3 | 4 | 348.2 |
| ASVDSGSSEEQGGSSRALVST | P01833 | Polymeric immunoglobulin receptor | 623-643 | 5.6 | 86.8 | 4 | 113.7 |
| SVDSGSSEEQGGSSR | P01833 | Polymeric immunoglobulin receptor | 624-638 | 5.5 | 66.2 | 4 | 133.3 |
| SVDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 624-639 | 6.7 | 47.6 | 11 | 338.8 |
| SVDSGSSEEQGGSSRAL | P01833 | Polymeric immunoglobulin receptor | 624-640 | 5.1 | 98.3 | 4 | 156.0 |
| SVDSGSSEEQGGSSRALV | P01833 | Polymeric immunoglobulin receptor | 624-641 | 5.3 | 67.9 | 4 | 145.1 |
| SVDSGSSEEQGGSSRALVST | P01833 | Polymeric immunoglobulin receptor | 624-643 | 6.0 | 67.6 | 4 | 136.3 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| SVDSGSSEEQGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 624-648 | 7.5 | 58.6 | 8 | 78.3 |
| VDSGSSEEQGGSSR | P01833 | Polymeric immunoglobulin receptor | 625-638 | 5.3 | 77.3 | 11 | 119.8 |
| VDSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 625-639 | 6.6 | 75.0 | 11 | 299.2 |
| VDSGSSEEQGGSSRALVST | P01833 | Polymeric immunoglobulin receptor | 625-643 | 5.6 | 68.1 | 2 | 68.8 |
| VDSGSSEEQGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 625-648 | 6.6 | 57.3 | 8 | 63.1 |
| DSGSSEEQGGSSRA | P01833 | Polymeric immunoglobulin receptor | 626-639 | 6.7 | 67.8 | 11 | 340.9 |
| DSGSSEEQGGSSRAL | P01833 | Polymeric immunoglobulin receptor | 626-640 | 5.8 | 49.6 | 4 | 200.8 |
| DSGSSEEQGGSSRALV | P01833 | Polymeric immunoglobulin receptor | 626-641 | 6.5 | 62.0 | 4 | 233.4 |
| DSGSSEEQGGSSRALVST | P01833 | Polymeric immunoglobulin receptor | 626-643 | 6.5 | 61.4 | 11 | 188.0 |
| DSGSSEEQGGSSRALVSTLVPL | P01833 | Polymeric immunoglobulin receptor | 626-647 | 6.7 | 82.9 | 1 | 68.8 |
| DSGSSEEQGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 626-648 | 7.1 | 108.5 | 4 | 125.5 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| SGSSEEQGGSSRALV | P01833 | Polymeric immunoglobulin receptor | 627-641 | 5.6 | 77.3 | 4 | 160.2 |
| SGSSEEQGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 627-648 | 6.3 | 95.8 | 5 | 92.1 |
| GSSEEQGGSSRALV | P01833 | Polymeric immunoglobulin receptor | 628-641 | 5.6 | 54.5 | 4 | 178.7 |
| SSEEQGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 629-648 | 6.0 | 64.0 | 5 | 113.7 |
| EQGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 632-648 | 5.7 | 101.5 | 9 | 109.2 |
| QGGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 633-648 | 6.0 | 78.3 | 4 | 110.9 |
| GGSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 634-648 | 6.2 | 66.3 | 4 | 125.7 |
| GSSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 635-648 | 6.5 | 60.1 | 8 | 114.8 |
| SSRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 636-648 | 6.3 | 76.5 | 8 | 109.4 |
| SRALVSTLVPLG | P01833 | Polymeric immunoglobulin receptor | 637-648 | 5.5 | 72.1 | 8 | 66.4 |
| SSTVAAEAQDGPQEA | P01833 | Polymeric immunoglobulin receptor | 750-764 | 5.5 | 77.6 | 5 | 130.0 |

Supplemental Table S 2: List with all identified peptides, including their precursor protein, sequence range, mean log10 LFQ intensity, inter-individual variation (CV), WGCNA cluster, and identification score. *(continued)*

| Sequence | Uniprot ID | Leading protein name | Sequence positions | Mean log10 LFQ intensity | CV (%) | WGCNA cluster | Identification score |
|---|---|---|---|---|---|---|---|
| STVAAEAQDGPQEA | P01833 | Polymeric immunoglobulin receptor | 751-764 | 5.2 | 93.3 | 4 | 58.7 |
| AVDKKAAGAGKVT | Q5VTE0 | Putative elongation factor 1-alpha-like 3 | 440-452 | 5.4 | 75.7 | 4 | 76.1 |
| AAGAGKVTKSAQKAQKA | Q5VTE0 | Putative elongation factor 1-alpha-like 3 | 445-461 | 5.7 | 100.5 | 5 | 136.3 |
| ESRAELTSDKDMY | Q58DD4 | Syndecan-2 | 19-31 | 6.2 | 155.0 | 2 | 172.9 |
| SRAELTSDKDMY | Q58DD4 | Syndecan-2 | 20-31 | 6.2 | 160.0 | 2 | 167.2 |
| SPVEESEDVSNK | P31431 | Syndecan-4 | 117-128 | 5.5 | 63.4 | 11 | 208.6 |
| SPVEESEDVSNKVS | P31431 | Syndecan-4 | 117-130 | 5.4 | 76.0 | 4 | 69.0 |

# Table with all identified metabolites.

Supplemental Table S 3: List with all identified metabolites, including their mean intensity, inter-individual variation (CV), inter-individual variation for secretor and Lewis positive subjects and the integrated NMR region.

| Metabolite | Mean intensity | CV (%) | CV (%) Se(+)Le(+) | Integrated region |
|---|---|---|---|---|
| 2'-FL | 11 | 50.6 | 37.2 | 5.31-5.284 |
| 3'-FL | 20 | 53.0 | 41.1 | 1.189-1.165 |
| Acetate | 100 | 15.9 | 17.0 | 1.91-1.894 |
| Alanine | 207 | 15.5 | 16.1 | 1.473-1.451 |
| Aspartate | 9 | 90.8 | 89.3 | 2.828-2.776 |
| Butyrate | 575 | 4.9 | 4.8 | 1.582-1.517 |
| Caprylate | 31 | 25.3 | 24.7 | 0.868-0.863 |
| Choline | 300 | 47.8 | 45.4 | 3.19-3.177 |
| cis-Aconitate | 63 | 13.8 | 11.2 | 3.165-3.149 |
| Citrate | 993 | 23.0 | 20.4 | 2.554-2.478 |
| CMP | 4 | 59.8 | 52.2 | 6.116-6.096 |
| Creatinine | 27 | 27.0 | 26.7 | 3.035-3.024 |
| CTP/CDP | 8 | 46.1 | 36.7 | 7.968-7.935 |
| Formate | 9 | 36.9 | 38.7 | 8.446-8.434 |
| Fucose-alpha-1,3GLcNAC | 1 | 72.2 | 58.1 | 5.146-5.128 |
| Fumarate | 1 | 67.4 | 64.7 | 6.515-6.499 |
| Galactose | 549 | 36.4 | 27.3 | 4.521-4.497 |
| GlcNAc | 363 | 41.0 | 38.4 | 2.018-2.008 |
| Glutamic acid | 669 | 26.6 | 26.9 | 2.362-2.319 |
| Glutamine | 182 | 29.9 | 26.8 | 2.463-2.416 |
| Glycerophosphocholine | 696 | 31.9 | 31.4 | 3.218-3.205 |
| Histidine | 4 | 48.9 | 50.6 | 7.072-7.046 |
| Lactate | 58 | 16.4 | 16.0 | 1.321-1.313 |
| Lacto-N-difucohexaose I | 187 | 30.7 | 21.9 | 5.189-5.172 |
| Lacto-N-difucohexaose II | 77 | 19.4 | 13.8 | 5.364-5.349 |
| Lactose | 97452 | 12.0 | 9.5 | 3.82-3.748 |
| LDFT | 23 | 52.6 | 44.6 | 5.451-5.437 |
| Leucine/isoleucine | 12 | 43.7 | 44.7 | 0.937-0.929 |
| LNFP I | 1 | 67.2 | 63.0 | 8.39-8.358 |
| LNFP III | 1 | 45.4 | 41.7 | 5.122-5.104 |

Supplemental Table S 3: List with all identified metabolites, including their mean intensity, inter-individual variation (CV), inter-individual variation for secretor and Lewis positive subjects and the integrated NMR region. *(continued)*

| Metabolite | Mean intensity | CV (%) | CV (%) Se(+)Le(+) | Integrated region |
|---|---:|---:|---:|---|
| Methionine | 54 | 19.4 | 18.7 | 2.144-2.139 |
| N-acetyl-neuraminic acid | 352 | 33.8 | 31.2 | 2.045-2.036 |
| N-acetyl sugar | 438 | 42.5 | 35.2 | 2.033-2.023 |
| Pantothenate | 7 | 63.9 | 64.1 | 0.926-0.919 |
| Phenylalanine | 6 | 44.7 | 46.7 | 7.335-7.304 |
| Phosphocholine | 674 | 35.7 | 36.6 | 3.205-3.196 |
| Tyrosine | 5 | 45.2 | 46.8 | 7.195-7.164 |
| Urea | 571 | 17.2 | 17.0 | 5.873-5.63 |
| Uridine | 14 | 20.7 | 18.9 | 5.908-5.886 |
| Valine | 20 | 16.2 | 17.1 | 1.056-1.035 |

# Listing S1 - Overview with the parameters of the NMR analysis

```
##TITLE= Parameter file, TopSpin 3.6.1
##JCAMPDX= 5.0
##DATATYPE= Parameter Values
##NPOINTS= 22 $$ modification sequence number
##ORIGIN= Bruker BioSpin GmbH
##OWNER= nmr
$$ 2020-07-08 11:17:21.887 +0200 nmr@AV600U
$$ /opt/nmrdata/path/Milk/10/acqu
$$ process /opt/topspin3.6.1/prog/mod/go4
##$ACQT0= 0
##$AMP= (0..31)
100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100
100 100 100 100 100 100 100 100 100 100 100 100 100 100
##$AMPCOIL= (0..19)
-1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$ANAVPT= 1
##$AQSEQ= 0
##$AQ_mod= 3
##$AUNM=
##$AUTOPOS= <1 A1 - 101 >
##$BF1= 600.36
##$BF2= 600.36
##$BF3= 600.36
##$BF4= 600.36
```

```
##$BF5= 600.36
##$BF6= 600.36
##$BF7= 600.36
##$BF8= 600.36
##$BWFAC= (0..63)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$BYTORDA= 0
##$CAGPARS= (0..11)
0 0 0 0 0 0 0 0 0 0 0 0
##$CHEMSTR=
##$CNST= (0..63)
1 1 145 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0.75 1 1 1
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##$CPDPRG= (0..8)
<> <> <> <>
##$D= (0..63)
0 4 0 0 0 0 0 0 0.01 0.06 0 0.03 2e-05 0 0 0 0.0002 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0
##$DATE= 0
##$DE= 10
##$DECBNUC=
##$DECIM= 1109.33333333333
##$DECNUC=
##$DECSTAT= 4
##$DIGMOD= 3
```

```
##$DIGTYP= 12
##$DQDMODE= 0
##$DR= 22
##$DS= 4
##$DSPFIRM= 4
##$DSPFVS= 0
##$DTYPA= 0
##$EXP=
##$FCUCHAN= (0..9)
0 2 0 0 0 0 0 0 0 0
##$FL1= 90
##$FL2= 90
##$FL3= 90
##$FL4= 90
##$FN_INDIRECT= (0..7)
0 2 2 2 2 2 2 2
##$FOV= 20
##$FQ1LIST=
##$FQ2LIST=
##$FQ3LIST=
##$FQ4LIST=
##$FQ5LIST=
##$FQ6LIST=
##$FQ7LIST=
##$FQ8LIST=
##$FRQLO3= 0
##$FRQLO3N= 0
```

```
##$FS= (0..7)
83 83 83 83 83 83 83 83
##$FTLPGN= 0
##$FW= 4032000
##$FnILOOP= 0
##$FnMODE= 0
##$FnTYPE= 0
##$GPNAM= (0..31)
<sine.100> <SMSQ10.100> <SMSQ10.100> <sine.100> <sine.100> <sine.100> <sine.100>
<sine.100> <sine.100> <sine.100> <sine.100> <sine.100> <sine.100> <sine.100>
<sine.100> <sine.100> <sine.100> <sine.100> <sine.100> <sine.100> <sine.100>
<sine.100> <sine.100> <sine.100> <sine.100> <sine.100> <sine.100> <sine.100>
<sine.100> <sine.100> <sine.100> <sine.100>
##$GPX= (0..31)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$GPY= (0..31)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$GPZ= (0..31)
0 50 -10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$GRDPROG= <>
##$GRPDLY= -1
##$HDDUTY= 20
##$HDRATE= 20
##$HGAIN= (0..3)
0 0 0 0
##$HL1= 1
##$HL2= 35
```

```
##$HL3= 16
##$HL4= 17
##$HOLDER= 101
##$HPMOD= (0..7)
0 0 0 0 0 0 0 0
##$HPPRGN= 0
##$IN= (0..63)
0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001
0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001
0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001
0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001
0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001 0.001
0.001 0.001 0.001 0.001
##$INF= (0..7)
0 0 0 0 0 0 0 0
##$INP= (0..63)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$INSTRUM= <>
##$INTEGFAC= (0..63)
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$L= (0..31)
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##$LFILTER= 10
##$LGAIN= -10
##$LINPSTP= 0
```

```
##$LOCKED= no
##$LOCKFLD= 0
##$LOCKGN= 0
##$LOCKPOW= -20
##$LOCKPPM= 0
##$LOCNUC= <2H>
##$LOCPHAS= 0
##$LOCSHFT= no
##$LOCSW= 0
##$LTIME= 0.1
##$MASR= 4200
##$MASRLST=
##$MULEXPNO= (0..15)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$NBL= 1
##$NC= 0
##$NLOGCH= 2
##$NOVFLW= 0
##$NS= 192
##$NUC1= <1H>
##$NUC2=
##$NUC3=
##$NUC4=
##$NUC5=
##$NUC6=
##$NUC7=
##$NUC8=
```

```
##$NUCLEUS=

##$NUSLIST=

##$NusAMOUNT= 25

##$NusFPNZ= no

##$NusJSP= 0

##$NusSEED= 54321

##$NusSPTYPE= 0

##$NusT2= 1

##$NusTD= 0

##$O1= 2822.737

##$O2= 2822.737

##$O3= 2822.737

##$O4= 2822.737

##$O5= 2822.737

##$O6= 2822.737

##$O7= 2822.737

##$O8= 2822.737

##$OVERFLW= 0

##$P= (0..63)

7.2 7.2 14.4 0 0 16.5 25 50 20000 0 0 80000 80000 1000 0 200000 1000 2500

100000 600 2500 0 0 0 0 180 100000 7.2 0 1000 0 0 20000 0 0 0 0 0 0 0 2000

0 0 0 200 0 80000 46600 10000 0 80000 0 0 0 0 0 0 0 0 0 0 0 0 0

##$PACOIL= (0..15)

1 0 4 2 3 0 0 0 0 0 0 0 0 0 0 0

##$PAPS= 2

##$PARMODE= 0

##$PCPD= (0..9)
```

```
100 70 100 100 100 100 100 100 100 100
##$PEXSEL= (0..9)
1 1 1 1 1 1 1 1 1 1
##$PHCOR= (0..31)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$PHLIST= <>
##$PHP= 1
##$PH_ref= 0
##$PL= (0..63)
120 6.5 120 120 120 120 120 120 120 60 15.18248 28.17752 120 120 120 120
120 120 6.5 21.80235 120 120 120 120 120 120 120 28.17752 120 120 120 120
120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120
120 120 120 120 120 120 120 120 120 120 120 120 120 120
##$PLSTEP= 0.1
##$PLSTRT= -6
##$PLW= (0..63)
0 4 0 0 0 0 0 0 0 8.3058e-06 0.33223 0.025635 0 0 0 0 0 0 4 0.042377 0
0 0 0 0 0 0 0.025635 0 0.33223 0 0 3.3223e-07 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$PLWMAX= (0..7)
0 0 0 0 0 0 0 0
##$PQPHASE= 0
##$PQSCALE= 0
##$PR= 1
##$PRECHAN= (0..15)
-1 3 0 2 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
##$PRGAIN= 0
```

```
##$PROBHD= <34>
##$PROBINPUTS= (0..15)
<> <> <> <> <> <> <> <> <> <> <> <> <> <> <> <>
##$PULPROG=
##$PW= 0
##$PYNM= <acqu.py>
##$ProjAngle= 0
##$QNP= 1
##$RD= 0
##$RECCHAN= (0..15)
0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$RECPH= 0
##$RECPRE= (0..15)
-1 0 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1
##$RECPRFX= (0..15)
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$RECSEL= (0..15)
0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
##$RG= 32
##$RO= 0
##$RSEL= (0..15)
0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0
##$S= (0..7)
83 4 83 83 83 83 83 83
##$SELREC= (0..9)
0 0 0 0 0 0 0 0 0 0
##$SFO1= 600.362822737
```

```
##$SFO2= 600.362822737
##$SFO3= 600.362822737
##$SFO4= 600.362822737
##$SFO5= 600.362822737
##$SFO6= 600.362822737
##$SFO7= 600.362822737
##$SFO8= 600.362822737
##$SOLVENT= <H2O+D2O>
##$SOLVOLD=
##$SP= (0..63)
1 76.59016 70.56956 120 120 0 66.23932 120 0 0 0 43.22378 0 0 120 0 150
150 120 68.53075 66.62075 69.93075 62.61075 150 150 150 150 150 150 120
120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120
120 120 120 120 120 120 120 120 120 120 120 120 120 120 120 120
##$SPECTR= 0
##$SPINCNT= 0
##$SPNAM= (0..63)
<Gaus1_270.1000> <Gaus1_180r.1000> <> <> <Sinc1.1000> <Squa100.1000>
<> <Squa100.1000> <Sinc1.1000> <Sinc1.1000> <>
<> <> <Sinc1.1000> <Sinc1.1000> <Sinc1.1000> <Sinc1.1000>
<Crp60,20,20.10> <Bip720,50,20.1>
<> <> <> <Rsnob.1000> <Gaus1_180r.1000> <Gaus1_180r.1000> <> <> <> <Gaus1_180r.1000>
<Squa100.1000> <> <> <> <> <> <> <> <> <> <> <> <> <> <> <> <> <>
<> <>
<> <> <>
##$SPOAL= (0..63)
0.5 1 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
```

```
1 1 1 1 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
0.5 0.5 0.5 0.5 0.5 0.5 0.5
##$SPOFFS= (0..63)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$SPPEX= (0..63)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$SPW= (0..63)
0 1.7238e-06 7.6612e-07 0 0 0.00059874 8.3058e-06 0 2.0764e-08 0 0.00059874
0.00059874 0 0 0 0 0 0 0 1.222967e-06 1.901063e-06 8.876617e-07 4.787086e-06
0 0 0 0 0 0 0.0079315 0.33223 0 0 0 8.3756e-06 7.6612e-07 4.9032e-05 0
0 0 7.6612e-07 2.0764e-08 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$SUBNAM= (0..9)
<"“> <’x‘> <’x‘> <’x‘> <’x‘> <’x‘> <’x‘> <’x‘> <’x‘> <”">
##$SW= 30.0299176948508
##$SWIBOX= (0..19)
0 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$SW_h= 18028.8461538462
##$SWfinal= 0
##$SigLockShift= 0
##$TD= 97352
##$TD0= 1
##$TD_INDIRECT= (0..7)
0 2 2 2 2 2 2 2
##$TDav= 0
```

```
##$TE= 300
##$TE1= 300
##$TE2= 300
##$TE3= 300
##$TE4= 300
##$TEG= 300
##$TE_MAGNET= 300
##$TE_PIDX= 0
##$TE_STAB= (0..9)
0 0 0 0 0 0 0 0 0 0
##$TL= (0..7)
0 120 120 120 120 120 120 120
##$TOTROT= (0..63)
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
##$TUBE_TYPE= <>
##$USERA1=
##$USERA2=
##$USERA3=
##$USERA4=
##$USERA5=
##$V9= 5
##$VALIDCODE= 0
##$VALIST=
##$VCLIST=
##$VDLIST=
##$VPLIST=
```

```
##$VTLIST=

##$WBST= 1024

##$WBSW= 4

##$XGAIN= (0..3)

0 0 0 0

##$XL= 0

##$YL= 0

##$YMAX_a= 0

##$YMIN_a= 0

##$ZGOPTNS= <-DFLAG_BLK>

##$ZL1= 120

##$ZL2= 120

##$ZL3= 120

##$ZL4= 120

##$scaledByNS= no

##$scaledByRG= no

##END=
```

# References

(1) Hettinga, K.; van Valenberg, H.; de Vries, S.; Boeren, S.; van Hooijdonk, T.; van Arendonk, J.; Vervoort, J. The host defense proteome of human and bovine milk. *PLoS One* **2011**, *6*, e19433.