**Online supplementary material**

 **Table 2s.** MS/MS-based identification and characterization of human plasma proteins that changed in abundance after 8 weeks of dietary intervention.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Metabolic process |  | Spot no | Protein name | Acc.no | No of  | Sequence coverage (%) |  Score | MWe; pIe |  MWth; pIth | ANOVA | Fold change | Observed (ms) | start-end | Peptide |
|  |  | peptides | (MDa;pH) | (MDa;pH) | p-value |
| Haeme transport and catabolism |  | 127 | Haemopexin | P02790 | 2 | 6 | 113 | 54.4; 6.4 | 52.4; 6.6 |  0.020 (ab; ac) |  1.5; 1.4 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 14,956,700 | 175 - 185 | R.YYCFQGNQFLR.F |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,364,120 | 108 - 128 | K.LLQDEFPGIPSPLDAAVECHR.G |
|  |  | 141 | Haemopexin | P02790 | 4 | 11 | 128 | 52.8; 6.7 | 52.4; 6.6 | 0.042 (ac)  |  2.4 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,129,660 | 356 - 363 | R.RLWWLDLK.S |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,495,690 | 175 - 185 | R.YYCFQGNQFLR.F |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,771,990 | 295 - 309 | K.LYLVQGTQVYVFLTK.G |
|  |  |  |  |  |  |  |  |  |  |  |  | 2364,150 | 108-128 | K.LLQDEFPGIPSPLDAAVECHR.G |
|  |  | 153 | Haemopexin | P02790 | 3 | 10 | 195 | 52.8; 6.6 | 52.4; 6.6 | 0.024 (ab) |  1.4 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,495,698 | 198-208 | R.YYCFQGNQFLR.F |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,772,021 | 318-332 | K.LYLVQGTQVYVFLTK.G |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,364,164 | 131-151 | K.LLQDEFPGIPSPLDAAVECHR.G |
|  |  | 460 | Protein AMBP | P02760 | 2 | 7 | 75 | 33.5; 4.0 | 40.0; 6.0 | 0.039 (ab) | -1.1 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,021,530 | 159-166 |  R.ETLLQDFR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,919,930 | 186-202 | R.GECVPGEQEPEPILIPR.V |
| Regulation of vasoconstriction |  | 136 | Angiotensinogen | P01019 | 2 | 6 | 99 | 52.9; 5.5 | 53.4; 5.9 | 0.019 (ac) |  2.2 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,529,720 | 103-116 | R.AAMVGMLANFLGFR.I + 2 Oxidation (M) |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,722,970 | 180-196 | K.VLSALQAVQGLLVAQGR.A |
| Blood haemostasis |  | 139 | Fibrinogen γ-chain | P02679 | 5 | 16 | 157 | 51.0; 5.1 | 52.1; 5.4 | 0.021 (ac) |  1.7 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 759,460 | 412-417 | K.IIPFNR.L |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,491,760 | 122-134 | K.YEASILTHDSSIR.Y |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,960 | 259-273 | K.IHLISTQSAIPYALR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,207,060 | 239-258 | K.EGFGHLSPTGTTEFWLGNEK.I |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,417,100 | 41-61 | R.FGSYCPTTCGIADFLSTYQTK.V |
|  |  | 151 | Fibrinogen γ-chain | P02679 | 3 | 9 | 108 | 49.2; 5.3 | 52.1; 5.4 |  0.011 (ab; ac) |  1.4; 1.4 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,491,760 | 122-134 | K.YEASILTHDSSIR.Y |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,545,820 | 418-432 | R.LTIGEGQQHHLGGAK.Q |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,960 | 259-273 | K.IHLISTQSAIPYALR.V |
|  |  | 167 | Fibrinogen γ-chain | P02679 | 4 | 14 | 110 | 50.2; 5.7 | 52.1; 5.4 | 0.022 (ac) |  2.5 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,116,520 | 274-282 | R.VELEDWNGR.T |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,956 | 259-273 | K.IHLISTQSAIPYALR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,207,027 | 239-258 | K.EGFGHLSPTGTTEFWLGNEK.I |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,661,215 | 200-222 | K.ANQQFLVYCEIDGSGNGWTVFQK.R |
|  |  | 172 | Fibrinogen γ-chain | P02679 | 3 | 9 | 198 | 50.2; 5.4 | 52.1; 5.4 | 0.044 (ab) |  2.5 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 759,450 | 412-417 | K.IIPFNR.L |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,970 | 259-273 | K.IHLISTQSAIPYALR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,417,100 | 41-61 | R.FGSYCPTTCGIADFLSTYQTK.V |
|  |  | 181 | Fibrinogen γ-chain | P02679 | 3 | 12 | 129 | 50.2; 5.6 | 52.1; 5.4 | 0.039 (ac) |  5.4 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,956 | 142-156 | K.IHLISTQSAIPYALR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,893,886 | 266-282 | K.ASTPNGYDNGIIWATWK.T |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,661,218 |  83-105 | K.ANQQFLVYCEIDGSGNGWTVFQK.R |
|  |  | 190 | Fibrinogen γ-chain | P02679 | 3 | 10 | 112 | 50.2; 5.9 | 52.1; 5.4 | 0.018 (ac) |  2.8 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,293,723 | 189-199 | K.QSGLYFIKPLK.A |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,920 | 259-273 | K.IHLISTQSAIPYALR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,417,000 | 41-61 | R.FGSYCPTTCGIADFLSTYQTK.V |
|  |  | 583 | Tetranectin | P05452 | 3 | 17 | 130 | 25.1; 5.5 | 23.0; 5.5 | 0.022 (ab) | -1.9 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 941,500 | 286-293 | R.GVGHPYRR.V |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,113,530 | 191-199 | R.TFAHYATFR.L |
|  |  |  |  |  |  |  |  |  |  |  |  | 155,830 | 200-213 | R.LLGEVDHYQLALGK.F |
| Complement casacade |  | 401 | Clustrin | P10909 | 2 | 5 | 47 | 35.6; 5.0 | 53.0; 5.9 | 0.048 (ab) | -1.3 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,075,570 | 215-222 | R.RPHFFFPK.S |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,998,953 | 199-214 | R.EPQDTYHYLPFSLPHR.R |
|  |  | 402 | Complement C1r sub-component | P00736 | 1 | 1 | 43 | 35.6; 5.1 | 81.6; 5.8 | 0.026 (cb) |  -3.6 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,667,790 |  | R.LPVANPQACENWLR.G |
| Anti-oxidative defence |  | 561 | Gluthatione peroxidase3 | P22352 | 3 | 12 | 36 | 26.4; 5.7 | 25.8; 8.3 | 0.015 (ab) | -1.1 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,314,648 | 186-197 | K.FLVGPDGIPIMR.W |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,330,641 | 186-197 | K.FLVGPDGIPIMR.W + Oxidation (M) |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,954,896 | 121-137 | K.YVRPGGGFVPNFQLFEK.G |
| Cellular movement |  | 275 | Actin, cytoplasmic1 | P60709 | 6 | 20 | 372 | 44.1; 5.3 | 42.1; 5.3 |  0.008 (ab; ac) |  2.2; 1.6 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 923,566 | 329-336 | K.IIAPPERK.Y |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,132,526 | 197-206 | R.GYSFTTTAER.E |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,198,704 | 29-39 | R.AVFPSIVGRPR.H |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,516,702 | 360-372 | K.QEYDESGPSIVHR.K |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,790,886 | 239-254 | K.SYELPDGQVITIGNER.F |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,954,055 | 96-113 | R.VAPEEHPVLLTEAPLNPK.A |
| Glycolysis |  | 190 | Glyceraldehyde-3-phosphate dehydrogenase | P04406 | 1 | 4 | 37 | 50.2; 5.9 | 36.2; 8.6 | 0.018 (ac) |  2.8 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,682,918 | 259-273 | K.IHLISTQSAIPYALR.V |
| Vitamin transport |  | 569 | Retinol-binding protein4 | P02753 | 4 | 36 | 317 | 25.9; 5.4 | 23.3; 5.8 | 0.019 (ab) | -1.8 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,198,629 | 106-115 | K.YWGVASFLQK.G |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,064,961 | 138-155 | R.LLNLDGTCADSYSFVFSR.D |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,612,149 | 79-101 | R.LLNNWDVCADMVGTFTDTEDPAK.F |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,693,095 | 116-137 | K.GNDDHWIVDTDYDTYAVQYSCR.L |
|   |  | 570 | Retinol-binding protein4 | P02753 | 2 | 12 | 146 | 25.9; 5.2 | 23.3; 5.8 | 0.026 (ac) | -1.6 |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  | 1,018,500 | 174-181 | R.QEELCLAR.Q |
|  |  |  |  |  |  |  |  |  |  |  |  | 2,064,960 | 140-157 | R.LLNLDGTCADSYSFVFSR.D |