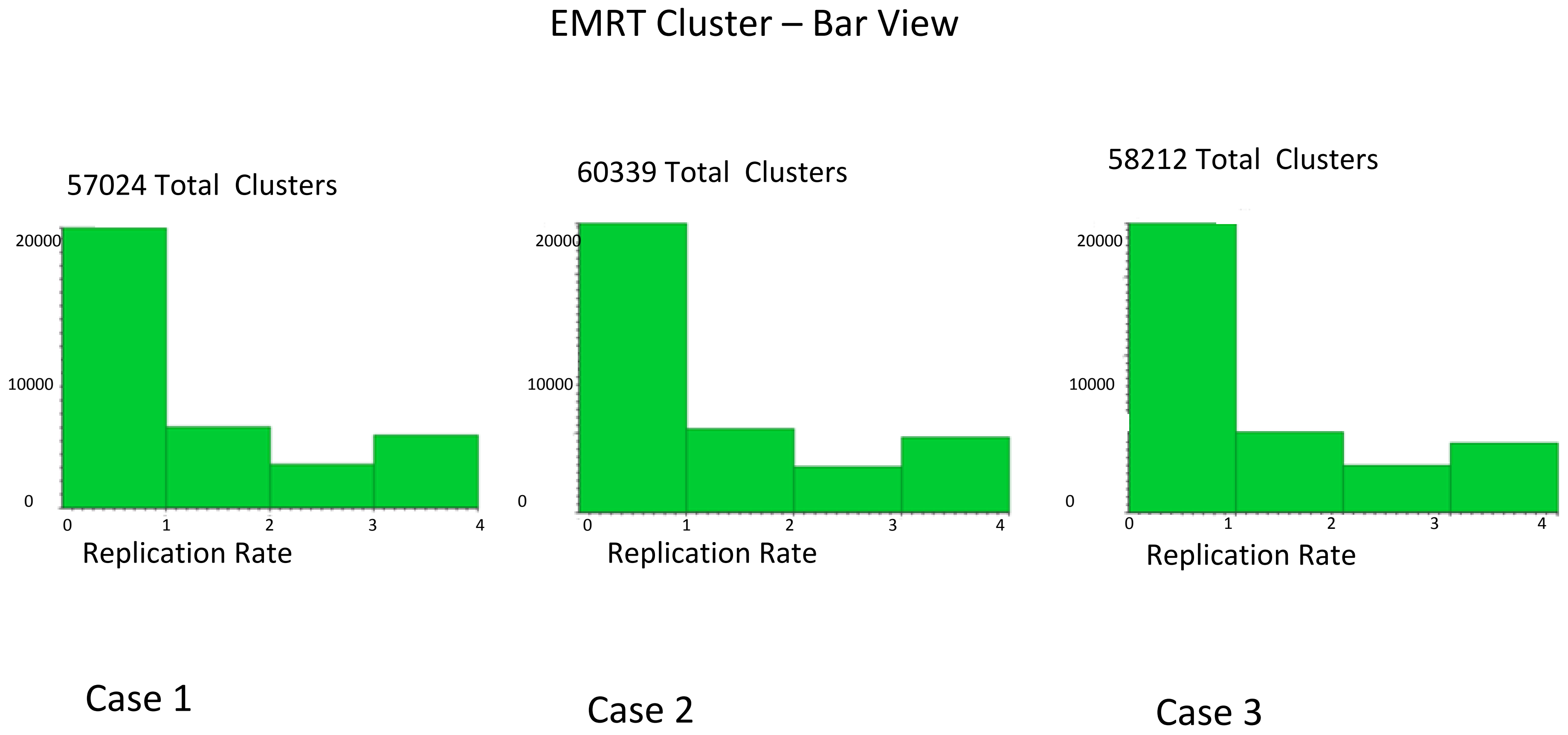

**Fig. S1** Exact Mass Retention Time (EMRT) cluster replication rate.
Four replicates data set were analysed for each patient to provide information about data quality. Histograms show replication rate of each mass peak, defined by its EMRT.

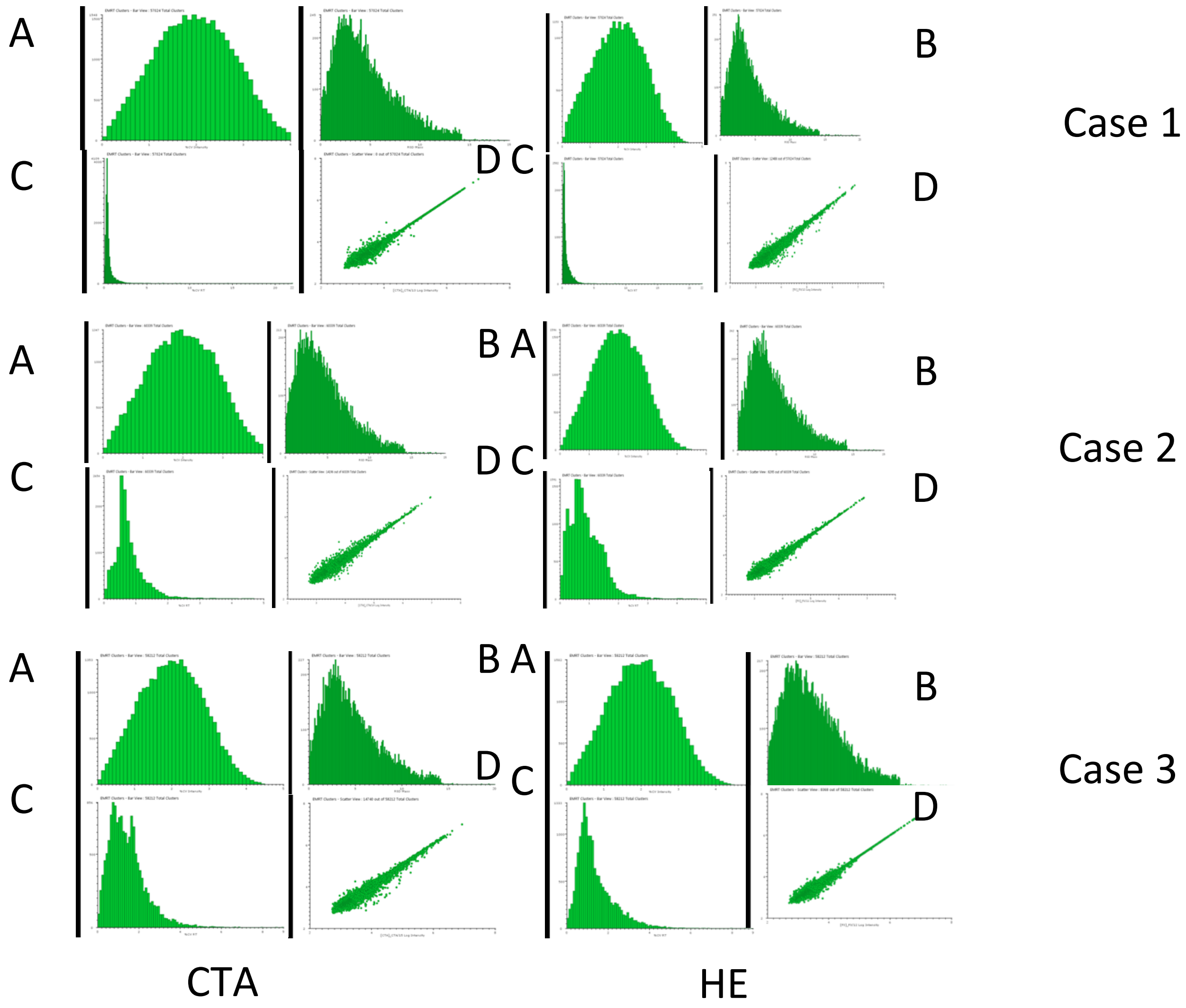

**Fig. S2** Analytical reproducibility of replicates LC-MS$^E$ experiments. (A) Average coefficient of variation of the measured signal intensity of the clusters. (B) Relative standard deviation from all the Exact Mass Retention Time (EMRT) components. (C) Average retention time coefficient of variation. (D) Binary comparison of the log intensity measurement obtained from the matched EMRT cluster for two replicates injection.

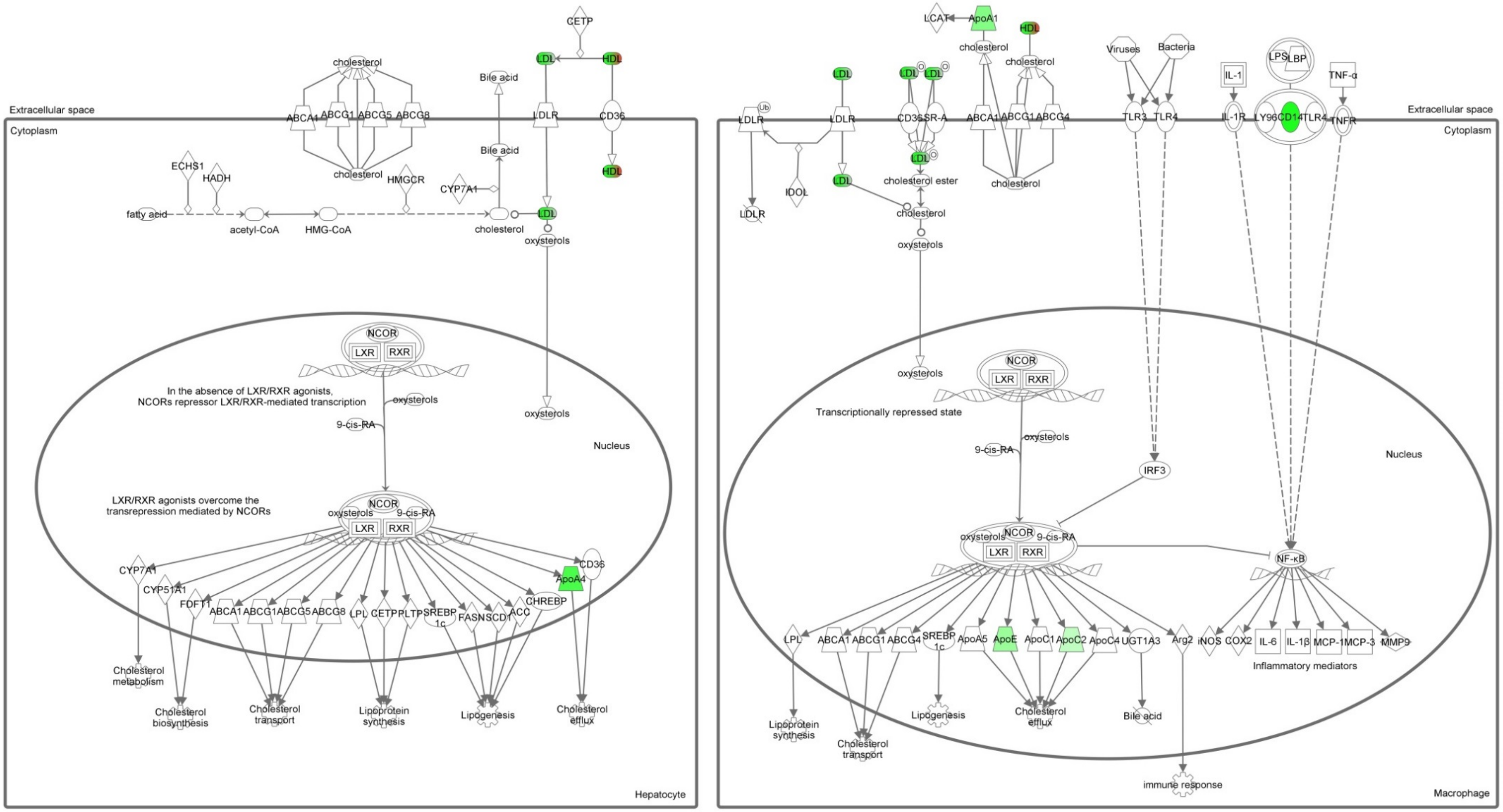

**Fig. S3** Ingenuity Pathway Analysis (IPA) of cellulose triacetate retained proteins pool of dataset. Proteins retained from cellulose triacetate-containing dialyser are involved in the LXR/RXR Activation canonical pathway.

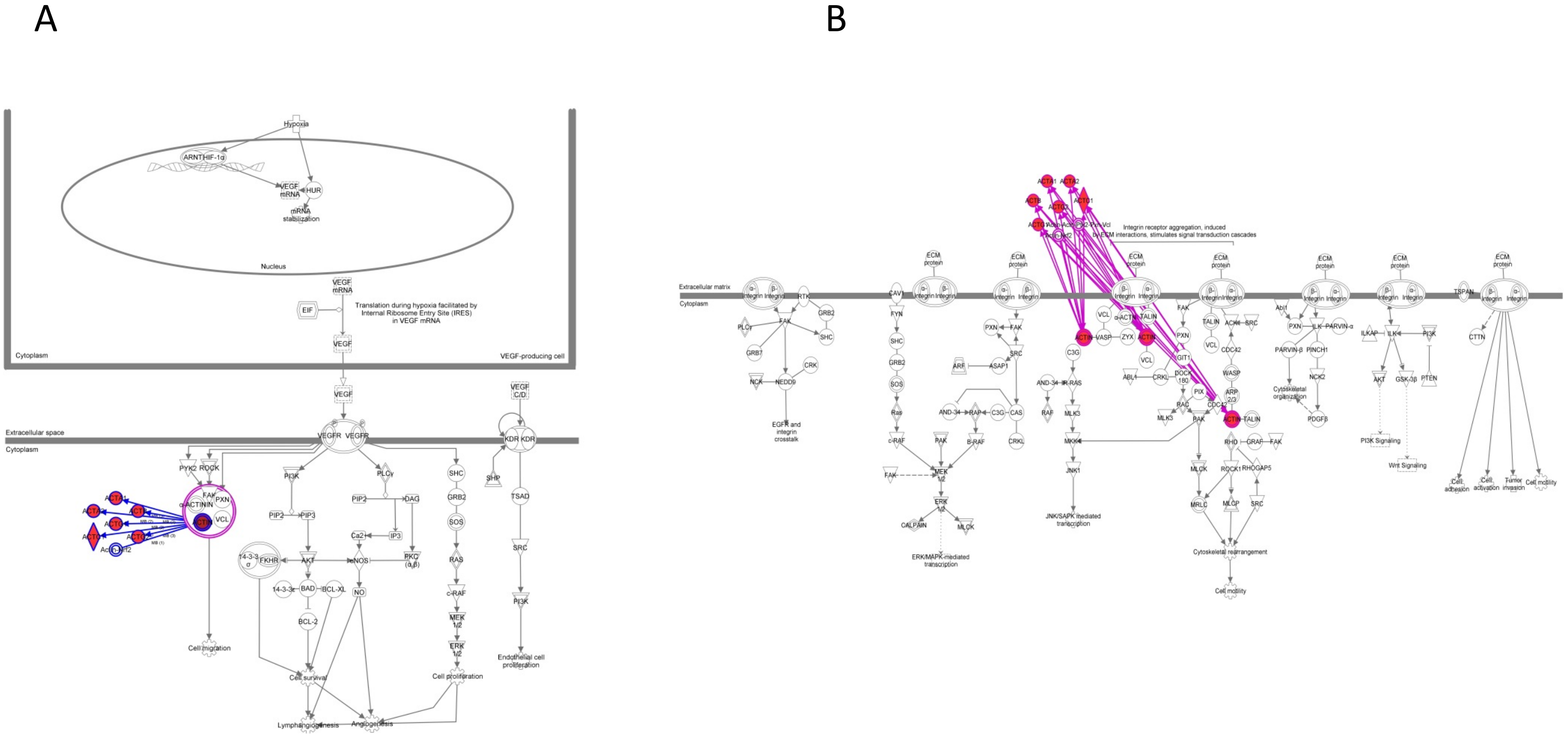

**Fig. S4** Ingenuity Pathway Analysis (IPA) of helixone retained proteins pool of dataset. Proteins retained from helixone-containing dialyser (red symbols) are involved in the VEGF Signalling canonical pathway (A) and in activation of the Integrin Signalling canonical pathway (B).

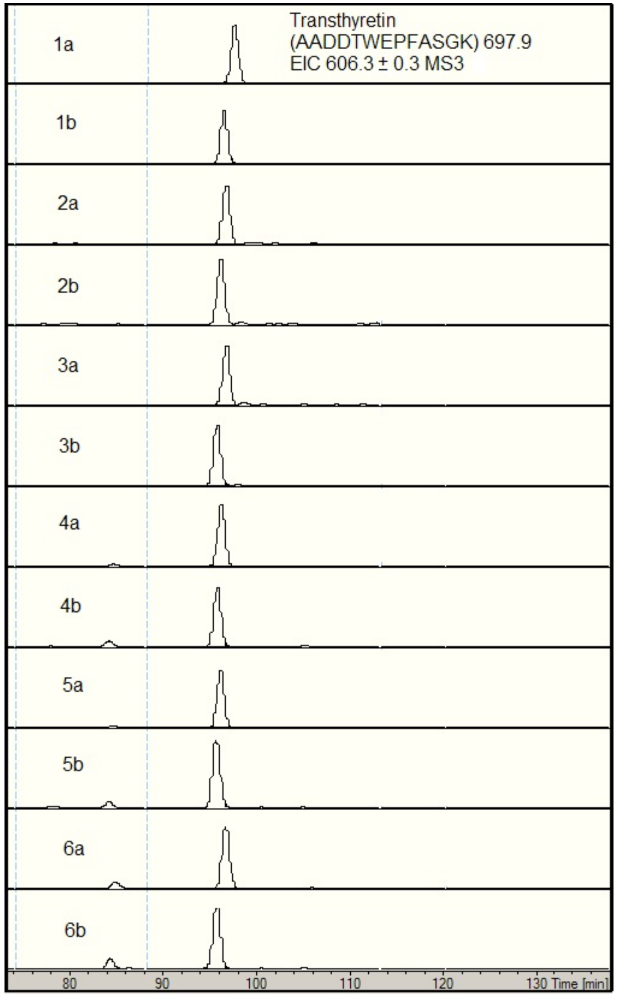

**Fig. S5** Transthyretin peptide AADDTWEPFASGK can be easily isolated in all biological and technical replicates, allowing to monitor the selected transition and integrate peak area in the EIC. Retention time variation was observed to be less than 3 seconds (CV% < 1%).

| **Table S1. BOTTOM UP DATA INDEPENDENT DIFFERENTIAL ANALYSIS** | | | | | | |
|---|---|---|---|---|---|---|
| **Case 1** | | | | | | |
| **Accession *** | **Description** | **PLGS Score †** | **Highly Represented‡** | **HE:CTA_Ratio§** | **HE:CTA_Log(e)Ratio** | **HE:CTA__Log(e)StdDev** |
| **1.** | *** Unique protein sequence identifier according to UniProtKB/Swiss-Prot Protein Knowledgebase, release 2014_03 of 19-Mar-14.** | | | | | |
| **2.** | **† ProteinLynx Global Server score.** | | | | | |
| **3.** | **‡ Protein found highly represented in Helixone (HE) or in Cellulose Triacetate (CTA) membrane retained proteins** | | | | | |
| **4.** | **§ Ratio of expression between HE and CTA membrane retained proteins** | | | | | |
| **5.** | **# colour code: green protein are more retained by CTA membrane, red protein are more retained by HE membrane** | | | | | |
| **P08571** | Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2 | 374,41 | CTA | **CTA** | CTA | CTA |
| **P01859** | Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 | 834,23 | CTA | **CTA** | CTA | CTA |
| **P01857** | Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1 | 5951,07 | CTA | **CTA** | CTA | CTA |
| **P01009** | Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3 | 5426,8 | CTA | **CTA** | CTA | CTA |
| **P08603** | Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4 | 264,67 | CTA | **CTA** | CTA | CTA |
| **P02753** | Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 | 10719,37 | CTA | **CTA** | CTA | CTA |
| **P04206** | Ig kappa chain V-III region GOL OS=Homo sapiens PE=1 SV=1 | 505,75 | CTA | **CTA** | CTA | CTA |
| **P36980** | Complement factor H-related protein 2 OS=Homo sapiens GN=CFHR2 PE=1 SV=1 | 1082,5 | CTA | **CTA** | CTA | CTA |
| **P02750** | Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2 | 947,04 | CTA | **CTA** | CTA | CTA |
| **P19652** | Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2 | 787,08 | CTA | **CTA** | CTA | CTA |

| | | | | | | |
|---|---|---|---|---|---|---|
| **P02749** | Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3 | 2168,58 | CTA | **CTA** | CTA | CTA |
| **P01042** | Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 | 2731,24 | CTA | **CTA** | CTA | CTA |
| **P02790** | Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 | 1482,22 | CTA | **CTA** | CTA | CTA |
| **P18136** | Ig kappa chain V-III region HIC OS=Homo sapiens PE=2 SV=2 | 1514,25 | CTA | **CTA** | CTA | CTA |
| **P18135** | Ig kappa chain V-III region HAH OS=Homo sapiens PE=2 SV=1 | 1514,25 | CTA | **CTA** | CTA | CTA |
| **P02787** | Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 | 1722,68 | CTA | **CTA** | CTA | CTA |
| **P01623** | Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1 | 1514,25 | CTA | **CTA** | CTA | CTA |
| **P01622** | Ig kappa chain V-III region Ti OS=Homo sapiens PE=1 SV=1 | 505,75 | CTA | **CTA** | CTA | CTA |
| **O76076** | WNT1-inducible-signaling pathway protein 2 OS=Homo sapiens GN=WISP2 PE=1 SV=1 | 755,1 | CTA | **CTA** | CTA | CTA |
| **P01620** | Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1 | 1514,25 | CTA | **CTA** | CTA | CTA |
| **P01034** | Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1 | 1122,23 | CTA | **CTA** | CTA | CTA |
| **P04196** | Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1 | 397,75 | CTA | **CTA** | CTA | CTA |
| **Q03591** | Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2 | 1239,95 | CTA | **CTA** | CTA | CTA |
| **P02774** | Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1 | 1450,24 | CTA | **CTA** | CTA | CTA |
| **Q12805** | EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 | 980,37 | CTA | **CTA** | CTA | CTA |
| **P01861** | Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1 | 2637,1 | CTA | **CTA** | CTA | CTA |
| **P01860** | Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2 | 2654,68 | CTA | **CTA** | CTA | CTA |
| **P02765** | Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 | 1165,65 | CTA | **CTA** | CTA | CTA |
| **P02763** | Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1 | 1920,05 | CTA | **CTA** | CTA | CTA |
| **P02760** | Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1 | 7358,24 | CTA | **CTA** | CTA | CTA |

| | | | | | | |
|---|---|---|---|---|---|---|
| **P06727** | Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3 | 33805,95 | | **0,03** | -3,68 | 0,07 |
| **P01834** | Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 | 25084,61 | | **0,07** | -2,64 | 0,12 |
| **P02768** | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 | 45043,62 | | **0,07** | -2,6 | 0,04 |
| **P02647** | Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 | 61850,12 | | **0,08** | -2,5 | 0,04 |
| **A0M8Q6** | Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=1 SV=2 | 12564,6 | | **0,13** | -2,05 | 0,16 |
| **P02649** | Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 | 8407,3 | | **0,13** | -2,04 | 0,11 |
| **P0CF74** | Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4 SV=1 | 26511,72 | | **0,14** | -1,94 | 0,07 |
| **B9A064** | Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2 | 50172,51 | | **0,14** | -1,94 | 0,07 |
| **P0CG04** | Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1 | 49479,4 | | **0,14** | -1,94 | 0,07 |
| **P0CG06** | Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1 | 48247,2 | | **0,15** | -1,93 | 0,08 |
| **P0CG05** | Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1 | 48247,2 | | **0,15** | -1,92 | 0,07 |
| **P02655** | Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1 | 29205,1 | | **0,29** | -1,25 | 0,05 |
| **P10909** | Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 | 3024,07 | | **0,33** | -1,11 | 0,07 |
| **P04004** | Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 | 468,71 | | **1,82** | 0,6 | 0,09 |
| **P02671** | Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2 | 6722,38 | | **2,36** | 0,86 | 0,03 |
| **P0DJI8** | Serum amyloid A-1 protein OS=Homo sapiens GN=SAA1 PE=1 SV=1 | 24619,64 | | **4,10** | 1,41 | 0,04 |
| **P01024** | Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 | 344,75 | | **4,66** | 1,54 | 0,08 |
| **P0DJI9** | Serum amyloid A-2 protein OS=Homo sapiens GN=SAA2 PE=1 SV=1 | 10540,51 | | **4,90** | 1,59 | 0,05 |
| **P63261** | Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 | 527,67 | HE | **HE** | HE | HE |
| **P01008** | Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1 | 883,3 | HE | **HE** | HE | HE |

| | | | | | | |
|---|---|---|---|---|---|---|
| **O75339** | Cartilage intermediate layer protein 1 OS=Homo sapiens GN=CILP PE=1 SV=4 | 147,31 | HE | **HE** | HE | HE |
| **Q9BYX7** | Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 | 375,42 | HE | **HE** | HE | HE |
| **P02748** | Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2 | 138,09 | HE | **HE** | HE | HE |
| **Q07507** | Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 | 1699,38 | HE | **HE** | HE | HE |
| **P62736** | Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 | 632,48 | HE | **HE** | HE | HE |
| **Q9H1Z8** | Augurin OS=Homo sapiens GN=C2orf40 PE=1 SV=1 | 428,7 | HE | **HE** | HE | HE |
| **P11684** | Uteroglobin OS=Homo sapiens GN=SCGB1A1 PE=1 SV=1 | 1203,53 | HE | **HE** | HE | HE |
| **Q6S8J3** | POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 | 412,27 | HE | **HE** | HE | HE |
| **O00187** | Mannan-binding lectin serine protease 2 OS=Homo sapiens GN=MASP2 PE=1 SV=4 | 316,3 | HE | **HE** | HE | HE |
| **P68133** | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 | 610,32 | HE | **HE** | HE | HE |
| **P68032** | Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 | 632,48 | HE | **HE** | HE | HE |
| **P48740** | Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3 | 3189,61 | HE | **HE** | HE | HE |
| **P60709** | Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 | 527,67 | HE | **HE** | HE | HE |
| **Q15485** | Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2 | 14175,09 | HE | **HE** | HE | HE |
| **Q16819** | Meprin A subunit alpha OS=Homo sapiens GN=MEP1A PE=1 SV=2 | 527,51 | HE | **HE** | HE | HE |
| **A5A3E0** | POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 | 412,27 | HE | **HE** | HE | HE |
| **Q562R1** | Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 | 387,04 | HE | **HE** | HE | HE |
| **P09382** | Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 | 705,03 | HE | **HE** | HE | HE |
| **P63267** | Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 | 632,48 | HE | **HE** | HE | HE |
| **Case 2** | | | | | | |

| **Accession** | **Description** | **Score** | **Unique** | **HE:CTA_Ratio** | **HE:CTA_Log(e)Ratio** | **HE:CTA_Log(e)Variance** |
|---|---|---|---|---|---|---|
| **P08571** | Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2 | 579,25 | CTA | **CTA** | CTA | CTA |
| **P01859** | Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 | 2259,19 | CTA | **CTA** | CTA | CTA |
| **P01857** | Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1 | 6413,42 | CTA | **CTA** | CTA | CTA |
| **P01009** | Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3 | 3687,61 | CTA | **CTA** | CTA | CTA |
| **P02753** | Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 | 6183,96 | CTA | **CTA** | CTA | CTA |
| **P04206** | Ig kappa chain V-III region GOL OS=Homo sapiens PE=1 SV=1 | 4908,27 | CTA | **CTA** | CTA | CTA |
| **P36980** | Complement factor H-related protein 2 OS=Homo sapiens GN=CFHR2 PE=1 SV=1 | 451,74 | CTA | **CTA** | CTA | CTA |
| **P00746** | Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5 | 528,9 | CTA | **CTA** | CTA | CTA |
| **P02749** | Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3 | 1858,94 | CTA | **CTA** | CTA | CTA |
| **Q13790** | Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2 | 629,42 | CTA | **CTA** | CTA | CTA |
| **P01042** | Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 | 1757,57 | CTA | **CTA** | CTA | CTA |
| **P41159** | Leptin OS=Homo sapiens GN=LEP PE=1 SV=1 | 1313,66 | CTA | **CTA** | CTA | CTA |
| **P18136** | Ig kappa chain V-III region HIC OS=Homo sapiens PE=2 SV=2 | 5203,02 | CTA | **CTA** | CTA | CTA |
| **P18135** | Ig kappa chain V-III region HAH OS=Homo sapiens PE=2 SV=1 | 5203,02 | CTA | **CTA** | CTA | CTA |
| **P02787** | Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3 | 330,94 | CTA | **CTA** | CTA | CTA |
| **P01623** | Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1 | 5203,02 | CTA | **CTA** | CTA | CTA |
| **P01622** | Ig kappa chain V-III region Ti OS=Homo sapiens PE=1 SV=1 | 4908,27 | CTA | **CTA** | CTA | CTA |
| **P01620** | Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1 | 5203,02 | CTA | **CTA** | CTA | CTA |

| | | | | | | |
|---|---|---|---|---|---|---|
| **Q03591** | Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2 | 441,31 | CTA | **CTA** | CTA | CTA |
| **Q12805** | EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 | 640,74 | CTA | **CTA** | CTA | CTA |
| **P01861** | Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1 | 3673,03 | CTA | **CTA** | CTA | CTA |
| **P01860** | Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2 | 3913,3 | CTA | **CTA** | CTA | CTA |
| **P02765** | Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1 | 356,51 | CTA | **CTA** | CTA | CTA |
| **P02760** | Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1 | 5439,31 | CTA | **CTA** | CTA | CTA |
| **B9A064** | Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2 | 31466,05 | | **0,11** | -2,2 | 0,07 |
| **P0CG06** | Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1 | 29832,89 | | **0,11** | -2,19 | 0,08 |
| **P0CG04** | Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1 | 31201,36 | | **0,11** | -2,19 | 0,08 |
| **P0CG05** | Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1 | 29832,89 | | **0,11** | -2,18 | 0,07 |
| **P02647** | Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 | 46886,76 | | **0,12** | -2,16 | 0,04 |
| **P02655** | Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1 | 31287,69 | | **0,17** | -1,75 | 0,04 |
| **P02649** | Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 | 25865,32 | | **0,22** | -1,5 | 0,05 |
| **P02768** | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 | 16971,69 | | **0,25** | -1,37 | 0,06 |
| **P02766** | Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1 | 12385,7 | | **0,32** | -1,14 | 0,06 |
| **P10909** | Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 | 7130,75 | | **0,41** | -0,9 | 0,06 |
| **P0DJI9** | Serum amyloid A-2 protein OS=Homo sapiens GN=SAA2 PE=1 SV=1 | 8149,26 | | **0,61** | -0,49 | 0,08 |
| **P02656** | Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1 | 26322,37 | | **0,64** | -0,45 | 0,02 |
| **P0DJI8** | Serum amyloid A-1 protein OS=Homo sapiens GN=SAA1 PE=1 SV=1 | 10976,76 | | **0,70** | -0,35 | 0,06 |
| **P01024** | Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 | 204,04 | | **2,59** | 0,95 | 0,11 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **P02671** | Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2 | 5598,27 | | **3,10** | 1,13 | 0,03 |
| **P02100** | Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 | 6580,57 | | **15,18** | 2,72 | 0,05 |
| **P69892** | Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 | 6580,57 | | **15,33** | 2,73 | 0,05 |
| **P69891** | Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 | 6580,57 | | **15,33** | 2,73 | 0,05 |
| **P68871** | Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 | 39537,09 | | **15,49** | 2,74 | 0,02 |
| **P69905** | Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 | 10931,45 | | **15,80** | 2,76 | 0,04 |
| **P02042** | Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 | 13029,13 | | **16,12** | 2,78 | 0,04 |
| **P63261** | Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 | 1547,43 | HE | **HE** | HE | HE |
| **Q16661** | Guanylate cyclase activator 2B OS=Homo sapiens GN=GUCA2B PE=1 SV=1 | 271,19 | HE | **HE** | HE | HE |
| **Q9BYX7** | Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 | 927,09 | HE | **HE** | HE | HE |
| **P62736** | Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 | 1266,59 | HE | **HE** | HE | HE |
| **Q9H1Z8** | Augurin OS=Homo sapiens GN=C2orf40 PE=1 SV=1 | 520,22 | HE | **HE** | HE | HE |
| **P0CG39** | POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 | 367,23 | HE | **HE** | HE | HE |
| **P0CG38** | POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 | 440,78 | HE | **HE** | HE | HE |
| **P32119** | Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 | 1049,99 | HE | **HE** | HE | HE |
| **Q6S8J3** | POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 | 1135,55 | HE | **HE** | HE | HE |
| **P00915** | Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 | 1312,63 | HE | **HE** | HE | HE |
| **P68133** | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 | 1366,42 | HE | **HE** | HE | HE |
| **P68032** | Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 | 1366,42 | HE | **HE** | HE | HE |
| **P48740** | Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3 | 757,39 | HE | **HE** | HE | HE |

| | | | | | | |
|---|---|---|---|---|---|---|
| **P60709** | Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 | 1554,04 | HE | **HE** | HE | HE |
| **Q15485** | Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2 | 8217,97 | HE | **HE** | HE | HE |
| **P61769** | Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1 | 9586,78 | HE | **HE** | HE | HE |
| **Q16819** | Meprin A subunit alpha OS=Homo sapiens GN=MEP1A PE=1 SV=2 | 407,86 | HE | **HE** | HE | HE |
| **A5A3E0** | POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 | 1112,19 | HE | **HE** | HE | HE |
| **Q562R1** | Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 | 793,81 | HE | **HE** | HE | HE |
| **Q96NZ9** | Proline-rich acidic protein 1 OS=Homo sapiens GN=PRAP1 PE=1 SV=2 | 417,82 | HE | **HE** | HE | HE |
| **P63267** | Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 | 1266,59 | HE | **HE** | HE | HE |
| **Case 3** | | | | | | |
| **Accession** | **Description** | **Score** | **Unique** | **HE:CTA_Ratio** | **HE:CTA_Log(e)Ratio** | **HE:CTA_Log(e)Variance** |
| **P01009** | Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3 | 3935,93 | CTA | **CTA** | CTA | CTA |
| **P04206** | Ig kappa chain V-III region GOL OS=Homo sapiens PE=1 SV=1 | 2008,35 | CTA | **CTA** | CTA | CTA |
| **P04004** | Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1 | 645,15 | CTA | **CTA** | CTA | CTA |
| **Q13790** | Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2 | 906,5 | CTA | **CTA** | CTA | CTA |
| **P01042** | Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 | 2566,82 | CTA | **CTA** | CTA | CTA |
| **P01623** | Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1 | 2304 | CTA | **CTA** | CTA | CTA |
| **P01622** | Ig kappa chain V-III region Ti OS=Homo sapiens PE=1 SV=1 | 2008,35 | CTA | **CTA** | CTA | CTA |
| **P01620** | Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1 | 2304 | CTA | **CTA** | CTA | CTA |
| **P01034** | Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1 | 1525,72 | CTA | **CTA** | CTA | CTA |

| | | | | | | |
|---|---|---|---|---|---|---|
| **P02760** | Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1 | 5134,18 | CTA | **CTA** | CTA | CTA |
| **P02647** | Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1 | 63912,05 | | **0,11** | -2,19 | 0,03 |
| **P01857** | Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1 | 11473,75 | | **0,13** | -2,02 | 0,08 |
| **P01834** | Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 | 41887,75 | | **0,15** | -1,87 | 0,07 |
| **A0M8Q6** | Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=1 SV=2 | 16305,53 | | **0,19** | -1,68 | 0,14 |
| **B9A064** | Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2 | 35557,46 | | **0,20** | -1,63 | 0,07 |
| **P0CG06** | Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1 | 34303,55 | | **0,20** | -1,63 | 0,06 |
| **P0CG05** | Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1 | 34303,55 | | **0,20** | -1,63 | 0,07 |
| **P0CG04** | Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1 | 35317,46 | | **0,20** | -1,63 | 0,05 |
| **P0CF74** | Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4 SV=1 | 21277,07 | | **0,20** | -1,62 | 0,08 |
| **P02655** | Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1 | 54640,04 | | **0,23** | -1,49 | 0,03 |
| **P02768** | Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2 | 33149,57 | | **0,24** | -1,41 | 0,04 |
| **P02753** | Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 | 6338,78 | | **0,33** | -1,12 | 0,11 |
| **P01861** | Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1 | 5375,98 | | **0,39** | -0,93 | 0,1 |
| **P01860** | Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2 | 3654,59 | | **0,40** | -0,91 | 0,08 |
| **P01859** | Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 | 5151,65 | | **0,41** | -0,89 | 0,08 |
| **P02649** | Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 | 22223,38 | | **0,41** | -0,88 | 0,05 |
| **P0DJI9** | Serum amyloid A-2 protein OS=Homo sapiens GN=SAA2 PE=1 SV=1 | 7627,79 | | **0,41** | -0,88 | 0,13 |
| **P0DJI8** | Serum amyloid A-1 protein OS=Homo sapiens GN=SAA1 PE=1 SV=1 | 14922,66 | | **0,57** | -0,56 | 0,06 |
| **P02656** | Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1 | 20768,14 | | **0,59** | -0,53 | 0,02 |

| | | | | | | |
|---|---|---|---|---|---|---|
| **P10909** | Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1 | 6694,86 | | **0,68** | -0,39 | 0,04 |
| **P02652** | Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1 | 7854,07 | | **0,70** | -0,36 | 0,08 |
| **P02671** | Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2 | 6093,66 | | **3,90** | 1,36 | 0,04 |
| **P02042** | Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2 | 9858,24 | | **35,16** | 3,56 | 0,06 |
| **P69905** | Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 | 6167,84 | | **38,09** | 3,64 | 0,07 |
| **P68871** | Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2 | 14496,8 | | **48,91** | 3,89 | 0,07 |
| **P02100** | Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2 | 4861,9 | | **64,07** | 4,16 | 0,1 |
| **P69891** | Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2 | 4861,9 | | **64,07** | 4,16 | 0,08 |
| **P69892** | Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2 | 4861,9 | | **64,72** | 4,17 | 0,1 |
| **P63261** | Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 | 4181,45 | HE | **HE** | HE | HE |
| **Q9BYX7** | Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1 | 1236,17 | HE | **HE** | HE | HE |
| **Q07507** | Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 | 956,65 | HE | **HE** | HE | HE |
| **P62736** | Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1 | 3309,59 | HE | **HE** | HE | HE |
| **P0CG39** | POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1 | 1633,23 | HE | **HE** | HE | HE |
| **P0CG38** | POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1 | 1675,94 | HE | **HE** | HE | HE |
| **P32119** | Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 | 2097,75 | HE | **HE** | HE | HE |
| **Q6S8J3** | POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3 | 2761,05 | HE | **HE** | HE | HE |
| **P00915** | Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 | 1646,18 | HE | **HE** | HE | HE |
| **P68133** | Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 | 3323,39 | HE | **HE** | HE | HE |
| **P68032** | Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 | 3323,39 | HE | **HE** | HE | HE |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| **P48740** | Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3 | 4272,76 | HE | **HE** | HE | HE |
| **P60709** | Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 | 4181,45 | HE | **HE** | HE | HE |
| **P08493** | Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2 | 7402,88 | HE | **HE** | HE | HE |
| **P01871** | Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 | 413,69 | HE | **HE** | HE | HE |
| **Q15485** | Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2 | 18406,43 | HE | **HE** | HE | HE |
| **P01024** | Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 | 997,36 | HE | **HE** | HE | HE |
| **P04220** | Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1 | 330,05 | HE | **HE** | HE | HE |
| **A5A3E0** | POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2 | 2761,05 | HE | **HE** | HE | HE |
| **Q562R1** | Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 | 1445,83 | HE | **HE** | HE | HE |
| **P09382** | Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 | 1333,56 | HE | **HE** | HE | HE |
| **P63267** | Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1 | 3309,59 | HE | **HE** | HE | HE |

**Table S2.** Proteins selected for targeted MRM analysis with their tryptic peptides and transitions.

| **Protein Description** | **Protein ID** | **Precursors (m/z)** | **RT (min)** | **Transition 1 (m/z)** | **Transition 2 (m/z)** |
|---|---|---|---|---|---|
| Antithrombin-III | ANT3 | 837.9<br>875.8 | 77<br>68 | 717.4<br>755.3 | 1108.54<br>973.4 |
| β 2 microglobulin | B2MG | 749.9<br>561.8 | 36<br>40 | 615.3<br>673.4 | 884.4<br>772.4 |
| Fibrinogen α chain | FIBA | 570.9<br>690.9 | 60<br>35 | 561.8<br>590.8 | 610.3<br>681.9 |
| Fibrinogen β chain | FIBB | 834.9<br>893.4 | 127<br>123 | 671.8<br>608.3 | 825.9<br>1178.5 |
| Fibrinogen γ chain | FIBG | 736.4<br>757.4 | 71<br>75 | 447.2<br>647.3 | 909.4<br>867.4 |
| Inhibin β C chain | INHBC | 904.9 | 52 | 444.3 | 895.9 |
| Inhibin β E chain | INHBE | 613.5<br>944.9 | 95<br>85 | 384.2<br>795.4 | 846.5<br>1306.6 |
| Insulin-like GF binding protein 2 | IBP2 | 808.4<br>711.4 | 101<br>70 | 644.4<br>630.3 | 709.3<br>889.4 |

| | | | | | |
|---|---|---|---|---|---|
| Integrin α-2b | ITA2B | 611.9 | 72 | 395.2 | 1009.5 |
| | | 764.8 | 58 | 662.8 | 1258.5 |
| Kininogen | KNG1 | 626.5 | 94 | 617.3 | 1051.5 |
| | | 502.5 | 82 | 493.3 | 606.3 |
| Plasminogen | PLMN | 667.4 | 65 | 707.3 | 964.4 |
| | | 897.4 | 64 | 716.3 | 966.5 |
| Retinol-binding protein 4 | RET4 | 1033.1 | 145 | 409.2 | 1496.7 |
| | | 559.3 | 45 | 675.8 | 725.3 |
| Serum amyloid A1 protein | SAA1 | 775.9 | 171 | 822.4 | 935.5 |
| | | 835.9 | 69 | 826.9 | 1080.5 |
| Serum amyloid A2 protein | SAA2 | 537.9 | 95 | 526.8 | 626.8 |
| | | 728.4 | 111 | 447.2 | 859.5 |
| Transthyretin | TTHY | 683.9 | 95 | 611.7 | 728.4 |
| | | 697.9 | 99 | 606.3 | 735.4 |
| Wnt1 inducible signalling pathway protein 2 | WISP2 | 917.0 | 115 | 916.9 | 1306.6 |
| | | 1031.1 | 92 | 1132.5 | 1212.6 |