Table S1. List of the proteins identified by LC-MS/MS in at least two samples out of three. The protein score and the sequence of the detected peptides are reported for each protein.

				sample 11			sample 12			sample 13		
UNIPROT ID	**Description**	**MW**	**pI**	**Score**	**N° peptides**	peptide sequences	Score	N° peptides	peptide sequences	Score	N° peptides	peptide sequences
O00300	Tumor necrosis factor receptor superfamily member 11B	45996	8.66	116	3	TVTQSLK VGAEDIEK SLMESLPGKK	92	3	TVTQSLK VGAEDIEK SLMESLPGKK			n.i.
O00391	Sulfhydryl oxidase 1	66818	8.85	129	1	DVQNVAAAPELAMGALELESR	257	7	GAVLGSR EGAVLAK VPVLMESR VLNTEANVVR AAPGQEPPEHMAELQR AHFSPSNIILDFPAAGSAAR RDVQNVAAAPELAMGALELESR			n.i.
O15232	Matrilin-3	52816	6.25	194	3	EPSSNIPK RPSPAAPDGAPASGTSEPGR MMASEPLEEHVFYVETYGVIEK	346	6	EPSSNIPK IEFQLQAYTDK IIDTLDIGPADTR AQASGIELYAVGVDR VAIIVTDGRPQDQVNEVAAR MMASEPLEEHVFYVETYGVIEK			n.i.
P00709	Alpha-lactalbumin	16214	4.83	55	2	SSQVPQSR GIDYWLAHK	211	3	SSQVPQSR CELSQLLK GIDYWLAHK			n.i.
P01011	Alpha-1-antichymotrypsin	47621	5.33	373	4	NLAVSQVVHK ITLLSALVETR AVLDVFEEGTEASAATAVK DYNLNDILLQLGIEEAFTSK	180	2	EQLSLLDR AVLDVFEEGTEASAATAVK			n.i.
P01024	Complement C3	187030	6.02	1368	9	QPSSAFAAFVK DFDFVPPVVR ENEGFTVTAEGK EVVADSVWVDVK SEETKENEGFTVTAEGK DAPDHQELNLDVSLQLPSR ILLQGTPVAQMTEDAVDAER VPVAVQGEDTVQSLTQGDGVAK EGVQKEDIPPADLSDQVPDTESETR	1509	19	LVLSSEK SVQLTEK NEQVEIR TGLQEVEVK QPSSAFAAFVK DFDFVPPVVR APSTWLTAYVVK KQELSEAEQATR SSLSVPYVIVPLK AGDFLEANYMNLQR SNLDEDIIAEENIVSR SEETKENEGFTVTAEGK TELRPGETLNVNFLLR LSINTHPSQKPLSITVR DAPDHQELNLDVSLQLPSR ILLQGTPVAQMTEDAVDAER SLYVSATVILHSGSDMVQAER YYGGGYGSTQATFMVFQALAQYQK EGVQKEDIPPADLSDQVPDTESETR	412	3	SEETKENEGFTVTAEGK ILLQGTPVAQMTEDAVDAERLK EGVQKEDIPPADLSDQVPDTESETR
P01833	Polymeric immunoglobulin receptor	83232	5.58	1780	14	APAFEGR VLDSGFR VYTVDLGR ILLNPQDK IIEGEPNLK LVSLTLNLVTR DGSFSVVITGLR DGSFSVVITGLRK QGHFYGETAAVYVAVEER FLCRQSSGENCDVVVNTLGK ILLNPQDKDGSFSVVITGLR GLSFDVSLEVSQGPGLLNDTK NADLQVLKPEPELVYEDLR ILLNPQDKDGSFSVVITGLRK	2063	13	APAFEGR VLDSGFR VYTVDLGR ILLNPQDK IIEGEPNLK LVSLTLNLVTR DGSFSVVITGLR QGHFYGETAAVYVAVEER LDIQGTGQLLFSVVINQLR ILLNPQDKDGSFSVVITGLR NADLQVLKPEPELVYEDLR KNADLQVLKPEPELVYEDLR IRLDIQGTGQLLFSVVINQLR	599	5	VLDSGFR VLDSGFREIENK DVSLAKADAAPDEK ADAAPDEKVLDSGFR ADAAPDEKVLDSGFREIENK
P01834	Immunoglobulin kappa constant	11758	6.11	602	3	DSTYSLSSTLTLSK TVAAPSVFIFPPSDEQLK VDNALQSGNSQESVTEQDSK	218	3	DSTYSLSSTLTLSK TVAAPSVFIFPPSDEQLK VDNALQSGNSQESVTEQDSK			n.i.
P01876	Immunoglobulin heavy constant alpha 1	37631	6.08	317	3	TPLTATLSK DASGVTFTWTPSSGK QEPSQGTTTFAVTSILR	393	3	SAVQGPPER DASGVTFTWTPSSGK QEPSQGTTTFAVTSILR			n.i.
P02647	Apolipoprotein A-I	30759	5.56	543	6	DLATVYVDVLK VSFLSALEEYTK DYVSQFEGSALGK DSGRDYVSQFEGSALGK EQLGPVTQEFWDNLEK	746	15	AHVDALR AELQEGAR LHELQEK AKPALEDLR LSPLGEEMR			n.i.

						LREQLGPVTQEFWDNLEKE TEGLR			LEALKENGGAR ATEHLSTLSEK DLATVYVDVLK VQPYLDDFQK THLAPYSDELR VSFLSALEEYTK DYVSQFEGSALGK LLDNWDSVTSTFSK EQLGPVTQEFWDNLEK LREQLGPVTQEFWDNLEK			
P02649	Apolipoprotein E	36132	5.65	397	3	VQAAVGTSAAPVPSDNH SELEEQLTPVAEETR WVQTLSEQVQEELLSSQVTQ ELR	322	5	ALMDETMK SWFEPLVEDMQR VQAAVGTSAAPVPSDNH SELEEQLTPVAEETR WVQTLSEQVQEELLSSQVTQE LR			n.i.
P02652	Apolipoprotein A-II	11168	6.26	213	4	SPELQAEAK EQLTPLIKK AGTELVNFLSYFVELGTQPA TQ KAGTELVNFLSYFVELGTQP ATQ	131	4	SPELQAEAK SKEQLTPLIK VKSPELQAEAK AGTELVNFLSYFVELGTQPAT Q	47	1	GKVKVGVNGFGR
P02748	Complement component C9	63133	5.43	112	1	GTVIDVTDFVNWASSINDAP VLISQK	68	2	TSNFNAAISLK LSPIYNLVPVK			n.i.
P02788-2	Lactotransferrin	78182	8.50	486	5	DGAGDVAFIR SDTSLTWNSVK YLGPQYVAGITNLKK GEADAMSLDGGYVYTAGK DVTVLQNTDGNNNEAWAK	2491	23	DSAIGFSR VPSHAVVAR EDAIWNLLR THYYAVAVVK FQLFGSPSGQK SDTSLTWNSVK THYYAVAVVKK GGSFQLNELQGLK LRPVAAEVYGTER DLLFKDSAIGFSR KGGSFQLNELQGLK SVNGKEDAIWNLLR YLGPQYVAGITNLKK GEADAMSLDGGYVYTAGK FQLFGSPSGQKDLLFK LRPVAAEVYGTERQPR ADAVTLDGGFIYEAGLAPYK IDSGLYLGSGYFTAIQNLR IDSGLYLGSGYFTAIQNLRK VPPRIDSGLYLGSGYFTAIQNL R FQLFGSPSGQKDLLFKDSAIGF SR VPPRIDSGLYLGSGYFTAIQNL RK ADAVTLDGGFIYEAGLAPYK LRPVAAEVYGTER			n.i.
P04114	Apolipoprotein B-100	515283	6.58	214	3	FPEVDVLTK SVSDGIAALDLNAVANK VPSYTLILPSLELPVLHVPR	883	14	FVTQAEGAK QIDDIDVR FPEVDVLTK TEVIPPLIENR AASGTTGTYQEWK AVSMPSFSILGSDVR TSSFALNLPTLPEVK ALYWVNGQVPDGVSK SVSDGIAALDLNAVANK NIQEYLSILTDPDGK VNWEEEAASGLLTSLK VPSYTLILPSLELPVLHVPR VNWEEEAASGLLTSLKDNVP K IADFELPTIIVPEQTIEIPSIK			n.i.
P04406	Glyceraldehyde-3-phosphate dehydrogenase	36030	8.57	171	2	VIISAPSADAPMFVMGVNH EK VIHDNFGIVEGLMTTVHAIT ATQK	300	5	VGVNGFGR GALQNIIPASTGAAK LVINGNPITIFQER VIISAPSADAPMFVMGVNHE K VIHDNFGIVEGLMTTVHAITA TQK	47	2	GKVKVGVNGFGR DGRGALQNIIPASTGAAK
P05814	Beta-casein	25366	5.52	2447	6	SPTIPFFDPQIPK VLPIPQQVVPYPQR ETIESLSSSEESITEYK AVPVQALLLNQELLLNPTH QIYPVTQPLAPVHNPISV LTDLENLHLPLPLLQPLMQQ VPQPIPQTLALPPQPLWSVP QPK VKHEDQQQGEDEHQDKIYP SFQPQPLIYPFVEPIPYGFLPQ NILPLAQPAVVLPVPQPEIM EVPK	4325	10	AKDTVYTK SPTIPFFDPQIPK VLPIPQQVVPYPQR ETIESLSSSEESITEYK VKHEDQQQGEDEHQDK VMPVLKSPTIPFFDPQIPK AVPVQALLLNQELLLNPTHQ IYPVTQPLAPVHNPISV LTDLENLHLPLPLLQPLMQQ VPQPIPQTLALPPQPLWSVPQ PK IYPSFQPQPLIYPFVEPIPYGFL PQNILPLAQPAVVLPVPQPEI MEVPK VKHEDQQQGEDEHQDKIYPS FQPQPLIYPFVEPIPYGFLPQNI LPLAQPAVVLPVPQPEIMEVP K	2660	13	GRVMPVLK AKDTVYTK DTVYTKGR SPTIPFFDPQIPK VLPIPQQVVPYPQR ETIESLSSSEESITEYK VMPVLKSPTIPFFDPQIPK GRVMPVLKSPTIPFFDPQIPK AVPVQALLLNQELLLNPTHQ IYPVTQPLAPVHNPISV LTDLENLHLPLPLLQPLMQQ VPQPIPQTLALPPQPLWSVPQ PK

												IYPSFQPQPLIYPFVEPIPYGFL PQNILPLAQPAVVLPVPQPEI MEVPK SPTIPFFDPQIPKLTDLENLHL PLPLLQPLMQQVPQPIPQTLA LPPQPLWSVPQPK VKHEDQQQGEDEHQDKIYPS FQPQPLIYPFVEPIPYGFLPQNI LPLAQPAVVLPVPQPEIMEVP K
P06396	Gelsolin	85698	5.90	107	2	GGVASGFK TGAQELLR	331	6	YIETDPANR HVVPNEVVVQR EVQGFESATFLGYFK EPAHLMSLFGGKPMIIYK DPDQTDGLGLSYLSSHIANVE R VPFDAATLHTSTAMAAQHG MDDDGTGQK			n.i.
P06858	Lipoprotein lipase	53129	8.4	534	7	APAVFVK LVGQDVAR DFIDIESK GLGDVDQLVK EPDSNVIVVDWLSR SIHLFIDSLLNEENPSK ITGLDPAGPNFEYAEAPSR	648	11	APAVFVK LVGQDVAR DFIDIESK GLGDVDQLVK AQEHYPVSAGYTK EPDSNVIVVDWLSR LSPDDADFVDVLHTFTR SIHLFIDSLLNEENPSK ITGLDPAGPNFEYAEAPSR TFMVIHGWTVTGMYESWVP K FINWMEEEFNYPLDNVHLLG YSLGAHAAGIAGSLTNK	277	6	DFIDIESK GLGDVDQLVK LSPDDADFVDVLHTFTR SIHLFIDSLLNEENPSK ITGLDPAGPNFEYAEAPSRLSP DDADFVDVLHTFTR FINWMEEEFNYPLDNVHLLG YSLGAHAAGIAGSLTNK
P07498	Kappa-casein	20293	8.97	1417	5	RPAIAINNPYVPR QYLPNSHPPTVVR RPNLHPSFIAIPPK RPNLHPSFIAIPPKK TYYANPAVVRPHAQIPQR	1626	8	RPAIAINNPYVPR QYLPNSHPPTVVR RPNLHPSFIAIPPK RPNLHPSFIAIPPKK TYYANPAVVRPHAQIPQR SFLLVVNALALTLPFLAVEVQ NQK MKSFLLVVNALALTLPFLAVE VQNQK TAPYVPMYYVPNSYPYYGTN LYQR	3509	10	RPAIAINNPYVPR QYLPNSHPPTVVR RPNLHPSFIAIPPK RPNLHPSFIAIPPKK TYYANPAVVRPHAQIPQR RPNLHPSFIAIPPKKIQDK TAPYVPMYYVPNSYPYYGTN LYQR QYLPNSHPPTVVRRPNLHPSF IAIPPK RPAIAINNPYVPRTYYANPAV VRPHAQIPQR TYYANPAVVRPHAQIPQRQY LPNSHPPTVVR
P07602	Prosaposin	58112	5.06	305	4	LPALTVHVTQPK NVIPALELVEPIK NVIPALELVEPIKK IPELDMTEVVAPFMANIPLL LYPQDGPR	92	1	NVIPALELVEPIKK			n.i.
P07996	Thrombospondin-1	129300	4.71	362	6	DLASIAR GPDPSSPAFR IEDANLIPPVPDDK GGVNDNFQGVLQNVR MENAELDVPIQSVFTR IEDANLIPPVPDDKFQDLVD AVR	207	5	DLASIAR SITLFVQEDR AGTLDLSLTVQGK GGVNDNFQGVLQNVR IEDANLIPPVPDDKFQDLVDA VR			n.i.
P08571	Monocyte differentiation antigen CD14	40051	5.84	282	5	ELTLEDLK LKELTLEDLK LTVGAAQVPAQLLVGALR RLTVGAAQVPAQLLVGALR ITGTMPPLPLEATGLALSSLR	609	10	QYADTVK ELTLEDLK FPAIQNLALR LKELTLEDLK STLSVGVSGTLVLLQGAR LTVGAAQVPAQLLVGALR SWLAELQQWLKPGLK RLTVGAAQVPAQLLVGALR AFPALTSLDLSDNPGLGER ITGTMPPLPLEATGLALSSLR			n.i.
P10451	Osteopontin	35442	4.37	860	7	GDSVVYGLR QNLLAPQTLPSK YPDAVATWLNPDPSQK AIPVAQDLNAPSDWDSR GKDSYETSQLDDQSAETHSH K QLYNKYPDAVATWLNPDPS QK QETLPSK	1303	8	GDSVVYGLR QNLLAPQTLPSK ISHELDSASSEVN YPDAVATWLNPDPSQK AIPVAQDLNAPSDWDSR QLYNKYPDAVATWLNPDPS QK RPDIQYPDATDEDITSHMESE ELNGAYK FRRPDIQYPDATDEDITSHME SEELNGAYK			n.i.
P10909	Clusterin	52494	5.88	4229	16	SGSGLVGR FMETVAEK EIQNAVNGVK IDSLLENDR TLLSNLEEAK TLLSNLEEAKK ELDESLQVAER KTLLSNLEEAKK ASSIIDELFQDR QQTHMLDVMQDHFSR LFDSDPITVTVPVEVSR EPQDTYHYLPFSLPHR LFDSDPITVTVPVEVSRK VTTVASHTSDSDVPSGVTEV VVK IDSLLENDRQQTHMLDVMQ DHFSR MQDHFSR	2096	15	SGSGLVGR FMETVAEK EIQNAVNGVK IDSLLENDR TLLSNLEEAK TLLSNLEEAKK KTLLSNLEEAK ELDESLQVAER KTLLSNLEEAKK ASSIIDELFQDR RELDESLQVAER YVNKEIQNAVNGVK QQTHMLDVMQDHFSR LFDSDPITVTVPVEVSR VTTVASHTSDSDVPSGVTEVV VK	1931	20	FMETVAEK EIQNAVNGVK TLLSNLEEAK TLIEKTNEER ELDESLQVAER NPKFMETVAEK TLIEKTNEERK ASSIIDELFQDR YVNKEIQNAVNGVK ELDESLQVAERLTR FMETVAEKALQEYR LFDSDPITVTVPVEVSR TNEERKTLLSNLEEAK YVNKEIQNAVNGVKQIK EPQDTYHYLPFSLPHR LFDSDPITVTVPVEVSRK VTTVASHTSDSDVPSGVTEVV VK

												LFDSDPITVTVPVEVSRKNPK ASSIIDELFQDRFFTREPQDTY HYLPFSLPHR VTTVASHTSDSDVPSGVTEVV VKLFDSDPITVTVPVEVSR
P15291	Beta-1,4-galactosyltransferase 1	43920	8.88	707	6	HISVAMDK LLNVGFQEALK GMSISRPNAVVGR YPLYTQITVDIGTPS ETMLSDGLNSLTYQVLDVQ R LPQLVGVSTPLQGGSNSAA AIGQSSGELR	372	5	HISVAMDK VAIIIPFR LLNVGFQEALK ETMLSDGLNSLTYQVLDVQR LPQLVGVSTPLQGGSNSAAAI GQSSGELR	274	2	LPQLVGVSTPLQGGSNSAAAI GQSSGELR DLSRLPQLVGVSTPLQGGSNS AAAIGQSSGELR
P19835	Bile salt-activated lipase	79272	5.13	1782	17	GIPFAAPTK EAQMPAVIR VTEEDFYK LVSEFTITK DQHMAIAWVK LGLLGDSVDIFK LGAVYTEGGFVEGVNK AISQSGVALSPWVIQK VGPLGFLSTGDANLPGNYG LR TTFDVYTESWAQDPSQENK TTFDVYTESWAQDPSQENK K TVVDFETDVLFLVPTEIALA QHR KTVVDFETDVLFLVPTEIALA QHR CLQATITQDSTYGDEDCLYL NIWVPQGR WVGADHADDIQYVFGKPF ATPTGYRPQDR TGDPNMGDSAVPTHWEPYT TENSGYLEITK TGDPNMGDSAVPTHWEPYT TENSGYLEITKK	6019	33	MGSSSMK ALTLAYK NPLFWAK GIPFAAPTK EAQMPAVIR VTEEDFYK LVSEFTITK KVTEEDFYK EAQMPAVIRF DQHMAIAWVK LGLLGDSVDIFK GNVIVVTFNYR AMIAYWTNFAK TYAYLFSHPSR KLGLLGDSVDIFK LGAVYTEGGFVEGVNK AISQSGVALSPWVIQK LGAVYTEGGFVEGVNKK ALENPQPHPGWQGTLK RAISQSGVALSPWVIQK VGPLGFLSTGDANLPGNYGL R LGLLGDSVDIFKGIPFAAPTK TTFDVYTESWAQDPSQENKK TVVDFETDVLFLVPTEIALAQ HR KTVVDFETDVLFLVPTEIALA QHR WVGADHADDIQYVFGKPFA TPTGYRPQDR TGDPNMGDSAVPTHWEPYT TENSGYLEITK NIAAFGGDPNNITLFGESAGG ASVSLQTLSPYNK TGDPNMGDSAVPTHWEPYT TENSGYLEITKK RNIAAFGGDPNNITLFGESAG GASVSLQTLSPYNK DLPVMIWIYGGAFLMGSGHG ANFLNNYLYDGEEIATR VPLAGLEYPMLHYVGFVPVID GDFIPADPINLYANAADIDYI AGTNNMDGHIFASIDMPAIN K	1409	15	NPLFWAK GIPFAAPTK LVSEFTITK LGLLGDSVDIFK ALENPQPHPGWQGTLK VTEEDFYKLVSEFTITK LGLLGDSVDIFKGIPFAAPTK TTFDVYTESWAQDPSQENK TTFDVYTESWAQDPSQENKK TTFDVYTESWAQDPSQENKK K AISQSGVALSPWVIQKNPLFW AK TVVDFETDVLFLVPTEIALAQ HR KTVVDFETDVLFLVPTEIALA QHR KKTVVDFETDVLFLVPTEIAL AQHR WVGADHADDIQYVFGKPFA TPTGYRPQDR
P22897	Macrophage mannose receptor 1	165905	6.11	122	2	YTNWAADEPK DSTFSAWTGLNDVNSEHTFL WTDGR	3559	37	GSGLWSR SSYSLMR FAWMDGSK KTWFESR GVHYTNWGK LITASGSYHK EEQQTIWR DYQYYFSK EGWNFYSNK IFGFMEEER ALGGDLASINNK YTNWAADEPK SQGPEIVEVEK TGIAGGLWDVLK EQAFLTYHMK IFGFMEEERK GEDLFFNYGNR FTHWNSDMPGR YFWTGLSDIQTK QFLIYNEDHKR GTFQWTIEEEVR WVSESQIMSVAFK NFGDLVSIQSESEK NFGDLVSIQSESEKK RNFGDLVSIQSESEK RNFGDLVSIQSESEKK NDAQSAYFIGLLISLDK YEQAFLTSFVGLRPEK SDPSLTNPPATIQTDGFVK NDAQSAYFIGLLISLDKK IQMYFEWSDGTPVTFTK MGSSLVSIESAAESSFLSYR ALGGDLASINNKEEQQTIWR			n.i.

									YVNRNDAQSAYFIGLLISLDK K FEGSESLWNKDPLTSVSYQIN SK DSTFSAWTGLNDVNSEHTFL WTDGR LHNSLIASILDPYSNAFAWLQ METSNER			
P23280	Carbonic anhydrase 6	35366	6.51	376	4	LENSLLDHR TTLTGLDVQDMLPR NYPENTYYSNFISHLANIK VVESNFPNQEYTLGSEFQFY LHK			n.i.	65	1	VVESNFPNQEYTLGSEFQFYL HKIEEILDYLR
P23284	Peptidyl-prolyl cis-trans isomerase B	23728	9.42	63	1	TVDNFVALATGEK	106	3	IGDEDVGR VLEGMEVVR TVDNFVALATGEK			n.i.
P24821	Tenascin	24085	4.79	7173	50	SSTITAK FSVGDAK AVDIPGLK STDLPGLK SFSTFDK VSIYGVIR AYAAGFGDR TRDITGLR IQALNGPLR FTTDLDSPR LDAPSQIEVK AATHYTITIR TPVLSAEASTAK ITAQGQYELR ETFTTGLDAPR DHGETAFAVYDK GHEHSIQFAEMK AVDIPGLEAATPYR EEFWLGLDNLNK QSEPLEITLLAPER REEFWLGLDNLNK EATEYEIELYGISK YAPISGGDHAEVDVPK KQSEPLEITLLAPER GLEPGQEYNVLLTAEK ESNPATINAATELDTPK LSWTADEGVFDNFVLK VEGYSGTAGDSMAYHNGR ASVTGYLLVYESVDGTVK DLQVSETAETSLTLLWK TTLTGLRPGTEYGIGVSAVK DHGETAFAVYDKFSVGDAK WQPAIATVDSYVISYTGEK EDKESNPATINAATELDTPK DLTATEVQSETALLTWRPPR TTLTGLRPGTEYGIGVSAVK EDK ASTEQAPELENLTVTEVGW DGLR TVSGNTVEYALTDLEPATEY TLR TAHISGLPPSTDFIVYLSGLA PSIR EVIVGPDTTSYSLADLSPSTH YTAK WQPAIATVDSYVISYTGEKV PEITR TISATATTEAEPEVDNLLVSD ATPDGFR DVTDTTALITWFKPLAEIDGI ELTYGIK TKTISATATTEAEPEVDNLL VSDATPDGFR DLAPPSEPSESFQEHTVDGE NQIVFTHR TTIDLTEDENQYSIGNLKPDT EYEVSLISR GHSTRPLAVEVVTEDLPQLG DLAVSEVGWDGLR ESNPATINAATELDTPKDLQ VSETAETSLTLLWK EDKESNPATINAATELDTPK DLQVSETAETSLTLLWK TTLTGLRPGTEYGIGVSAVK EDKESNPATINAATELDTPK	4702	53	SSTITAK FSVGDAK AVDIPGLK SFSTFDK LRPSNFR SMEIPGLR VSIYGVIR AYAAGFGDR IQALNGPLR FTTDLDSPR AYAAGFGDRR LDAPSQIEVK AATHYTITIR TPVLSAEASTAK ITAQGQYELR ETFTTGLDAPR VATYLPAPEGLK DHGETAFAVYDK GHEHSIQFAEMK AVDIPGLEAATPYR AGTPYTVTLHGEVR VSQTDNSITLEWR QSEPLEITLLAPER EATEYEIELYGISK YAPISGGDHAEVDVPK KQSEPLEITLLAPER GLEPGQEYNVLLTAEK ESNPATINAATELDTPK LSWTADEGVFDNFVLK AATPYTVSIYGVIQGYR VEGYSGTAGDSMAYHNGR ASVTGYLLVYESVDGTVK DLQVSETAETSLTLLWK QTGLAPGQEYEISLHIVK YGDNNHSQGVNWFHWK TTLTGLRPGTEYGIGVSAVK LKVEGYSGTAGDSMAYHNG R WQPAIATVDSYVISYTGEK EDKESNPATINAATELDTPK DLTATEVQSETALLTWRPPR TTLTGLRPGTEYGIGVSAVKE DK VTEYLVVYTPTHEGGLEMQF R VPGDQTSTIIQELEPGVEYFIR ASTEQAPELENLTVTEVGWD GLR TVSGNTVEYALTDLEPATEYT LR TVSGNTVEYALTDLEPATEYT LR TAHISGLPPSTDFIVYLSGLAP SIR EVIVGPDTTSYSLADLSPSTHY TAK WQPAIATVDSYVISYTGEKVP EITR TISATATTEAEPEVDNLLVSD ATPDGFR DVTDTTALITWFKPLAEIDGIE LTYGIK DLAPPSEPSESFQEHTVDGEN QIVFTHR GHSTRPLAVEVVTEDLPQLG DLAVSEVGWDGLR	253	4	GLEPGQEYNVLLTAEK VDLRDHGETAFAVYDKFSVG DAK IKYAPISGGDHAEVDVPKSQQ ATTK WQPAIATVDSYVISYTGEKVP EITR
P47710	Alpha-S1-casein	21671	5.32	2154	9	NNVMLQW LPLRYPER QTDEIKDTR EEYMNGMNR EKQTDEIKDTR MESSISSSSEEMSLSK LQNPSESSEPIPLESR LNEYNQLQLQAAHAQEQIR LNEYNQLQLQAAHAQEQIR R	4584	12	NNVMLQW EKQTDEIK LPLRYPER QTDEIKDTR EEYMNGMNR EKQTDEIKDTR MESSISSSSEEMSLSK LQNPSESSEPIPLESR LNEYNQLQLQAAHAQEQIR LNEYNQLQLQAAHAQEQIRR	285	5	NNVMLQW LPLRYPER EEYMNGMNR LQNPSESSEPIPLESR LQNPSESSEPIPLESREEYMNG MNR

									MNENSHVQVPFQQLNQLAA YPYAVWYYPQIMQYVPFPPFS DISNPTAHENYEK RMNENSHVQVPFQQLNQLA AYPYAVWYYPQIMQYVPFPP FSDISNPTAHENYEK			
P47989	Xanthine dehydrogenase/oxidase	146330	7.86	178	4	DPPADVQLFQEVPK ITYEELPAIITIEDAIK TLLSPEEILLSIEIPYSR SVASVGGNIITASPISDLNPV FMASGAK	1232	22	LGLSGTK MGGGFGGK MVQVASR GVLEQLR TLVDAVAK MLGVPANR LDSPATPEK LGQENLEDK EGEYFSAFK DEDMLITGGR VTWIQASTLK NNSFYGPELK EGDLTHFNQK IPAFGSIPIEFR TADKLVFFVNGR STVVSTAVALAAYK LVVGNTEIGIEMK NADPETTLLAYLR LDPTFASATLLFQK DPPADVQLFQEVPK TVQMDHTFFPGYR SVASVGGNIITASPISDLNPVF MASGAK	44	2	IEKGDLKK SVASVGGNIITASPISDLNPVF MASGAK
P49327	Fatty acid synthase	273254	6.01	64	1	GVDLVLNSLAEEK	516	9	LLEQGLR VFTTVGSAEK VTAIHIDPATHR VVVQVLAEEPEAVLK LPEDPLLSGLLDSPALK VTVAGGVHISGLHTESAPR LQLNGNLQLELAQVLAQERPK LHLSGIDANPNALFPPVEFPAPR ALGLGVEQLPVVFEDVVLHQ ATILPK	86	2	TPEAVQK GGNVGINSFGFGGSNVHIILR PNTQPPPAPAPHATLPR
P58499	Protein FAM3B	25981	8.97	64	2	NAIEALGSK GLELPSEIQR	20	1	LLSGGGR			n.i.
P60709	Actin, cytoplasmic 1	41710	5.29	210	2	VAPEEHPVLLTEAPLNPK TTGIVMDSGDGVTHTVPIYE GYALPHAILR	145	8	IIAPPER EITALAPSTMK HQGVMVGMGQK TTGIVMDSGDGVTHTVPIYEG YALPHAILR IIAPPER EITALAPSTMK HQGVMVGMGQK YPIEHGIITNWDDMEK	56	1	VAPEEHPVLLTEAPLNPK
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	83550	6.46	184	2	NLAYDTLPVLIHGNGPTK IQGGYENVPTIDIHMNQIGF ER	92	1	IFQNLDGALDEVVLK			n.i.
Q08431	Lactadherin	43105	8.47	195	2	NAVHVNLFETPVEAQYVR AGMVNAWTPSSNDDNPWI QVNLLR	66	1	NAVHVNLFETPVEAQYVR			n.i.
Q13410	Butyrophilin subfamily 1 member A1	58923	5.38	807	8	FPSTSESR ATLVQDGIAK TPLPLAGPPR GEKFPSTSESR EQEAEQMPEYR NPDEEGLFTVAASVIIR FPSTSESRNPDEEGLFTVAAS VIIR KATLHAVDVTLDPDTAHPH LFLYEDSK	243	4	FPSTSESR ATLVQDGIAK EQEAEQMPEYR NPDEEGLFTVAASVIIR			n.i.
Q14697	Neutral alpha-glucosidase AB	10687	5.74	363	3	EPWLLPSQHNDIIR DVHNIYGLYVHMATADGL R FSFSGNTLVSSSADPEGHFET PIWIER	66	1	VTEGGEPYR			n.i.
Q6WN34	Chordin-like protein 2 OS=Homo sapiens	49643	6.75	252	2	LPSPDPGAEGHGQSR GPGTPAPTGLSAPLSFIPR	561	7	VTASPDKVTK GIFHLTQIK ADPGHSEISSTR VLVHTSVSPSPDNLR VLVHTSVSPSPDNLRR FALEHEASDLVEIYLWK LLAGPHEGHWNVFLAQTLEL K	146	4	GAGSTTVKIVLK LPSPDPGAEGHGQSR SLERLPSPDPGAEGHGQSR RGPGTPAPTGLSAPLSFIPR
Q96DA0	Zymogen granule protein 16 homolog B	22725	6.74	200	3	VSVGLLLVK YFSTTEDYDHEITGLR LGALGGNTQEVTLQPGEYIT K	203	3	VSVGLLLVK YFSTTEDYDHEITGLR LGALGGNTQEVTLQPGEYITK			n.i.
Q96S86	Hyaluronan and proteoglycan link protein 3	40868	6.07	40	1	DLLNGVK	143	3	DLLNGVK LTLTEAR LSENGAPEKDVLVAIGLR			n.i.

Q99102	Isoform 10 of Mucin-4	225293	5.78	78	1	TVDFTSPLFKPATGFPLGSSLR	119	2	TVDFTSPLFKPATGFPLGSSLR GTTFYQEYETFYGEHSLLVQQAESWIR	n.i.
Q9H173	Nucleotide exchange factor SIL1	52052	5.27	109	1	MFAEEEAELTQEMSPEK	73	2	VQVEAIEGGALQK LLVILATEQPLTAK	n.i.

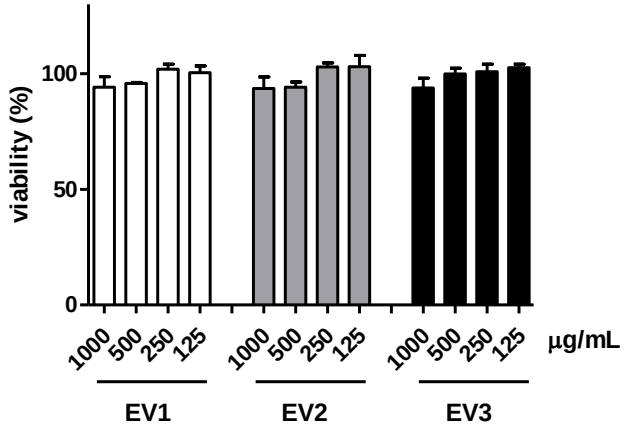

Figure S1. Cell viability assay. Evaluation of the effect of three EVs preparations (EV1, EV2 and EV3) on HFF-1 viability at 5 days. HFF-1 cells were treated under the same conditions as the antiviral assays and processed by means of an MTS assay. Data are reported as percentages of viable cells in comparison to the controls as determined by MTS assay for 1000, 500, 250, and 125 µg/mL concentrations. Three independent experiments were performed.