

# SUPPLEMENT

## POST-ACQUISITION TARGETED SEARCHES (PATS) FOR NOVEL PEPTIDES IN BIG MASS SPECTROMETRY DATA-SETS

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**Supplementary Figure 1.** Detailed PATS workflow comparing to conventional approach.

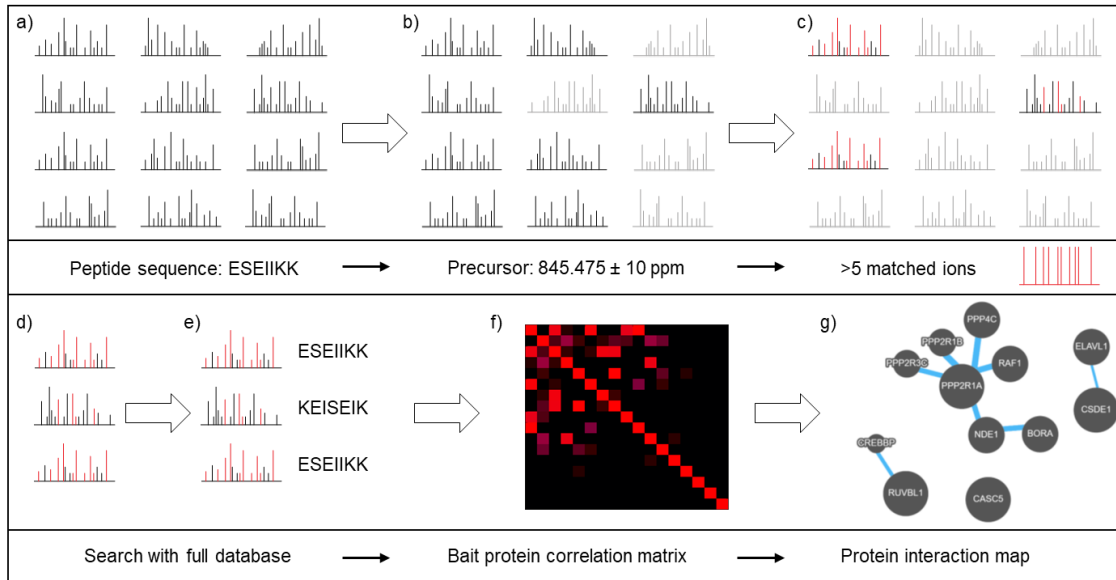
**Supplementary Table 1.** Small encoding peptide (SEP) numbering and sequences.

**Supplementary Table 2.** Detected microprotein peptide sequences from human interactome data.

**Supplementary Spectra 1-18.** Spectra of synthetic and PATS detected microprotein peptides

## Supplementary Figure 1

### Supplementary Figure 1



Supplementary Figure 1. PATS workflow comparing to conventional approach. a) High quality MS/MS spectra were selected. b) MS/MS spectra were filtered by precursor mass of target peptide. c) MS/MS spectra were filtered by number of matching y and b ions to the target peptide. d) Filtered MS/MS spectra were combined into single file. e) Filtered MS/MS spectra were searched against database to generate peptide identifications. e) Bait protein correlation matrix was generated based on peptide identification, bait proteins and STRING-DB correlation score. f) Protein interaction network related the target peptide was generated based on correlation matrix.

**Supplementary Table 1.** Small encoding peptide (SEP) numbering and sequences.

SEP	Sequence	Additional Note
SEP1	AEDCASALQPRRQRETL SQKKKKKGLKLLNKITLTPILSTSLYCH STILCFIL	chr2:73685032- 73686486_strand=+ ALMS1- IT1:NR_046762.1
SEP2	MKVVWGLAAACFLQHHGMPAQFTLPPAPRDETSPADAVCPG LGRDLCGSSRCCLRPPSQPDWKEPSGAALRARAPRGR	chr6:24403092- 24425750_strand=+ MRS2:NM _001286265.1
SEP3	WRAASRRPVSDGTSTLSRHHWRVTSPGSVCGALACPSSTFPR GPGEAGMSWEEAGGLAPHLCCRGQQRKTMWTCHCLVPLCL AQGSRLKGPQVDLETLRVENGGRPA	chr6:36646489- 36655106_strand=+ CDKN1A:N M_001220777.1
SEP4	MNFKNGPIFYPRGSSDIISVPCEFPSPMGRMPLLFI SNKL	chr9:5784555- 5791478_strand=-  ERMP1:XM_005251587.1
SEP5	MSSMPLICFLILEGLRSWRATPTTPEEV	chr3:42700959- 42709057_strand=+ ZBTB47:X M_006713415.1
SEP6	MKACTTVPPAPGCSMPPTTAGTRRAVPAQGLLQSTPTCMPWT PYLCLCWVWVQGW	chr1:160061136- 160068413_strand=-  IGSF8:XM_005245613.1
SEP7	TKYLCNYLITLVNRWNMNAWKIKL	chr12:115108455- 115109381_strand=-  TBX3:NM_005996.3
SEP8	FIQILEDQGLSSFILG	chr5:53783495- 53783605_strand=+ NONANN OT
SEP9	IMYALGNENPVTFLNKFLYLHHL	chr14:44572751- 44572856_strand=-  NONANNOT
SEP10	MRHLQIALRQL	chr9:127023982- 127024178_strand=+ TBC1D32 :XM_005266861.1
SEP11	ARGDAPGAGPQAGSACRYRGHRQGCGQPQAGQALQGLQ WCRDHVRLPRG	chr9:124030419- 124094730_strand=+ GSN:XM _005251940.1
SEP12	DWRITRRALTSSQEPFKSSFLCLVEEIGGIKPKKVFC	chr20:62284523- 62286347_strand=+ NONANN OT
SEP13	VWVEQVIIRMSQGEAGNRNESGWSR	chr6:161645965- 161646164_strand=-  NONANNOT

SEP14	EVFDRYFEINMVCISLWKLTSQWRFPSLYIYVYIYVYVYVCIYNSYL CLFEVRGYMQTNNEIY	chr8:25292135- 25292495_strand=-  NONANNOT
SEP15	ARVCKPDTLYVFTHVSTYTHAPAAHASVSSSSHPPFSCCLPSQA GAGSFLGDGGSPGCRQPSRQYEDRRPTGLAVRGVAPHRFMIL KSQLPLPAS	chr17:40925462- 40948763_strand=+ NONANN OT
SEP16	MYNHNNIFLRLRSAQSTYRPHFIAEETSSERLHDMSTDYLTSK WQS	chr3:185498033- 185499568_strand=+ NONAN NOT
SEP17	NKEAKNHTYKHSIFIIFFRTPKSL	chr12:19580521- 19580665_strand=+ NONANN OT
SEP18	QVAHTLRILLKQFLMVGKKLNNPKHLKL	chr5:27252217- 27253483_strand=+ NONANN OT
SEP19	MFRRLTFAQLLFATVLGIAGGVYIFQPVFEQYAKDQKELKEKM QLVQESEEKKS	chr15:55609385- 55613829_strand=-  LOC101928527:XR_253377.1
SEP20	LRKGRLEEEKIVEVENGELSAGCLLNI	chr6:10782384- 10784044_strand=-  NONANNOT
SEP21	SEYKRGETHCLIFLPCSYSQRRVHQAVRLMNFGLIKQILKMEF K	chr5:38972236- 38973378_strand=-  NONANNOT
SEP22	VKVKSYTARCRKICFNESNDTDLITKFELLIV	chr11:33278931- 33378550_strand=+ HIPK3:NM _001278163.1
SEP23	NVQCSKNETCKEIGTCDSYTGKTRNYLQDKQMLILVNDFKA AIIIFKEIKATMFN	chrX:100353186- 100424873_strand=+ NONAN NOT
SEP24	KGKKTPOFYRLEITTLIDIMTNFFWRFFTHIFVFLCLPKTSNLLSTL FLHFYCYEYFPSY	chr6:143805412- 143806379_strand=-  NONANNOT
SEP25	ELFFPLKNGGEDDPPVATQFAPSQDATAEKAHVWTLWRAAS SRWLPSL	chr7:100434573- 100435233_strand=+ NONAN NOT
SEP26	HWLIYCTSGSRLCFLWGEGRAGSRSALSPELEFSGGISAASWSW AIKRSFHRSPLSSWDHRCAPSCLGDL	chr7:66117889- 66118600_strand=+ NONANN OT
SEP27	VSIFLPKIVILGRDKGVFLEDVLRHTLLKHWRLF	chr9:68400605- 68402846_strand=+ NONANN OT

SEP28	MEFFITRK	chr7:151922816- 151923301_strand=-  NONANNOT
SEP29	MLSPLQQVCLEFCSVSPTSPDCIFSAAQNTSPTPPSSTLLAPPLSR LEEALAAAGGAQAARGQVCPAAADVPLLGTGIGCLLTKRMGKY KLPIPLLANYKPQMGKSRVRGEGWKAEMGVLYRRHLKAREV KKG	chr9:35725443- 35728861_strand=+ NONANN OT
SEP30	KDQLSLFKNNSPSTIITSR	chr11:76248705- 76254909_strand=-  NONANNOT
SEP31	MKFLDLTLALRIQDGNYNNGHEDRL	chr7:86606421- 86606768_strand=-  NONANNOT
SEP32	QPLISKNSHWWNKPHQGSKNHGHTQSPTV	chr3:15247751- 15301267_strand=+ SH3BP5- AS1:NR_046084.1
SEP33	MQLFVYSAYLSLNGES	chr4:166327097- 166327492_strand=+ NONAN NOT
SEP34	SQFSEESVSLMIGASQTEIEREKIVLKKDRPFNDCTIISKHVTHISA IPEERENRVQTTYTVTLVENFPKLITATKSQTQEDERTPNRMNT KGNTFIHILFKLQTNKRKENIFKVARGKGWSLGG	chr15:87878674- 87879358_strand=+ NONANN OT
SEP35	LIKMGIMVKAEVLARCMAYSKHHKVTYASNYSLCGLMMRIR SKI	chr3:12568054- 12568215_strand=-  NONANNOT
SEP36	RGSEMIPCLTSQLGGASTSVKLST	chr5:138275241- 138283167_strand=+ NONAN NOT
SEP37	MGWRISTPFSSKRTRCIYQRAFLGPTSCLLLFSTGTPGYATVRS SIFVAGCRTMLKMSTYGSKVWTSRP	chr17:4835352- 4837123_strand=+ GP1BA:NM _000173.5
SEP38	MGSQHLPLRVTVRCRCEQGLRLGKKSMSATQQGAMAGAVRG RLG	chr12:117151124- 117175823_strand=-  C12orf49:XM_005253937.1
SEP39	MDEWISKMWYLHTMEYYLGLKRKEILSHATTWVTLEGSMLGE ISQMQDKCCMIPFI	chr10:95057205- 95057400_strand=-  NONANNOT
SEP40	MPTQFFFKREL	chrX:15843934- 15863636_strand=-  NONANNOT

SEP41	LYQRREELKLQWRSFNLDKIVYGDIRKEGILNALETMGSSF	chr8:17873932- 17874063_strand=+ NONANN OT
SEP42	MSRGQFGQGQEPLDMFFWVNEISGEITYPPQKADAPAVSPES PQKKPPFQPRSVQEAPCSPQGPQAQRPALAPPSKPSLKDSGSR NPCPSAPTWARPKPEE	chr3:44462454- 44493083_strand=-  XR_133338 LOC100506301
SEP43	MLLYGVTLAAKRECLKTSPNVQVVIKSLFASHLLMSHWPKQV TWSPESVWEGTTQGCEYQEAWVCGGHQYIPYTS	chr20:45298911- 45299385_strand=-  NONANNOT
SEP44	MPKNFFISKIKALAYIGARC	chr9:88428049- 88428393_strand=+ NONANN OT
SEP45	MPGRDGGRQLAPECGRRRCSPQPSGSGMAGASALLPTDPPEA ETESPRAPSSLPSKSRCSHCRRHDAETKEAESSPATDTAAAPAA RAGRDWR	chr6:30522829- 30531396_strand=+ NM_0252 63 PRR3
SEP46	MAGGDPAAGRAVGAAKAKRAAGICGDTAAPALSGHPPDCLPE SPGRGGLTCSPSQRFSPLAAGGVRGCGAQLVTVGCSEPSW SPGEGAGPGEQQSLDVEAAEALQAGPASPRCRLLLPCPCCFG	chr6:32780349- 32806575_strand=-  NM_018833 TAP2
SEP47	IRKYLDLHERQIFHSNKHLNINIINCKAQTRVK	chr16:33121842- 33122879_strand=+ NONANN OT
SEP48	RTLSEITQGLGGGIGIRTQLLDLETGFLKGKEGACTLGSDVESEIS KFMVQVCGRAELTLQNC	chr17:48178065- 48178330_strand=+ NONANN OT
SEP49	MGFYHIGQAGLELLTSGDPPASASESVEIKGMSHLVWPKEVL RHYT	chr19:40327193- 40330486_strand=+ NONANN OT
SEP50	MGLSKVSVSVTVTLNLVSSVDESEPGICEGEGALVPAGNGIKGT GSGGGG	chr14:58955358- 58955764_strand=-  NM_001244189 KIAA0586
SEP51	DGGISGKCLIEEYSVGVTTMYDLKKEKDTLLEVL	chr13:34124857- 34125083_strand=-  NONANNOT
SEP52	MVIAMLFVAVKKWKWSKCHQRTG	chr11:11803558- 11805863_strand=-  NONANNOT

SEP53	MLYDCLCTSFCVDVCFVSRIQKVRILSDKFNKESEIHKKNQAEILEL KMQLTY	chr6:118017079- 118018042_strand=+ NONAN NOT
SEP54	DWSSGDEFPPQFKVFLLNK	chr4:84156218- 84156708_strand=-  NM_052834 WDR7
SEP55	MMKNQWMEIGHHQLHQPSRFLHLKHPEILPTVQGSLVQQVA LRLEVLLRKEVLEQLMKMIL	chr3:33537746- 33759712_strand=-  NM_001207044 CLASP2
SEP56	MNVRNVRRLNVLVVINLFYITGFMSLRDPMNAKSVGRTFVVAIN LLYIKDFILVRNPMNVQNVGRTLEVVIS	chr19:38230342- 38231032_strand=-  NM_001172692 ZNF573
SEP57	MEFHSLPRLECNGTISAHRNLRLLVQAILLPQPPK	chr8:124471523- 124472268_strand=+ XR_1117 95 LOC100509315
SEP58	GHLRPSSLSTKLEIILESMSELPYELVLKYNTGS	chr14:56021802- 56026332_strand=-  NONANNOT
SEP59	NLGFQRPLETLVERSWSPLHFQCLVACLAPSGAQ	chr5:149891915- 149892156_strand=+ NONAN NOT
SEP60	VNFCNKASWDLKKIYNRLYFLEKF	chr18:9345769- 9345975_strand=+ NONANNO T
SEP61	MTTGERDSAKPIRATATRQEDRSPEGGWQRQVEGTGTPKSKQG SRVLAAQEETQHPEAVPQRADPKGASASPLRRQ	chr16:624062-629182_strand=-  NONANNOT
SEP62	MDELSQYLKVIPLSTVVLDVILLQLSFLLYIANFLFSLGSLP	chr4:83831822- 83832435_strand=-  NONANNOT
SEP63	SQHFGRSRQVDQEVRSRTAWPRW	chr6:17701564- 17701878_strand=+ NONANN OT
SEP64	GWGGRGPSNPPSPCLSLLCFSSHFRVHVQCLIESPPPGGAGSC PPGAYGLSRPSRAPAQLGCCASFTSPSSLNLPLFS	chr3:184053746- 184068183_strand=+ NM_144 635 FAM131A
SEP65	DFVFNSLSKILVENRPAFVNENIPDITKPKHF	chr6:10801828- 10803161_strand=+ NONANN OT
SEP66	FFLAFRLFETKAILFCGCCAALKRWISYFFLC	chr1:160313607- 160313730_strand=+ NONAN NOT

SEP67	MYLLFAAPSLNLQSKFERGRETERERID	chr2:156867321-156871777_strand=+ NONAN NOT
SEP68	RVAEIIERLVSHGINLALIFSIWKCLKENHFHCRKSFFKYLLYPREI SLYLPPQAVISCFREWNPPCPSIFWFLGLNSSLVKSPWLGILSWE QILSCSLMCLHSPKTLTYTCLLRA	chr12:122714123-122751118_strand=-  NONANNOT
SEP69	MVAIVVARVVTIPKIMHQPVLSFLNFHVPLYTFMSVYVDLSLV	chr8:9565334-9565564_strand=+ NONANNO T
SEP70	AGDFLNLRIGISYQFCKFSPINYFFLFSPCLLYGILLDIS	chr2:108294549-108364747_strand=-  NONANNOT
SEP71	MADDKDSLPLKDLAFLKNQLESQRVEDEVNSGVGQDGSLL SSPFLKGLAGYVVAKLRAVAVLGFVGTCTGIYAAQAYAVPNV EKTLRDYLQLLRKGPD	chr5:139941187-139946658_strand=+ NM_080 670 SLC35A4
SEP72	GTTFSWVIRLLFAGKLNYSMS	chr8:99962637-99963699_strand=-  NONANNOT
SEP73	QRVQAERLAIRARLKREYLLQYNDPNRQGLIENPALIRWAYART TNVYPNFRPTPKNSLMGALCGFGLIFIIYIIKTERDRKEKLMQE GKLDRTVHLSY	chr4:43901065-43901402_strand=+ NONANN OT
SEP74	TFISPHIYEETLEIAARKCTP	chr2:82967185-82967587_strand=+ NONANN OT
SEP75	LFFHDFINLKAHRKVAPLITCMETSVLVNSISQS	chr5:127419792-127524262_strand=+ NR_0462 07 SLC12A2
SEP76	IWSRVVTLTLQSSENQRQNIKGLENILQKEAATCVDNGLFMPLL LSLTV	chr16:15198209-15199311_strand=-  NR_003610 PDXDC2P
SEP77	MAPLGLKDPLSSWLTPVAGKLVMAVS	chr2:65855310-65855473_strand=-  NONANNOT
SEP78	NSTNFFLLIKQRSFGGFIPIADKRGKDGKCSRFLSFHKQEFHALPL LKQRKE	chr16:11933549-11935884_strand=+ NONANN OT
SEP79	TGAGILLLRWLTHWLLAGSLRSSPGVPLHVLLHGLMMWHEPH SV	chr18:9864909-9865248_strand=+ NONANNO T





SEP93	NTHPHLLDNNIFPFNNALILIRHKHFNGG	chr13:108521011-108526878_strand=+ NONAN NOT
SEP94	TQEVEGAVSRDCITALQPGKQSEVMSQKQTTKIFNNHTLIK	chr1:52960264-52960434_strand=+ NONANN OT
SEP95	SSGKGKSNSQRDFTSHQLERLSSKRQNIKRVGKNAEKRPPLYTI GWNLNWYSHYKKQHGGSSKN	chr7:12450740-12451773_strand=-  NONANNOT
SEP96	SQPPLKCLCLIKINALLKGNILLSNKCGCVFYHTSILRKCWTSEYH KTGN	chr13:108521486-108526772_strand=-  NONANNOT
SEP97	VRMLDLLIQLQVPAAVW	chr11:64002664-64006302_strand=-  NONANNOT
SEP98	ESCPEPTEQKGLSFQPPHHVQSSPDVKSQFWF	chrX:119745582-119754975_strand=-  NM_014060 MCTS1_v1v2
SEP99	MCLPFLYTVLLPKLPSVDL	chr8:9403098-9403311_strand=- NONANNOT
SEP100	HSLLNIRSFILVRSHLNVRSVGRPLIVAQTLFNLRVFILVRNPMNV RSVGRLLDFTYNFLCIKNLYR	chr19:40529109-40596836_strand=-  NM_001005851 ZNF780B
SEP101	APFLGGLPCVLEEGERARILGSWLSELPDTGSEHVPGILSCQQ GPG	chr11:134094604-134117677_strand=+ NM_052 875 VPS26B
SEP102	QTKTRLLITTSRLIVNSKRPRNSEGRLSDTPTSIRLEYPS	chr9:115980741-115983650_strand=+ NONAN NOT
SEP103	MMTNSTFPRRYNRSHYQKPYNNNLRETLAQKP	chr19:50840986-50856670_strand=+ NONANN OT
SEP104	MPSPQKIGTAFLNKKE	chr16:53728816-53730245_strand=+ NONANN OT
SEP105	KLLLDLNKSQLGKISRQKIFMAC	chr10:15478885-15479329_strand=+ NONANN OT
SEP106	YTDAVVLVYFKQVKALIK	chr16:72452815-72454466_strand=+ NONANN OT
SEP107	RVFICIFRASFKINYKKVQLKIGESFEKSKITVCPEEELLHSYSKEGQ N	chr3:197787735-197789967_strand=-  NONANNOT

SEP108	VISTYEMGVDFLPQKINIKKKIIQYI	chr8:91519522-91520168_strand=- NONANNOT
SEP109	TLLSDHVLGAVSNQLIPKHNLKPNLSLQKGFILRGRYQKRT	chr21:35275511-35288046_strand=+ NONANNOT
SEP110	VPSGAWGTCVAIFSRGSLALFLPRGPCPCRAPSVVEGENMK	chr11:2391037-2391433_strand=- NONANNOT
SEP111	GVSLEPKVESGRQPELRLPQDSDLRITPPTSNPESIFLLGENAYI YFL	chr16:16170189-16236878_strand=+ NM_004996 ABCC1
SEP112	KFLENNDDGNATDQKLWDTTKAGLRGKFIAIIAYIKKEKNL	chrX:120338054-120341958_strand=- NONANNOT
SEP113	WSWRLLLLPLNIRTPGSEVFELLNLHKQALRFSGLQLKTES	chr12:74853896-74854278_strand=- NONANNOT
SEP114	DILLHDFLASIEVIIRFFSINL	chr21:20167140-20167299_strand=+ NONANNOT
SEP115	IKSINYICIWEIEKVHISHDFEVKRERIFGKEG	chr5:34183374-34185173_strand=+ NONANNOT
SEP116	KYWATPTIKIPLSIVIRKRFIKMFSNRLTHMRQVRFAHATPEAV SG	chr5:81078543-81079471_strand=- NONANNOT
SEP117	MNYPSRYILRSFDFINLRGRKQLFPLY	chr16:8991978-8996350_strand=+ NONANNOT
SEP118	KNNKFLKSTLFSGLFVIKCNVFKSSIS	chr2:69476143-69476401_strand=+ NM_032208 ANTXR1
SEP119	ITRVKIHQHLALGALRSDFRLTY	chr22:26860929-26864708_strand=+ NONANNOT
SEP120	ESLTEKDPTFKFMKLNKDEFNYC	chr7:6789180-6793491_strand=- NONANNOT
SEP121	LSELSNGVFLHENLEGIATKPGKERTMVPMEKVHK	chr20:25712848-25713130_strand=- NONANNOT
SEP122	MVHCSLDLPGPILLPQLAVVAGITGVYHHTWLIFFFFGRHGVS LCGPGSSLIPGLK	chr5:80597485-80605440_strand=- NONANNOT
SEP123	ISCPEKYPRFSFILNFPLSRSHSLLSLSSHSD	chr1:161284832-161284990_strand=+ NONANNOT

SEP124	IAAPGQACSGRWVDTQKTGPESVGGGTEPRGGQVGARRSSP HYQGLVD	chr7:44800637- 44801496_strand=-  NONANNOT
SEP125	WFHSCQLLGLKGKKYNIH	chr9:128724377- 128729551_strand=+ NR_0241 23 PBX3
SEP126	LPCDLYRNIRGGEAGDITSRIAAGALSPLRCGS	chr11:3408735- 3430083_strand=+ NONANNO T
SEP127	PHSVTNTQKSLNSVISEVILR	chr16:18089134- 18089599_strand=+ NONANN OT
SEP128	MCAEIEEGAEGVTARDQYGHLIPTKVASGPQGLSGARKPSFPSP RLRGSCHFLSQVGGWGI	chr16:29982572- 29984370_strand=-  NONANNOT
SEP129	AKIVPLHSSLGDRVRPCLKTKQTKEFRNDLAFIFLPDRQCIHQDG TLTGNQVLAPLLAGKEHEVF	chr15:31218600- 31220691_strand=+ NONANN OT
SEP130	KGLFLLLGQKISLTKQKGALSSELPQTIYWGPVKRQMSKDSKFI	chr17:56066228- 56086144_strand=+ NONANN OT
SEP131	GFLFQLCLHYLHSIIPSSLNLLMGRTQPPTTKLTVRVL	chr14:95645271- 95645404_strand=+ NONANN OT
SEP132	WSCGLKCVISDRLLLLSIAPGDGSSEKVSYLASWRSDKDSPCGV GLCRKSINKSLEETFCILGIGVLCANQGSVFSMSFSGIVVALNCFC LVLGCLEFWEKLLGSMALFLLSKYAEISS	chrX:154159069- 154159686_strand=+ NM_000 132 F8_v1
SEP133	MQLAFICSSITTATSEVLVTIISRLAM	chr13:98012703- 98018647_strand=-  NONANNOT
SEP134	KKNFRRSPAVNISAVRILGRRHGS	chr2:234384197- 234469870_strand=-  NM_018218 USP40
SEP135	QSKTPSQKKKKKKKSQQHTHGDIFLKNSHKIK	chr11:114325616- 114326071_strand=+ NONAN NOT
SEP136	MPSLSVPLSYLDRQMGSVLVLIHHSYRHCSDBGTQGTSQRGSLS REQLTEH	chr1:161136224- 161147286_strand=-  NONANNOT
SEP137	KVLVETHAFLTVTQELL	chr17:76001568- 76001690_strand=+ NONANN OT

SEP138	MMKKWATMNTLNFNISKLVLHVSVDNVLDVLF	chr8:66567401- 66567615_strand=+ XM_0038 46486 LOC400682
SEP139	FGEVKARPPLGLKGHFQTFLSVTWSVYASHISLINSSTFYLTAVI MVGRGARDGFTYCTEM	chr3:10157357- 10169022_strand=+ NM_0184 62 BRK1
SEP140	MSMCVRNSIQGWRRHFWF	chr16:15112097- 15124265_strand=-  NONANNOT
SEP141	MLFSSTLPMPISIFLMFRSHLRCHFHCSTSS	chr13:33080751- 33086968_strand=-  NR_026928 N4BP2L2-IT2
SEP142	SRHSWKAERYRPLIKDLIFILNPRPPKRGKCHGTRCVAFLSSAPL	chr12:57411725- 57411927_strand=-  NONANNOT
SEP143	LCDLLSKHDMVKIRIRHDEG	chr3:110639864- 110640215_strand=-  NONANNOT
SEP144	MNFVSDMLNLRCSWSQSNMSLVLRKELWSQGSSNSLQSMGI C	chr21:34020720- 34021204_strand=-  NONANNOT
SEP145	MRGPPPGRRALEANEACLPIWEWRGEEET	chr8:80942254- 80942687_strand=+ NONANN OT
SEP146	NTYCLALCRKSLTLPDVNFKLHKKTG	chr8:124530101- 124530292_strand=-  NONANNOT
SEP147	MLLIPTSPHPQHLLSAQSTPITRKGLFLKGPTGLVLLWNPVLES TL	chr6:17759506- 17762318_strand=+ NONANN OT
SEP148	MYIDECLQLQQVFLHALAVDVLQDTRAARPRRPWRGQQPPST SPMQDGELNRFPGRYPAGGSNASCLTLISSSKDRLPKDGSGEW GPAPFFFFFLPGWSEMARSRLTATSASQVQAIFLPQPPE	chr19:55649318- 55653007_strand=+ NONANN OT
SEP149	GWDQVYGEENDFLILFPCACVCM SVYIFRDVVFVPLHKCYSFM FHGYLE	chr5:88014045- 88018690_strand=+ MEF2C NM_001193350
SEP150	RVPDRWSPTPKKEAETWSCARQWQWPVHAGLASIAAGRPSH RPRRGGEQPHHAAPAQEAEEKEGRARQP GALWPAQPENSKF EKEEENESDVKLGGAQRGAGVRSWATPGSGKQWDLQFPEEA EAEGRERLCEV	chr21:45105748- 45115959_strand=+ NONANN OT

SEP151	MWVQGPHVPLPLPVMCESEGLWHLLEAQGVNERELLWLES LWGLGCQSTRQARTWRAQTLSPGGQEARWGPCLKDWSP	chr1:31342371- 31361123_strand=-  SDC3:NM_014654.3
SEP152	FFSIFRRDRFSRWPGWSRYPDLVIRLPLPPKVLGLQV	chr1:150343960- 150344120_strand=+ MPL:NM _005373.2
SEP153	LKAKLQITSYKYNICWELNTYIKYWTVQNVEMKHKR	chr15:49280838- 49285216_strand=+ SECISBP2L
SEP154	GERACSKINLMLDRD	chr17:67992904- 67996880_strand=+ NONANN OT
SEP155	CKSELNIKNCVNTIDIGITLKY	chr10:124768480- 124817809_strand=+ ACADSB: NM_001609.3
SEP156	MEALFVPEKKKLKTQRPTNRMDKMNISIQSNIVNE	chr7:32735224- 32735731_strand=-  NONANNOT
SEP157	EQQRHPQEPGIAGGGGERGVGHGAQQTRREAVREAGELAGR CLRPGLCGSPRSANPFYAWLRLESPPERPGQNSRSSRSIRSPEG RRRPRPRGGVGYG	chr4:74904262- 74904922_strand=+ CXCL3
SEP158	MLLDIQYILKKFSMNPSIKQIIQGAIKFMFSKIKSS	chr2:17844495- 17850489_strand=+ SMC6
SEP159	GKYSYLEKENFLDKFLKL	chr8:9423769- 9423869_strand=+ NONANNO T
SEP160	KGAWVLVNCLLDLEIKENTGERRFSIECGFFTQETLQGIRGTCPO YFNVGSFYFP	chr13:70234870- 70235374_strand=-  NONANNOT
SEP161	MRIIPALLEADEGYPFVRSWRPAWPIW	chr3:163403983- 163404349_strand=-  NONANNOT
SEP162	KEFDLLSKVFQTLKLHICH	chr1:83599137- 83599370_strand=+ NONANN OT
SEP163	SKKKVKDRKLENLMPAKDGLIIVERSLALCMLR	chr6:99387016- 99387302_strand=-  NONANNOT
SEP164	GCEADDVHTAQVSILADNCPFKLFQPHPVRYQRRQQLAQPGLL AGQAREGSSGPEAPKPLHDTCPYVQCLEDGGLRGDQGPAFHA GESPAAPGPPEAQPHISDPHLVLR	chr20:42295716- 42345131_strand=+ MYBL2:N M_001278610.1

SEP165	ASRTLQSFFIGSIRCLFPTRAIQQVLKEN	chr8:125467607- 125470995_strand=-  NONANNOT
SEP166	RPTWSRCGTNKVLRVSFAAFCWQRECTLVMKPLEFLKREFLQ PPIHQIVCSRMMWMMKGRSLSWATYLRT	chr2:239152640- 239197306_strand=- PER2 NM_022817
SEP167	SSRVKDYLFKFMCSHTYFVT	chr2:47600600- 47601323_strand=-  NONANNOT
SEP168	AYQGREYRQRKGSPLLFLQVFQHEGVREMGRKPHKD	chr4:86297867- 86298058_strand=-  NONANNOT
SEP169	MVYFCFTIIPRMLSFRLSNQRILPESQPWRSYTFNVRPSSLPKYTT HVFSFLANKSPLQSKSRLNSKFNF	chr5:44812872- 44828662_strand=- GATA6- AS1
SEP170	MQSHQALPLLLLQVEVDHHVNAAVDGTVELLRQIAGQDQHE SVGQGWGRKRWGCQLRCPEGNGGSSAPSGRLFGRI	chr1:1424437- 1425809_strand=- NONANNOT
SEP171	LVTFEDLGLIWNNQRKQELPLY	chr2:205660031- 205660209_strand=+ NONAN NOT
SEP172	ECKMVQLLKLEVEVPEKIKHRVMFMY	chr2:10244681- 10248113_strand=+ NONANN OT
SEP173	SPSDENYKAASSKEVNTDESSAAGVFHMR	chr11:77319073- 77325243_strand=- AQP11 NM_173039
SEP174	LKVGKIAWLEFKSLPLGPKPEILHLQPTENALEGCSPLIR	chr3:128996926- 128997117_strand=-  NONANNOT
SEP175	EPNGIKRIESEGGGEGWGRESIQESW	chr2:231589548- 231590185_strand=+ BANF1:N M_003860.3
SEP176	MPMEPALIVAFCFDEFELEPEQDCCKQ	chr1:67751219- 67751585_strand=+ NONANN OT
SEP177	LWTFILYCRNQYLFLGGYVKDLKNYYLVCSL	chr1:150317600- 150318971_strand=-  WDFY3:NM_014991.4
SEP178	ERGAGAGPHLGPQVEGGLQVQVQRGSALLRERPPRAGVRRHL QCL	chr22:22308818- 22337181_strand=-  TOP3B:NM_003935.3
SEP179	GNITHQILLGGMWQGEEDH	chr1:195789567- 195789749_strand=+ NONAN NOT

SEP180	LLAENLPIDFLNIRKIPN	chr8:30535597-30585324_strand=-  GSR:NM_001195104.1
SEP181	GRIESWNRKTGEKHRVCSLISTIVRLIS	chr7:22510284-22510452_strand=+ NONANN OT
SEP182	MAMGKGQEVLRWEVSALTGLSGGL	chr5:10158411-10158577_strand=+ NONANN OT
SEP183	HPTQPAQRLPIISDPLLLLPSHTAWL	chr1:24034077-24035038_strand=-  NONANNOT
SEP184	MLLNPPMKIFHYKTVFHTTAS	chr1:212531453-212535680_strand=-  PPP2R5A:NM_006243.3
SEP185	NCPAHGKPYLVYFGIILLILLYCCGIYCCCTLCVIRMQDKLAKIFLN GTYIHLDPVTFCKDSEL	chr8:56636872-56637117_strand=-  NONANNOT
SEP186	TPPISIESRGEKCRIQQFLTNCNILSWLPYINKE	chr6:4823265-4824846_strand=+ NONANNO T
SEP187	NCTRTADGCELPRLNKINYNKLLTLFSM	chr15:41849141-41849860_strand=+ NONANN OT
SEP188	THTFCGVYSFLVNAVQLLM	chr9:100689089-100700593_strand=-  HEMGN:NM_018437.4
SEP189	TSTTSLSGTTWTRCTSPLASISWTKSFQEMLPPLVLRFRRLMTT AMTSKVRSRRYIWSSRSRRLSSEPAEKQKGETNT	chr16:89590029-89594505_strand=- SPG7 NM_003119
SEP190	RSTNSLLSTNSGVEKVGCHCL	chr12:69813707-69814545_strand=+ NONANN OT
SEP191	TLQIINHRLNSERLINSNTEVREKQDLKWTLVCGIE	chr3:112539900-112542022_strand=+ NONAN NOT
SEP192	KSGQFSYFFVCLAIIILSERDALKVAGRQTDLL	chr1:110882061-110914912_strand=+ NONAN NOT
SEP193	TWEAEVAVSQDGAIALQPGRQERNISISKKRKKENGNLTFSLIA FKGLALCLKDIL	chr9:95194519-95194749_strand=+ NONANN OT



SEP194	DVSLVETEQNIVALELRFAGTEDTLVSQVLVHLLQALQALGHVLI IDLGIKGGHGLLTHEVGTVDVKPGALLNQGHRQGVTEVLLRDIL ATGEGEDHSHIPMQRGNREKDHATTSISHFSI	chr21:47685600- 47693148_strand=+ NONANN OT
SEP195	ELRKAKVLFCLFLFIYLYNY	chr4:145030055- 145038548_strand=+ NONAN NOT
SEP196	LYRQDNWVGLLWGNPPSITIWGCGEAILQRSFQLKGDGVFVLK SGRAWFLGFKDWAF	chr12:94688630- 94690814_strand=+ NONANN OT
SEP197	MTVQRRHGDEITHGALTGNELGSFDVHIRSCRFLPLGLMAQE HCYILPAAFELEVGW	chr1:53384961- 53385662_strand=-  NONANNOT
SEP198	LLELAPLTCFGCLDCKWKSILLTHIGAPPHTP	chr14:59925205- 59931181_strand=-  NONANNOT
SEP199	HLLQLRFFLSWNFLGFIVANQLTINLEFVSGLRILFH	chr5:27717055- 27717588_strand=-  NONANNOT
SEP200	CIGICIYTHHLKVIIMENTKDIFTSTIRSKARISSNYAIIHHITGNIS QYS	chr2:160547202- 160547607_strand=-  NONANNOT
SEP201	NGVGPDRLLGLESLLFLQMTS	chr14:23741387- 23746392_strand=+ NONANN OT
SEP202	QMPSEVTVTAIARDDD	chr14:57430195- 57430368_strand=-  NONANNOT
SEP203	CCNKVELQTSQRNLRAMSEFWKEINWNIPLLSWQPPKGFNA PCQIFDSIF	chr1:165664398- 165664673_strand=+ NONAN NOT
SEP204	EKERTLQVLRLEIHGCAQPVLSRPETLGVGARRQRSQIVVS	chr8:126009798- 126010145_strand=-  NONANNOT
SEP205	KSEGMLEQKSQIKMKYENIT	chr6:88240174- 88240816_strand=+ NONANN OT
SEP206	NLIKITVCACVCSVTIDEIRLFMSVKIEAGRWWCEDSVCHSFYN TFLYV	chr6:148065557- 148066827_strand=+ NONAN NOT
SEP207	GSEIFKPPGPRCKPSAKISAGGRSAF	chr14:61744089- 61748530_strand=-  TMEM30B:NM_001017970.2

SEP208	MPTGSSPHLLPSRLNSAHLGPCNSQPSSGLMSSKGLDDPLPQP PSPEGLCPVCSPVDQGRSQGATPSKGCWLTLESQGGAVPHP VMTLSEQGGARGRAEWGWAPAGHQGLRASSPWATLFLRGIL KTSENPKCVRVS	chr13:29283091- 29289675_strand=-  NONANNOT
SEP209	SIGFIIGINLVLDFIKLYLVQLILTITTVFLAIVCSD	chr14:75745481- 75748937_strand=+ FOS:XM_0 05267488.1
SEP210	RRHPPDQQLIFAGKQLEDGGTLDYNIQKESTLHLVLRGG MKIFVKTLTGKTITLEVEPSDTIENVKAKIQDEEGIPDQQLIFA GKKLEDGRTLSDYSIQKESTLHLVLRGGC	chr17:21729873- 21731760_strand=+ NONANN OT
SEP211	GFPWLFSSGLSYCASGSYWCHFMIVKKLPNLKQNDQKPSGKR EPIHSTEDPQVLLKM	chr2:160958233- 161056589_strand=-  ITGB6:NM_001282355.1
SEP212	QVGAGWGLNVKRQWQAAGVERAQQP	chr17:77751977- 77761449_strand=+ CBX2:NM _005189.2
SEP213	MQRVQMHLLEKLLLLLPCGLCQVCPGLHLQRGVGVQVLLRL MLGQPRSQM	chr16:56642478- 56643409_strand=+ MT2A:NM _005953.3
SEP214	FCLSNDFFKSIIYIGIFQNSNCHIKKHNDLNDLNKNTVPIKIRQL	chr2:160802326- 160919126_strand=-  PLA2R1:NM_001007267.2
SEP215	MPSRGTRPEDSSVLIPTDNSTPHKEDLSSKIQKIVVDELSNLK KNRKVYRQQNSNIFFLADRTEMLSESKNILDELKKEYQEIENLD KTKIKK	chr2:190526125- 190535557_strand=+ ASNSD1 (NM_019048)
SEP216	ILSLGWWKLIFEIKNPARTVKPQGMALQVRRSLGP	chr14:51800111- 51832275_strand=+ LINC0064 0:NR_038358.1
SEP217	RTYVLPQTIFLCPFHSLVTLPLLRGNCYSDFYCCIFLLPLEFYMSG ITH	chr17:35990853- 36002800_strand=-  NONANNOT
SEP218	MDYIMKEYVKRTYSNAQSLICV	chr20:13370036- 13619583_strand=-  TASP1:NM_017714.2
SEP219	LLSRIPWYGCTTVCLTIHLLKDKRVVFSFLPLLIKLL	chr8:146220251- 146224283_strand=+ TMED10 P1:NR_002807.3

SEP220	MSRLLPVITLLSRHVAQLLSKVKQTQPVAISITQVTGFAGMMM G	chr18:31158541- 31327399_strand=+ ASXL3:XM _005258356.1
SEP221	MVTKIQMAQKRIFSLALMEGMKQLQVMIPAQMKALLPSQM TSVMSLSILLKRRRRRMRKTLGEWQKGTMLILKV	chr9:470294- 746103_strand=+ KANK1:NM_ 015158.3
SEP222	HKYNLKVILENMEILKFYFTFS	chr1:186265405- 186283688_strand=+ PRG4:N M_001127710.1
SEP223	LCRAIDIERPNNRLQWGL	chr10:76871393- 76941881_strand=+ SAM8:N M_001174156.1
SEP224	GPASGVLTTGGARTPRETAGAERAAPGPRGTATGGRRAGPGAG RLRAAALDPTRRERPRDAEQEEVQRAVPAGADQEDHADGRR DWEGGGGGACHHLPGARALPRVAVEEGLPGDPVAEREDHDH IPPEAVHRAGAAV	chr11:65686728- 65689048_strand=+ DRAP1:N M_006442.3
SEP225	EVRSFSGNPAVEEGTTQEN	chr20:306239- 310867_strand=+ SOX12:NM_ 006943.3
SEP226	ARGPGPGEQAAPGPAAPAEGRVHCGGAARPARATDGAPRA GGGGRQGGAGHPPGQSPLIRDCPPAAACLWHPLGPWPQPLPG T	chr1:228395861- 228566575_strand=+ OBSCN:N M_001098623.2
SEP227	LDPGQDARAHIHSETLVTSRHRVAVGGGR	chr15:65488337- 65503840_strand=-  CILP:NM_003613.3
SEP228	PPGGEAASTVRTAQTAGRAAWRRRRCRPPPTCCATSR	chr17:3827163- 3867758_strand=-  ATP2A3:XM_005256658.1
SEP229	EIHKKLKKILEMELIQE	chr1:78409737- 78425885_strand=+ NONANN OT
SEP230	FIGSLITYPKPSSVLGNWETGVVSAIVELVKI	chr19:522521-522833_strand=-  NONANNOT
SEP231	FQYMEINTAGQSLERMGVENEKLVVRLVRIVFAHF	chr2:99862519- 99863895_strand=+ NONANN OT
SEP232	SSSPKQPQNYMALVLITRLDKPQLKQVLSKQSLCMWTKK GPTIQTNLKSHLIFLWGTAFPNYVTVLWLNLFSTLSSQGQR TECPKS	chr17:40970559- 40972008_strand=+ NONANN OT

SEP233	IISYKSTLLNNHIIKIIARKWTIFTMFCKLASVWICTLLVKYI	chr11:14665294-14895861_strand=+ PDE3B:XM_005252972.1
SEP234	KYNLQMIQCHFIDSFLLFLTLYSIPLCGPNMIYSTTLCMSL	chr14:27991709-27992439_strand=+ NONANN OT
SEP235	AAGGQAACGLAQSRAAGGGWTQGHTGCGSEQAAGRGGE RRKGVLTGTEPARWAPGTSCGRRRAGRVGAGHRARSGRS PWRLELPALPRRPRVEREPGRERAGLVGVRGQARP GPWSW SSCAGRHGTESLPARGP	chr4:1803098-1810596_strand=- NONANNOT
SEP236	MGLSICIQVEVCLVAGKQSRKKETLGLLVQAERWGLDWRGGF	chr2:74257245-74259066_strand=+ NONANN OT
SEP237	MVCLEVRFPARTSWPPHTVQDVVFKMHH	chr17:37682110-37691204_strand=-  NONANNOT
SEP238	MHRLHFSDRGDNRVTGFVTPGERGQKVDQENHSCGLQSQ GPILDLVKSNS	chr17:37710622-37710961_strand=+ NONANN OT
SEP239	WWCTPVVPAIQEAKVAGSPEHKSSRLQ	chr7:757156-757313_strand=+ NONANNOT
SEP240	TLLASRLPTMHSAAHKLNHWMGEGTMAQRGQVTCLRSRSL TTITFGLAPPTSPGPGPKHLPQGTAPQSGRGG	chr3:14520433-14530859_strand=-  NONANNOT
SEP241	LAGLLAFIQRTKDQ	chr17:35684526-35684974_strand=-  NONANNOT
SEP242	QTRVATVSNNILCISKLEERT	chr16:8742491-8744671_strand=+ NONANNO T
SEP243	KDLSFAIQINPWPDI	chr6:104975101-104975201_strand=-  NONANNOT
SEP244	PGVALSSLPRCQRGKQMVAPG	chr6:31606802-31611451_strand=+ NONANN OT
SEP245	MRDSELLGVHYLRPFLVKELRTLKCKMQDENVSGEALSG	chr19:23921996-23938778_strand=-  ZNF681:XM_005259770.1
SEP246	MICYTSQLVLYHLVTDITKHWFY	chr9:2039912-2046006_strand=+ NONANNO T

SEP247	AWFSSAPPGVSGPGPALIQPWEQLSSQQQPREGARLAGRDEG GQSGQKKQDMPGQWSREQACRAGRQEVGWSHK	chr16:67963770- 67967286_strand=-  NONANNOT
SEP248	TYFINLSIILIFYYSFIREFVEHLFYVIDTRNEIVKKENLLPRNIHSGI KV	chr17:68010245- 68038237_strand=+ NONANN OT
SEP249	KTLLLMCMKLLVPLSNWRNDFSFKKNYSGIHLLFKIHWVNHLYL E	chr6:143771955- 143810369_strand=+ PEX3:XM _005267181.1
SEP250	MQQRQERQSLENVKVMKCAGLD	chr17:20056612- 20057839_strand=+ NONANN OT
SEP251	MAGGLGCDVCYWFVEDTQEKEGILPERAEEAKLKAKYPSLGQK PGGSDFLMKRLQKGYFDSGDYNMAKAKMKNKQLPSAGPDKN LVTGDHIPTPQDLPQRKSSLVTSKLAGGQVE	chr1:150581888- 150601599_strand=-  NONANNOT
SEP252	MSQKQEEENPAEETGEEKQDTQEKEGILPERAEEAKLKAKYPSL GQKPGGSDFLMKRLQKGYFDSGDYNMAKAKMKNKQLPSAGP DKNLVTGDHIPTPQDLPQRKSSLVTSKLAGGQVE	chr1:150595298- 150602077_strand=-  NONANNOT
SEP253	MSTGLRLAESRVPALEKQAQLEEQLRDKVLHEKDLSQQQMQ SDLDKADLSARRVPGGCCMRQASLQKSDRAGPGSEASTEAE GEGSGRQGPHERA	chr1:16905808- 16970994_strand=-  NONANNOT
SEP254	LLEITSSVIFSSFLQEAASEAYLVGLFEDTNLCAIHAKRVTIMPKDI QLARRIRGERA	chr1:226256967- 226259277_strand=+ NONAN NOT
SEP255	SRIVPLSLCFVYSECTKDGVELSPTAAANFTRRNLDCLRSRTPY HVNLLLAGYDEHEGPALYYMDYLAALAKAPFAAHGYGAFLLSI LDRYYTPTISRERAVELLRKCLEELQKRFILNLPFSVRIIDKNGIH DLDNISFPKQGS	chr1:36064590- 36107159_strand=-  PSMB2:NM_001199780.1
SEP256	VFFCLSEDKKNIIIEEGKEILVGDVGTNNLYATFVKMLPYKDY RYTLYDTTYETKESKEEDLVFIFWAPESAPL	chr1:51623500- 51624038_strand=-  NONANNOT
SEP257	LCEHTRAGAVLYTRN	chr1:91276134- 91276678_strand=+ NONANN OT

SEP258	MTSWPGGSFGPDPLLALLVILLARLILWSCLGTYIDYRLAQRRP QKPKQD	chr11:68925212- 68926307_strand=+ NONANN OT
SEP259	MSYCFDRDDVALKNFAKYFLHQSHEREHAEKLMKLNQRGG RIFLQDIKKPCDDWESGLNVMICALHLEKNVNQSLLELHKLAT DKNDPHLCDFIETHYLNEQVKAIKELDHVTNLHKMGALESGL AEYLFDKHTLGSDNES	chr11:77445415- 77445967_strand=-  NONANNOT
SEP260	FSPDQLQGEPSGNRQESRRSAGVQAGSHHRVHGAEASIQAGIY ATRSGGTLVLVGLGSEMTTVPLLHAAIREVDIKGVFRYCNTWPV AISMLASKSVNVKPLVTHRFPLEKALEAFETFKKGLGLKIMLKCD PSDQNP	chr15:45117467- 45154252_strand=-  NONANNOT
SEP261	VERSAAETVTRGGIMLPEKSQGKVLQAIVVAVGSGSKGKGGEI QPVSMKVGDKVLLPEHGGTKVILDDKDYFLFRDGDILGKYVD	chr16:74646473- 74646748_strand=-  NONANNOT
SEP262	SPPTNLTFISILTKQSVVIPHIWSSSKPVSGDTRLRYGWIF	chr18:32947243- 32947540_strand=+ NONANN OT
SEP263	GNAICIQTPGLRGQRRDPPLPPVPEAGSGAGDKPGPARGLGFR DPLVLEGPRAPERQGSQGHGDQRARNLRRRGLEAGSARSGSF CPSVLGDRTAPGR	chr19:49458275- 49460071_strand=-  NONANNOT
SEP264	MDKPCGCPPGVCDHGTGDRRDPWYSTVGLLPPVRAMSQRNL NAKTEQGPTGVTMTSNPITWGQIKKTTQEAELLERQGGQAKT PDSMFLAMLAVVSCASIGSGEPPTGN	chr19:58816741- 58827140_strand=+ NONANN OT
SEP265	MGKGSFKYAWVLDKLAECEHGITIDTSLWKFETSKYYVTIVDA PGHRDFIKNMITETSQADCAVLIVAAGVGEFEAGISKNGQTQE HALLAYTLGVKQLIVGVNKMDSTEPYPYSQKRYEENC	chr2:107313599- 107315077_strand=-  NONANNOT
SEP266	GLWISHNKHTKLLKSAKKKCNQHILSDVWVPLTSVFYIEILNS PEKACCLAKTAFDEAIAELDTLSEESYKDSMLIMQLLRDNLTLWT SDTQGDAAEAGEGGEN	chr2:127314648- 127315784_strand=-  NONANNOT

SEP267	GIKQGVPDFKGTSAQAQIYII	chr2:242272175- 242277881_strand=-  NONANNOT
SEP268	MQIFVKTLMGKTITLQIEPLDTTENVKAKIQDKEEIRLDRQTLMF DGKQLEDERTLSNYNIQKESTLHLVLRLCDVIKEEFLYNSQEE	chr2:48109321- 48110972_strand=+ NONANN OT
SEP269	MLVRVVLNSQPQVICPPQPPKVLGLQA	chr2:61275508- 61277771_strand=-  NONANNOT
SEP270	MSLRNLWRDYKVLVVMVPLVGLIHLGWYRIKSSPVFQIPKNDD IPEQDSLGLSNLQKSQIQGK	chr20:10385838- 10414846_strand=-  MKKS:NM_018848
SEP271	MSGSCQRSGEDKKQEEEATAACGRLAGVPEAKQGPKADSDSD LETGARGRGQARLLPLGASPAGVVGGLAPRRQETSVQQG T	chr22:21368073- 21368526_strand=-  TUBP3FP:NR_003608
SEP272	MAPWSREAVLSLYRALLRQGRQLRYTDRDFYFASIRREFRKNQ KLEDAEARERQLEKGLVFLNGKLGRII	chr22:39898321- 39914136_strand=+ MIEF1:N M_019008.4
SEP273	MQKEDPHVTHLQVAQDTVPEAAQISSEHPQEKQA	chr3:75673790- 75674212_strand=-  NONANNOT
SEP274	QEKLKLEAELGNMQLLEDFKNKYEDEINKRTGMENEFFLIKDD VDKAYMTR	chr5:60040072- 60040365_strand=-  NONANNOT
SEP275	MQASIEKGGSLPKVEAKFINYVKNCFRMTNQEAIQDLWQWRK SL	chr5:93018209- 93019492_strand=-  NONANNOT
SEP276	LPDHLNSRLEESLVMQEEVWRKGN	chr6:127588051- 127664224_strand=-  NONANNOT
SEP277	MIKGVTLGFHYKMRSVYAHFPINVVIQENGLVEIRNFLGKKYIR RVWVRAGVVCSVSAQKDELILEGNDIELVSNSAALIQQATTV KKKDIREFLDGIYVSEKGTGQQADE	chr6:64325724- 64326136_strand=-  NONANNOT
SEP278	RVGAELNLWLLKLHWLALDVLSNPLDFVVVVVLFVCFRLAA	chr6:80253441- 80254311_strand=-  NONANNOT
SEP279	METLQSETKTRVLPWLTAQVATKNVAPMKAPKRMRAAVP VAAARCDSSGQKTPANLTPCDKDCVLHE	chr7:134844506- 134855399_strand=-  c7orf49:MRI-2

SEP280	MAEALNKYKLSVKGKAQLGVQAFADVLLVIPKVL AQNSGFDLQ ETLVKI	chr7:65216074- 65234525_strand=+ CCT6P1:N R_003110.2
SEP281	CGITASSPLSVKGNTFGYLLKLLIITVLPNCT	chr7:91826459- 91831812_strand=+ NONANN OT
SEP282	MMMHSLQRGTFKQNTSRQLQRLDSEAKLEGLRKDEEPPLREE AAAAAAAAAATPPLPHLPGNNAASDIQAVRWELLQTHAQHE GAEATGCDGHQPGAEPGPGGPHP	chr8:38001128- 38009539_strand=-  STAR:XM_005273620
SEP283	MRKKQQIENASKRNKWKLSTKQHVIYSNKKYISFWAQSINPVT EKRIQVEQTRDEDLDTDSL	chr9:15470968- 15475652_strand=-  PSIP:NM_021144
SEP284	KNSLLDLTPLPSSDTRLLSSQRS	chrX:44168529- 44172000_strand=+ NONANN OT
SEP285	MVEITSKHEERQDEHGYISRCFTRKYTLPPGVDPTKVSSLSPEG TLTVEAPMPKLATQSNEITLESRAQLGGLGAAKSDQSAK	chrX:49089935- 49090674_strand=-  NONANNOT
SEP286	LQLETEIEALREELLFMKNHEEEVKGLQAQIASFRLTVEVDAPKS QDLAKIMADIRAQYDDLAKNREELDKYWPQQFEENTTVVTT VRRGWSC	chrX:91714698- 91716013_strand=+ NONANN OT
SEP287	MMMGCGESELKSADGEEAAVPGPPPEPQVPQLRAPVPEPG LDLSLSPRPDSQPQRHGSPGRRKGRAERRGAARQRRQVSGGG WPPARDGLAPTWSLPCPLLPGPLPPDAALPGAVRAAACGAAG AGDARAEQPLGPGAAGRSREPL	chr7:100032991- 100034106_strand=-  NONANNOT
SEP288	MAAGRGRGRADGAGERDAADCAARRAEVAESRAAPGALPEA AVGPRGPSRGRGEAAGLGLGLAALKLRAGAGARGGSGARGGG ALPARLHLQGLRD	chr9:139256352- 139264369_strand=- DNLZ
SEP289	LGAGAVGSQTRLSASSHFSQGGCACAQLPGRAGRRGLKSLVPS LERERRAPQTSVPASGEEAGKKDAASGEHPGSKTGPLSTVGS VTRLGKAGAPAVGLLLANERSPRRRRGANDPTQDGE	chrX:16859470- 16888534_strand=- RBB7



SEP290	ECLAGSGFRVRPCSGFARSSAPAGNQAPSEARTAPGARTGGH AVPEGGGRGSRGGGGGGRGGRQLPPAAAVGDAGQLGRGG PAGGPDRRDAAAGRGAGQPGLAVRAPGGAAAGPGAPGCGG AGGQGPAPGGAAAAAARFG	chr10:99092201- 99094454_strand=- FRAT2
SEP291	MATPGLQQHQPPGPRHRWPPPPGGAAPAPVRGMTDSPP PGHPEEKATPPGGTGHEGLSGGAADVASGVGSRHRARLPAR P	chr9:139557342- 139567132_strand=+ EGFL7
SEP292	MGSGCRCGGATSRRRTPSWTPSSASLRARAVSSSPTLGWRTA PSSTATTASASCAATRGRPR	chr7:150646564- 150675053_strand=- KCNH2
SEP293	MRLVARLQVGPADTQPRVSGEADGESSGSRDSGLLWCHQPP PQQGGPGEGQEQLQRLDVQTDGGPVCAPVDRWPVLPRED QEGQQL	chr9:123611620- 123639498_strand=- PHF19
SEP294	MSLFDENELLRSHWYLYWGNIAKQEAYSLGENFFMSETENS CSRLCHPFFSRQKIPKSCNQSLHLIDKATNPKCLSMSTAACQT SSIATRCPV	chr14:103799905- 103808641_strand=+ EIF5
SEP295	SGQHGRAAAAAPCPPPGSRPGSSAAVGPRPGLESRVPRQARE GAAVHGQQASGGPRRGWRPSSAELTIETANPYL	chr16:89574814- 89623783_strand=+ SPG7
SEP296	ITQARLSGQHGRAAAAAPCPPPGSRPGSSAAVGPRPGLESRV RQAREGAAVHGQQASGGPRRGWRPSSAELTIETANPYL	chr16:89574814- 89623783_strand=+ SPG7:NM _003119.3
SEP297	RGEEAEPRSAAGGWGRKSEVSADVRVESGRSRLGAEVRLG SLSAIVDPRSREREGEEERASGKDGPLPPTPEREALILGSQRTAA AAAAGTITRPRATANCCECTGRGPGSGGGGSRVAVKNVSH	chr8:64080459- 64125260_strand=+ YTHDF3
SEP298	PSPPSAAAGARAAHPHHAQVHPAVALQPARGVGGQAALFAA GRAGGDLPLQPQPGGAAARRQPAARAAQAFFPAAELAQAGP ERQRDPAVASRGGQLHAAGGAGRVPERYP	chr8:144873093- 144897592_strand=- SCRIB

SEP299	ERAVTATAAAEEAAAAGPGPVRLSAPRGCESAAAEAAAAEEAAA GGGVGEPAPGRRGAEDEAAAWRSWRGGRRAVAAAAAAAP DPGGRARTHVSR	chr10:98277876- 98346768_strand=- TM9SF3
SEP300	AGLGCDRRLRLFFGRVVGASGRLGRVHAAWRRRLIPPSTPGSSD VGQLCAGACDPRGGLGAASIAADGAPRGPGEYQPGKGSARPT TADPGRAGGTEVREPAGSSAAAEAEDETGCTP	chr4:122734431- 122745077_strand=- CCNA2
SEP301	PSPRNVTSSSEAWSSPKLGRKRKKKSQKKFSFLESQTRCGTEEG VKARGSLQDRCLSPFPGHVGAHLAAPEAAGARQSPSGEGD PPRHPGATTGPRSSTPAPPQGQFLPPSI	chr7:100464771- 100471014_strand=+ TRIP6
SEP302	MKSREGSVHPQVEIANLLLIQSSLANLLSLQDPAGFALLALKWK NIWWSTSAHIATLPWPKEAYLMTMSSSCLLDTTSQWWSFQQ RW	chr10:101992050- 102027406_strand=-  CWF19L1:NM_001303407.1
SEP303	MPSVPKELSSAELPPQPAAGQYGPDSADAPNPWSREPRDRS GHLSQTPRSPEALLRGRRRGHLCGVPRIQEPQTAQRGAIGGGG AGVQQQTAGARGTTEEAPGGSAAEDESQGGEASDRTEEPDEV AGSGGLGVWATDTVSG	chr5:180650039- 180662529_strand=+ TRIM41
SEP304	MAPPALQRGQRVAAVAVGSQAVLQILSRVSGRQAPPQPSGSG GVGAGPVVVPDGGGEGPQPHSSSQSPPDLPLKAK	chr19:42701592- 42724264_strand=- DEDD2
SEP305	MSAPYSAAPPESAPPSPAPKTSRSPPPPGPSQTPDFSRNPPLV QDTVSGKGWPTSRSRFPPRERGDPGDSSGQEVPAASRPHQARN VRLWESALCIATAPEPQAPSEPTQI	chr1:150521860- 150532550_strand=+ ADAMTS L4
SEP306	ALQYQTAFGKWYESLLNRLIVSKQHVLTLKLNGRITILACGNLT GMNYLKKLKMKSLMKLSV	chr3:193310939- 193412467_strand=+ OPA1
SEP307	MAVAGAAAGAGRRRTRMVPEPGDHAGVAAGEAAGRRAEAS GEGAAHRRVHGQDATDDCELA AAAAGELGEGPG	chr19:13058987- 13068000_strand=-  GADD45GIP1

SEP308	KNTTQESLEKGPPSVLKGGRSRSRCPRTTRTS	chr22:41697661-41756143_strand=+ ZC3H7B:X M_011530016.1
SEP309	MERAELPQTAGQAGRGSPLPSRPPSPGLESPAPAPVPHR LPRRPRALPCPPSALR	chr11:118964582-118972602_strand=- H2AFX
SEP310	CCLKGTWYPNKAGNLILLQGHTV	chr3:124944633-124949368_strand=- ZNF148
SEP311	MLRYCFFPKMCFSTTIGGMNQRGKRK	chr12:48732236-48745011_strand=- ZNF641
SEP312	MDHQPGQTAKASEIQSTGGQRDPQPERERPANSLIDQCSQRD HQTEPPKDRHLC	chr2:131113651-131132956_strand=+ PTPN18
SEP313	AVFFKNLLAFARSMISDASHIY	chr6:80194734-80199064_strand=- LCA5
SEP314	MRSSFVLWERPALGEWVSSQPTSHLPSALCFLGFFPPVFLKTS LSLAELSFLNRSAFAIDPGQVKISF	chr16:86563765-86575431_strand=- MTHFSD
SEP315	MEGVFPSVKLTTWLPSCEDLTPGGGRGLTPSIIAVTLPSLVVSL GSVC	chr7:158799383-158814542_strand=+ LINC006 89
SEP316	MADRAPRQPTSLGSSPQRCGSPSAPPPPPDRGERIEDCLAPLC PPVVGRRGGCALSRLFVDSLRLSSRTAAVELVAGGVCRRSPQ EN	chr1:155532795-155708399_strand=+ ASH1L- AS1
SEP317	LVLFSFSASWLTVLPSSLSSYGACSRFYALIFLHKRYRSVVKLGIPL QCLLCAGLRVGVINNGLEASSP	chr17:35441928-35444379_strand=+ ACACA_an tisense
SEP318	MGGETDGAGRTRDGADGGGGAGSAGQIQRKSGGSAQGCEA GAPRGPSGTQEMGPLSRTQERSHGASGLAGDGAHARGLLAP QHPAPRLQGDPRAPGRPLP	chr19:3610043-3626771_strand=- CACTIN
SEP319	DQRSPGNCLIGKTFLTGGAPEAARRNQRGDAAAGAGPRAAAA DGAGAEGAGGAEGQNRGADGSAAPKRAGPGQQWSRAPEPG AVLAPAEVVLRAVWGVRRGLPVPARGEHCGRGTPERPQVN	chr22:46973128-47073068_strand=+ GRAMD4
SEP320	MAGRARSVQIILQESQTTTFTSPPAGQHRLVSGSPSAETLPLR WGLDAREPFSAKSLKRSEAAPRNRGGSEASPATLQTGPPPRPP SPQS	chr5:34914296-34925392_strand=+ NONANN OT

SEP321	DAAIRHSYKTSSGSCFKCQKSGHWAKECPQPRIPKPCPICAGT HWKSDCPARPTATPGAPKALAQGSLTPSQIYSA	chr22:17092426- 17095991_strand=+ NONANN OT
SEP322	RSSSSQVEERKRQREEDAGGGGGERPLPGVGSRRGGAGPPGAP GCGGPHGRRPAPRAPPELAPGPPAAADARRGAALGRDRRRDS GQRPASRLSAPQPGPDILQAPARGELPGAERLGS	chr19:54693858- 54697432_strand=+ TSEN34
SEP323	VLLKNEQTELLYNKSQPF	chr12:118649944- 118650075_strand=. NONANN OT
SEP324	RKRRRRRRTPCRPKRPLSRRSGVKFKILEDLPPSSSRPQS	chr2:85132483- 85133801_strand=+ TMSB10
SEP325	MPPKFDPNKIVGACSGCGRGCMEHPSALPRVQSFPRLMGLL KPLPPRDLPGVAPRPSLSLSP	chr9:130209955- 130216851_strand=-  NONANNOT
SEP326	MSRGTMPQPEAWPGASCAETPAREAAATARDGGKAAASGQ PRPEMQCPAEQTEIKRSS	chr5:14664778- 14699800_strand=+ NONANN OT
SEP327	GRGPTAPAVRDPNAIPAQRSHGSYRQHERGGPRGRDPQPETQ RSSCTARAQHGVHSNTASPLPAGAPRATAEIPQ	chr7:150778172- 150779835_strand=- TMUB1
SEP328	MVALPPAGPEAEAGAAELHVQTRSETALLALDRPLLPPALRRP QTAQPGGMEARKQGGFVQVSANALAVTGLGSPQSGGAATLA AQARLQPVHLDVWGEHERGRCGGPASLPQPQRVLPQAQAEAA GPACLWPAQRD	chr22:32014539- 32021921_strand=- PISD
SEP329	GEEGWGGCGGRGAPPGRKLNINQSIAVSTATQRRRGCEGGRG TGEGRVGGREEGRGRGESAVGAG	chr2:200322928- 200323580_strand=+ NONAN NOT
SEP330	TRAGQGEPASEAQPLSEPGPQTPEPEPRPAQPGAERLPG QATTQQTFDQRR	chr19:56165091- 56185542_strand=+ U2AF2
SEP331	CCYVDGQQQANKLVSAVLAGKEVLKNGHSPGAVARTFKIPAL WEAEAGGCLSTGV	chr1:7863564- 7864928_strand=- NONANNOT
SEP332	MPEPSLGESHSPHLPQPQPKPAVAAAATLHLPAAPEGPHRQQQ QAGSPAP	chr7:100169852- 100183655_strand=- LRCH4

SEP333	SPGEEDGPAGCVSHHRGAQELIGASLHTARCDPRRGPQFQQL QQQAAGPGGLPGHSHGRRQRAPCLPRGCQRQCGLGCFWH GQPGGGGHHGGGGRGRGRRRRLCDGGVPGHTQPWGS	chr1:228544743- 228549628_strand=+ OBSCN
SEP334	HGVRHPAWAFRLCLPCPSRRVTTSARTQQKGQDTQRRWRTH LGTEGQCDLPGAGGPARAFPEETAKEPRPGTAEKQGGGRRGP VPSSSAVPGGRSARLSA	chr10:11925853- 11937442_strand=- PROSER2- AS1
SEP335	GACVGLATRLANPPRPARPPRLRTPEVPTRTSDAPRPSATPPGA DPLNSAGPGARGPHDPRAPARTPRAPAPARVPDAAPATHRA PQQGPEPPAAGRGGAPR	chr19:55737961- 55770381_strand=-  NONANNOT
SEP336	MCCVKLVTSWDGQNPPRSRLKFLWPYKVVISLGLQKLALERQ APLLCPF	chr12:12966292- 12982381_strand=+ DDx47
SEP337	GRKRGEFGERRGLGDTEPSGAGAGAQAQKKAAPGPTAAAAA QASAAAARRQPREPLGSRPPAQPPPPREPVAGSRSGRKTTEGPS VRATPRGPNEQPEAAAAEDGSDDAEAEKGTGPAP	chr2:231577583- 231685792_strand=+ CAB39
SEP338	AWHPSSSVFPSLACDPPFPLSHLPLLEASGGIYKKRLLIPPEKS	chrX:5214450- 5216144_strand=+ NONANNO T
SEP339	FGQCQSYVGVTSAAEETTGSRITCSPTTDSYGIPQGCKKK	chr1:175913967- 176176388_strand=- RFWD2
SEP340	DYILSLEMFSILLWGFGINVSSLIMELLFPEAS	chr3:88101102- 88108113_strand=- CGGBP1
SEP341	FFHPETAVAGARTEAAAGARLASGLRVGPAEPDAAPGAGRWW CLAASGPPRAATSEPSATAGVRRRAAGPAGPGARSCPPGRGGA DQNNVQHQPPEPEGVHQQSASPGGLHDQRKRHGHSPDP GLLLQNQGD	chr7:66386203- 66420643_strand=+ TMEM248
SEP342	VLKCVCAASVHDASSPLGPPRVHFLDHTHIPPKNYLWWVVVY SSRLLGVIVPQNM	chr16:87435666- 87438903_strand=-  NONANNOT

SEP343	LIPAHTAHVEFACLVVYVLDLITDACTIKPLFNKVLQNDNAFPKI	chr9:130128866-130129660_strand=+ NONAN NOT
SEP344	KRNKKKKKFWTRCSWEGSCPGGRPGNEHRPAAGREPGRASP GEAGPAGGAAAGQGAPREGPVPAADAKRPGQG	chr1:16905808-16970994_strand=-  NONANNOT
SEP345	MPARRLLLLLTLPLGLGVSDRGAWGGGQLATAGSGPGQRRG AGAGVRAGSATAAARCPVSPAVGGSGRA	chr17:62205639-62207524_strand=-  NONANNOT
SEP346	TASKNIKQYLQIQGEKHTSTIVVGAFNDRTEKTDTEVLINTMSKL KI	chr1:4036227-4073316_strand=+ NONANNO T
SEP347	MEWWGQCMTEENSRQKGLFQKKKVYKWLLCNVERCSPILVI	chr1:157243513-157253900_strand=+ LOC1053 71455
SEP348	DLKPVFLLLLSIRDQCADLAVERRLWAASLEA	chr11:3532972-3542051_strand=+ NONANNO T
SEP349	MRSWAKRGLATCLRSYSQHCLILKPMNKVAFIPTEAWYSAGR QTHKQVQLAHLASRSASMDSTKNGFKILGKKQIIKQLKNTNFKI	chr11:82783129-82805398_strand=+ NONANN OT
SEP350	MLHSRKRELRQVLITNKNQVRLTLLTLG	chr11:65266554-65273981_strand=-  NONANNOT
SEP351	MCLKSVMLTWGPGCPWAGADGTSTLIKFLLAPEENKVTLPLL	chr16:3054772-3058645_strand=+ NONANNO T
SEP352	NHESFLNSVYRQVRIFLSEPERIKGGFELDKIELKVQTNGGRIVKI LQRIPCVVILTFFKVLHGFSVNKKLK	chr19:23278060-23286908_strand=+ NONANN OT
SEP353	NLGSPRRIRRIWSPRLWKTLPMMGMIRNGER	chr2:107137814-107160732_strand=+ NONAN NOT
SEP354	QHSDKGSSQSKVNLEQVNEETLKTGGLRKMHPLRACSEGSAEL IQGKEILPQTIDHSFNLSHESLLQLLVRGNCRFILDHLCNITEFSN ALWLRQLYNQLDVVLSDTTLSHFQFCFPVFLFSFSLFLSYIKL KNVFICCHRQIYMNQVDQETK	chr3:107852804-107857456_strand=+ NONAN NOT
SEP355	VHCQMSSNILKEIFLSEQHVSAMSLKYSVNQGINRCAVPRLLCS YRAQEE	chr15:31059077-31065344_strand=+ LOC10028 8637

SEP356	PATAACFCTAWQAKNGFHIFEYLKKIFQEYHFVAHENYMKFKF QCPQIKFYRNIACSLI	chr21:35345400- 35353552_strand=+ NONANN OT
SEP357	TIARTKNQTPHILTHRWELNNEITWTQEGEHHTLGTVVGWGE GGGIALGDIPNAR	chr1:144672440- 144676693_strand=+ LOC1053 76128
SEP358	SRLSATSASWVQAVLLDQHQRP	chr6:141167105- 141170052_strand=-  LOC102723724
SEP359	TYKIKDFKTFTISSTAIYYELQRGTRSTEGA	chr1:995566- 1002621_strand=+ NOTANNOT
SEP360	MGEMERGEIKEKKVIPET	chr17:41380977- 41381147_strand=- LINC00854
SEP361	GRPSPSLAAALQFDLRLLC	chr1:61105899- 61106128_strand=-  NONANNOT
SEP362	VASGIWWGLCISLPPQLGIGLCCFTSSTSGAPGDCHSLPCDLQ VLGDAQLRCQDILEAGKRDGVSLLLPRLECIIPISAYYNLRPGSS DSPTSAS	chr19:23449149- 23457064_strand=- IPO5P1
SEP363	MRTASPYSRPEGGQKADSLQAARPLHRPHRPRTRQLRTEPSP SRGCR	chr2:66649993- 66662138_strand=- MEIS-AS3
SEP364	AHHCPVGSPFWAGQQSRLPNVEGGVEGEAPVGTGAARSVC RPAGVPGGRGLGGRTRSRRLARPAPGNEGLSTWASGWGGC TGAPSSASPLALRSISHQG	chrX:118466927- 118467907_strand=+ LOC1019 28336
SEP365	MGDQPCASGRSTLPPGNAREAKPPKKRCLLAPRWDYPEGTPN GGSTTLPSAPPPASAGLKSHPPEK	chrX:56755414- 56843979_strand=+ LINC0142 0_NoBody

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**Supplementary Table 2.** Detected microprotein peptide sequences from human interactome data<sup>1</sup>.

<b>Detected peptide sequence</b>	<b>SEP #</b>
LAGRDEGGQSGQK	SEP247
DEDLDTDSL	SEP283
CQDILEAGKR	SEP362
MQASIEKGGSLPK	SEP275
EAVLSLYRALLRQGRQLR	SEP272
DAASGEHPGSK	SEP289
MADDKDSLPLK	SEP71
LDRQTLMFDGK	SEP268
YWTVQNVEMKHKR	SEP153
GTRPEDSSVLIPTDNSTPHKEDLSSK	SEP215
MQASIEKGGSLPKVEAK	SEP275
EFLDGIYVSEK	SEP277
MTNQEAIQDLWQWRK	SEP275
SVCRPAGVPGGRGLGGPR	SEP364
EPSGAALR	SEP2
GPTIQTNLK	SEP232
IVVDELSNLK	SEP215
TLSNYNIQKESTLHLVLR	SEP268
QVEGTGTPK	SEP61
GRPSPSLAAALQFDLRLLC	SEP361
SLLTPDVNFK	SEP146
EGSSGPEAPK	SEP164
TKYLCNYLITLVNR	SEP7
DNLTLWTSDTQGDEAEAGEGGEN	SEP266
YPSLGQKPGGSDFLMK	SEP252
QDEHGYISR	SEP285
SVYAHFPINVVIQENGLVEIR	SEP277
RGCEGGRGTGEGR	SEP329
NILDELKKEYQEIENLDKTK	SEP215
CDSSGQKTPANLTPCDK	SEP279
LQKAVVRVRVTIKKKKYK	SEP82
LLPLGASPAGVVGGGLAPRR	SEP271
YAWVLDKLLK	SEP265
QVQLAHLASRSASMDSTKNGFK	SEP349
SVCRPAGVPGGR	SEP364
TEMLSESKNILDELK	SEP215
KCLEELQKR	SEP255
EHALLAYTLGVK	SEP265
YYTPTISR	SEP255



YIWSSRSRRLSSEPAEKQKGETNT	SEP189
FLDGIYVSEK	SEP277
RWRTHLGTEGQCCLPGAGGPARAFPEETAKPR	SEP334
RAAGPAGPGAR	SEP341
GGLGAASIAADGAPR	SEP300
PAGVPGGRGLGGPRTRSR	SEP364
QKDELILEGNDIELVSNNSAALIQQATTVK	SEP277
ADSLQAARPR	SEP363
PVSDGTSTLSPR	SEP3
GPVPSSSAVPGGRSAR	SEP334
TRDGADGGGGAGSAGQIQRKSGGSAQGCEAGAPR	SEP318
FSFILNFPLSR	SEP123
TADGCELPR	SEP187
DELILEGNDIELVSNNSAALIQQATTVK	SEP277
FCLSNDFFKSIYIGIFQNSNCHIKKHDNLNDLNKNTVPKIKRQL	SEP214
MKFLDLTLALRIQDGNYNHEDR	SEP31
DETSPADAVCPGLGRDLCGSSRCCLR	SEP2
DGYELSPTAAANFTR	SEP255
EPGRASPGEAGPAGGAAAGQGAPR	SEP344
SADGEEAAVPGPPPEPQVPQLR	SEP287
KLNINQSIQVSTATQR	SEP329
KYKGRKER	SEP82
RPTWSRCGTNK	SEP166
GAWGGGQLATAGSGPGQR	SEP345
GAGAGPHLGPQVEGGLQQVQR	SEP178
GRGPTAPAVR	SEP327
TLRDYLQLLR	SEP71
MGETDAGRTRDGADGGGGAGSAGQIQR	SEP318
LPNVEGGVEGEAPVGTGAARSVCR	SEP364
NGIHDLDNISFPK	SEP255
VFFCLSEDKKNIIIEEGK	SEP256
DGLAPTWSLPCPLLPGLPPDAALPGAVR	SEP287
KYEDEINKR	SEP274
IIPALLEADEGYPFVRSWR	SEP161
QHGGSSK	SEP95
ATANCCECTGRGPGSGGGGSRVAVK	SEP297
EFDLLSKVFQTLK	SEP162
HGTESLPARGP	SEP235
GRAEWGWAPAGHQGLR	SEP208
IMADIR	SEP286
RKGVLTGTEPAR	SEP235
ADAPAVSPESPQKKPPFQPRSVQEAPCSPQGPPAQRPALAPPSKPSLK	SEP42
PAGVPGGRGLGGPR	SEP364

MAVAGAAAGAGGR	SEP307
STLLNNHIIKIIARKWTIFTMFCKLASVWICTLLVKYI	SEP233
QLPSAGPDK	SEP252
FILNLPTFSVR	SEP255
ERAVELLRK	SEP255
ERSCLHSIK	SEP80
EDHDHIPPEAVHR	SEP224
KEKDTLLEVLK	SEP51
QDLKWTLLVCGIE	SEP191
PGVALSSLPR	SEP244
RDAAAGRGAGQPGLAVR	SEP290
PRRGGEQPHHAAPAQEAEEKEGRAR	SEP150
FIAIIAYIKKEK	SEP112
AEPLQTAGQAGR	SEP309
GRDPQPETQRSSCTAR	SEP327
VRFAHATPEAVSG	SEP116
TAPGARTGGHAVPEGGGRSRRGGGGGGGR	SEP290
TAFDEAIAELDTLSEESYK	SEP266
TRMVPEPGDHAGVAAGEAAGR	SEP307
PSPPSAAAGAR	SEP298
GLVFLNGK	SEP272
AEEQPGLGPGAAGR	SEP287
EALILGSQRTAAAAAGTITRPRATANCCECTGRGPGSGGGGGSRVAVKNVSH	SEP297
NEQTELLYNK	SEP323
RQVSGGGWPPAR	SEP287
GPGSGGGGGSRVAVK	SEP297
EYQEIENLDKTK	SEP215
TITLEVEPSDTIENVKAK	SEP210
RKKIEKRKSFR	SEP82
DPQPERERPANSLIDQCSQR	SEP312
RTGMENEFFLIK	SEP274
TFLTGGAPEAAR	SEP319
IVVDELSNLKKNR	SEP215
AAALDPTR	SEP224
PEDSSVLIPTDNSTPHKEDLSSK	SEP215
IIDKNGIHDLDNISFPK	SEP255
ASEIQSTGGQRDPQPERER	SEP312
HPQEPGIAGGGGER	SEP157
IPLSIVIRK	SEP116
SFSGNPAVEEGTTQEN	SEP225
WDYPEGTPNGGSTLLPSAPPPASAGLK	SEP365
PRPGTAEKQGGGR	SEP334
MSYCFDR	SEP259

IIDKNGIHDLDNISFPKQGS	SEP255
KYTLPPGVDPTKVSSSLSPGTLTVEAPMPK	SEP285
AGAVLYTR	SEP257
AGDFLNLR	SEP70
NILDELKKEYQEIENLDK	SEP215
IESEGGGEGWGR	SEP175
APARTPRAPAPAR	SEP335
GGEIQPVSMKVGDKVLLPEHGGTK	SEP261
LGAGAVGSQTR	SEP289
RAGPGAGRLRAAALDPTR	SEP224
NLRAMSEFWKEINWNIPLLSWQPPK	SEP203
FINYVK	SEP275
SFQLKGDGVFVLKSGR	SEP196
RNLADCLR	SEP255
QLEDGGT LSDYNIQKESTLHLVLR	SEP210
CQDILEAGKRDGVSLLLPR	SEP362
QVSGGGWPPAR	SEP287
SPGNCLIGK	SEP319
LLAENLPIDFLNIRKIPN	SEP180
SGHLSQTPRSPEALLR	SEP303
APERQSGHGDQRARNLRGRRGLEAGSAR	SEP263
HEERQDEHGYISR	SEP285
QSKTPSQKKK	SEP135
GPHDPRAPAR	SEP335
VAGSPEHKSSR	SEP239
AVAAAAAAPDPGGR	SEP299
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AMSQRNLNAK	SEP264
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LRAAALDPTRR	SEP224
TAQTAGRAAWR	SEP228
PGQGNSRSSRSIRSPEGR	SEP157
QVLITNK	SEP350
SRLQLRDSEAKLEGLR	SEP282
QQQNSNIFFLADR	SEP215
RVTIMPKDIQLARR	SEP254
AGAPAVGLLLNER	SEP289
DALKVAGRQTDLL	SEP192
VTIMPK	SEP254
IMADIRAQYDDLAKG	SEP286

TLSDYNIQK	SEP210
MGSQHLPLR	SEP38
FYALIFLHK	SEP317
MGETDGAGR	SEP318
ESTLHLVLR	SEP268
ESTLHLVLR	SEP210
TITLEVEPSDTIENVK	SEP210
RVTIMPKDIQLAR	SEP254
LVTSWDGQNPPR	SEP336
TGGLRKMHPLR	SEP354
PAPRAPPELAPGPPAAADARR	SEP322
CLSMSTAACQTSSIATR	SEP294
IEDCLAPLCPVVGGRGGCALSR	SEP316
ERAVELLR	SEP255
GGSLPKVEAK	SEP275
ELDDHVTNLHK	SEP259
MRAGVVCVSQAQKDELILEGNDIELVSNAAAIQQATTVK	SEP277
TAAAAAAGTITRPRATANCCECTGRGPGSGGGGGSRVAVK	SEP297
ATATRQEDRSPEGGWR	SEP61
VTIMPKDIQLAR	SEP254
MYLLFAAPSLNLQSK	SEP67
ATANCCECTGR	SEP297
IQDEEGIPPDQQRLIFAGK	SEP210
SPGNCLIGKTFLTGGAPEAARR	SEP319
TGAGILLLR	SEP79
TEMLSESK	SEP215
RAPQTSVPASGEEAGKKDAASGEHPGSK	SEP289
YSVNQGINR	SEP355
KSMSATQQGAMAGAVR	SEP38
RSEAAPRNRGGSEASPATLQTGPPPR	SEP320
RVEDEVNSGVGQDGSLLSSPFLK	SEP71
QLRYTDRDFYFASIRR	SEP272
IVVDELSNLKK	SEP215
GAEDEAAWRSWRGGGR	SEP299
MITETSQADCAVLIVAAGVGEFEAGISK	SEP265
LLLLSIAPGDGSSEK	SEP132
ESEIHK	SEP53
VSSLSPEGTLTVEAPMPK	SEP285
KSSLVTSK	SEP252
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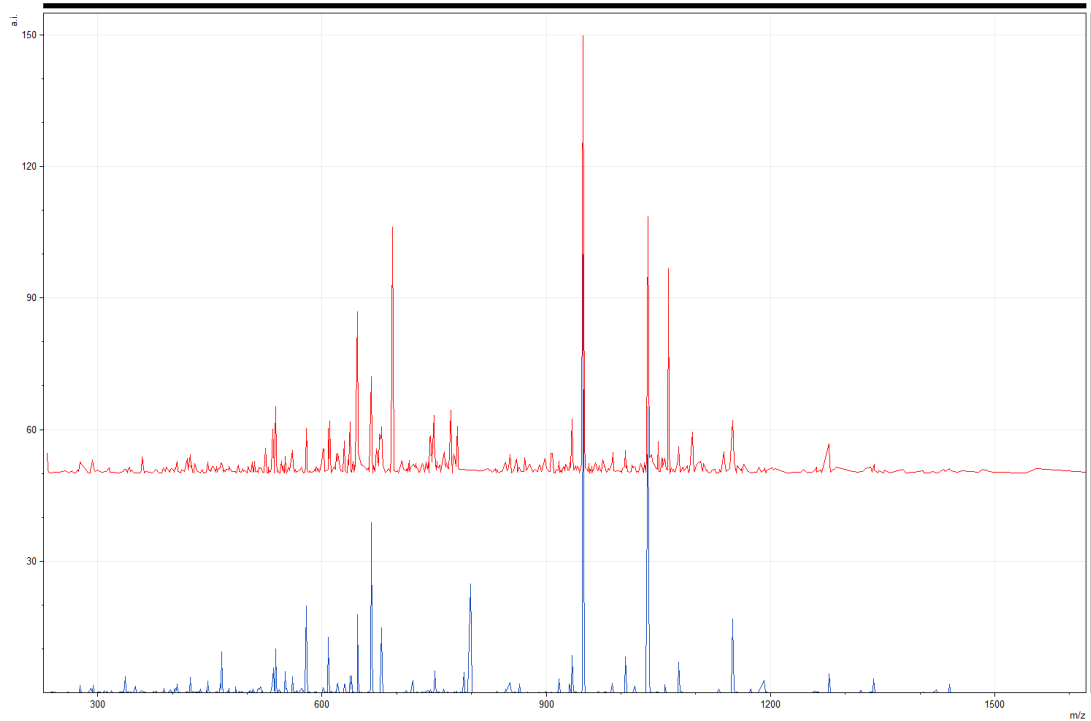
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KILEMELIQE	SEP229
TAFDEAIAELDTLSEESYKDSMLIMQLLR	SEP266
EGAAVHGQQASGGPR	SEP296
EYQEIENLDK	SEP215
NKYEDEINKR	SEP274
EDLSSKIKEQKIVVDELSNLKKNRKVYRQQNSNIFFLADR	SEP215
HCSDGTQGTSQRGSLSR	SEP136
QSPSGEGDPPR	SEP301
AAAADGAGAEGAGGAEGQNR	SEP319
LGAEVRLGSLSAIVDPRSR	SEP297
KEGILNALETMGSSF	SEP41
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AGPGAGRRLR	SEP224
MTNQEAIQDLWQWR	SEP275

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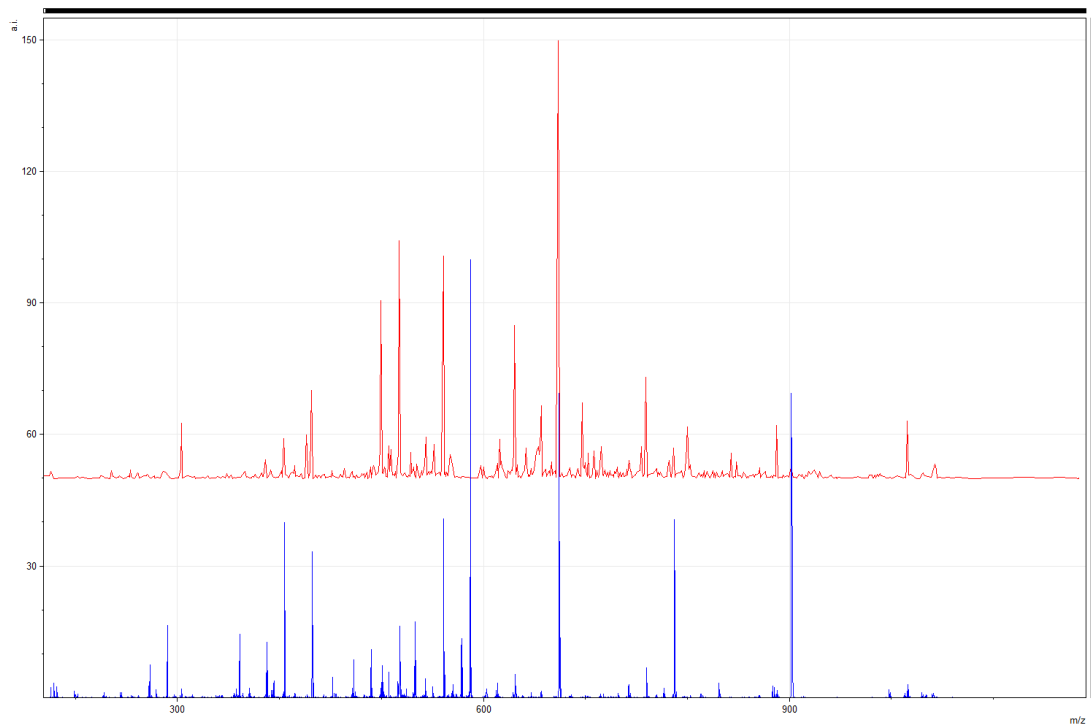
## Spectra of synthetic and PATS detected microprotein peptides

Spectrum in blue is the synthetic peptide and the one in red is from experimental MS/MS.

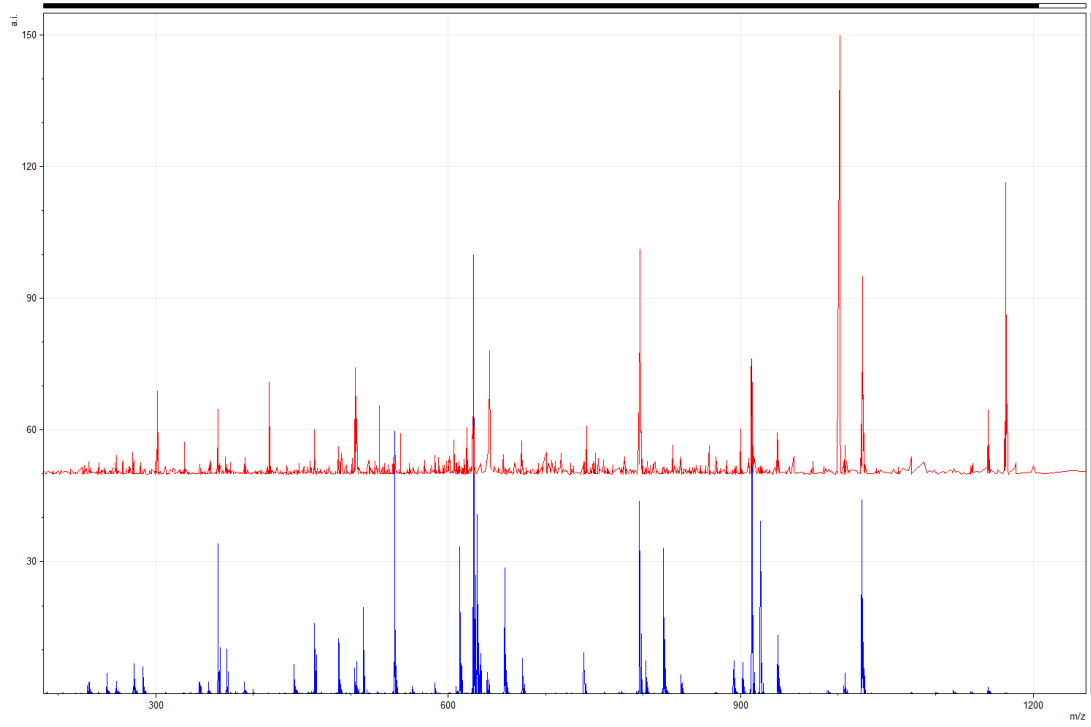
### 1. CQDILEAGKR



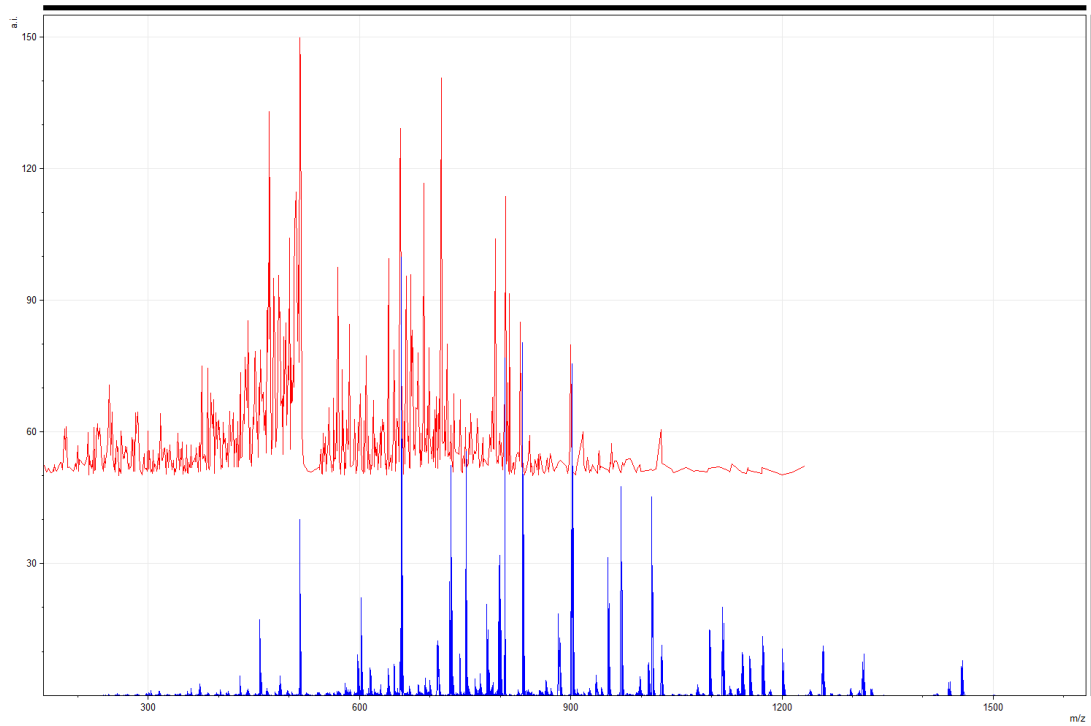
### 2. DGYELSPTAAANFTR



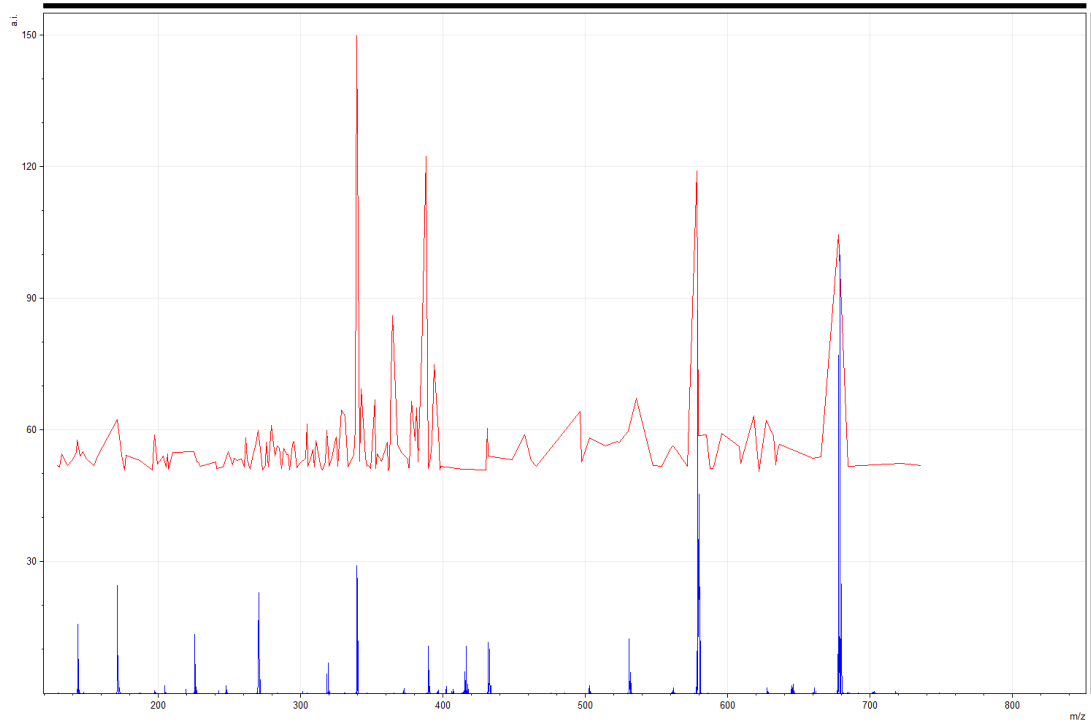
### 3. EFLDGIYVSEK



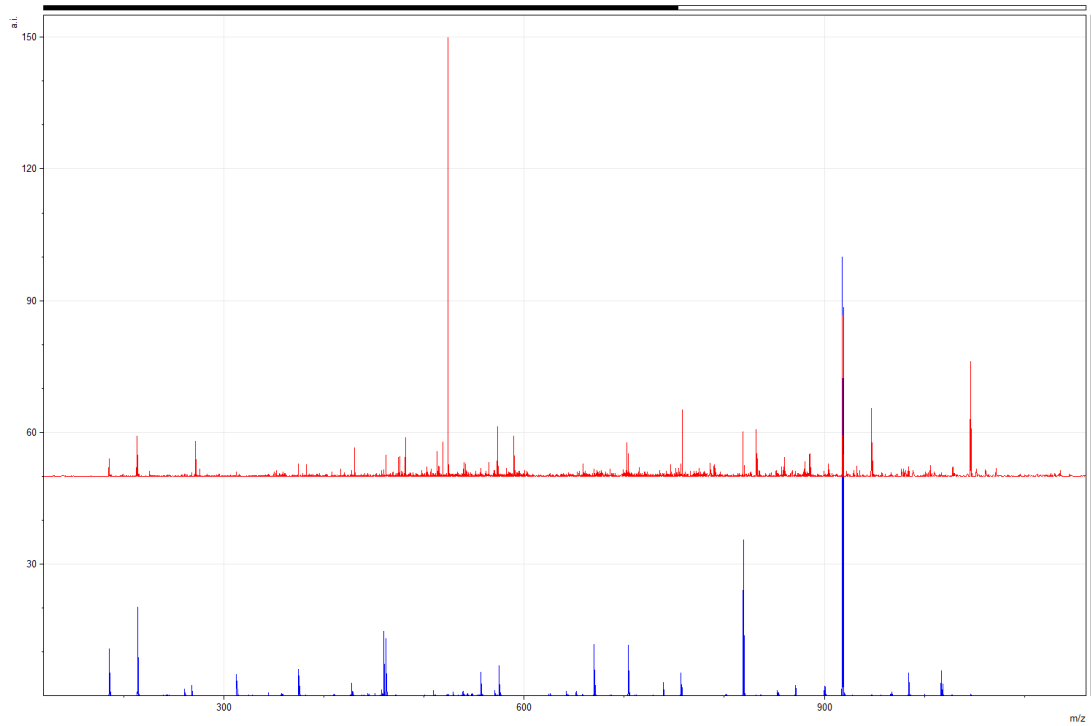
### 4. GAWGGGQLATAGSGPGQR



### 5. GLVFLNGK

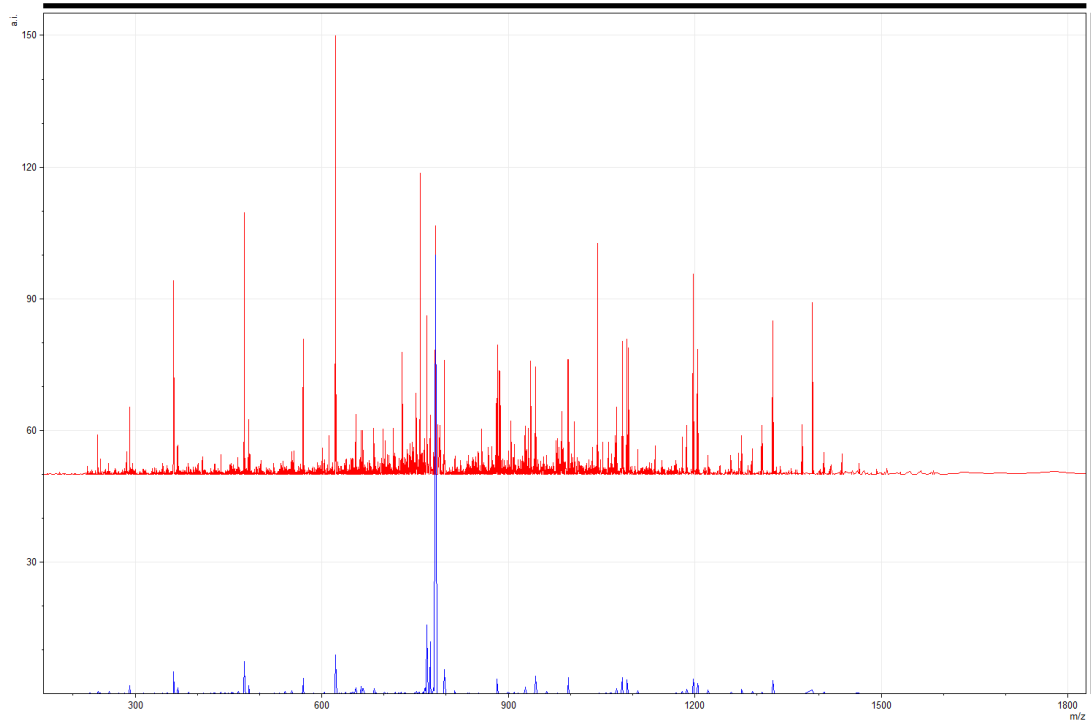


### 6. IVVDELSNLK

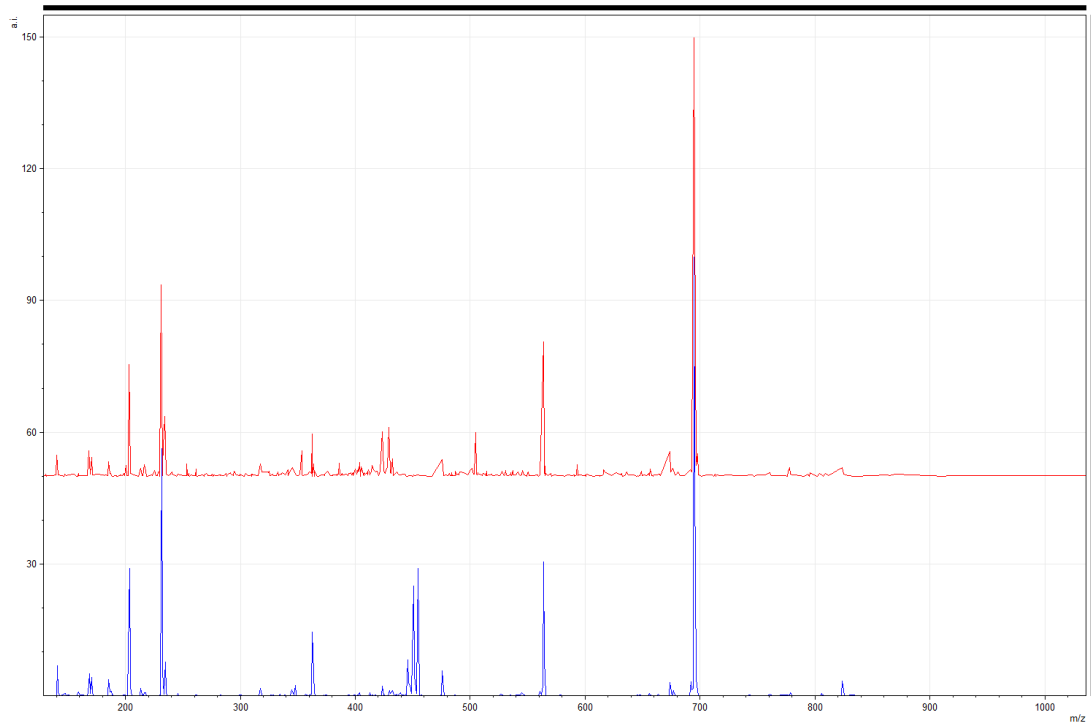




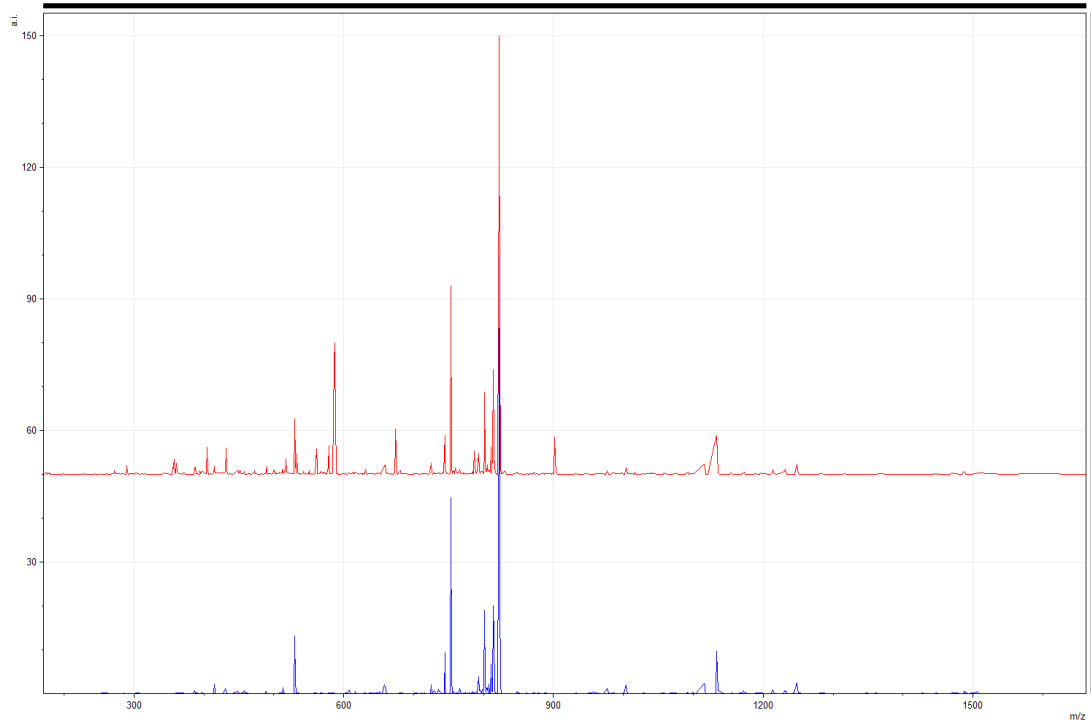
## 7. QQQNSNIFFLADR



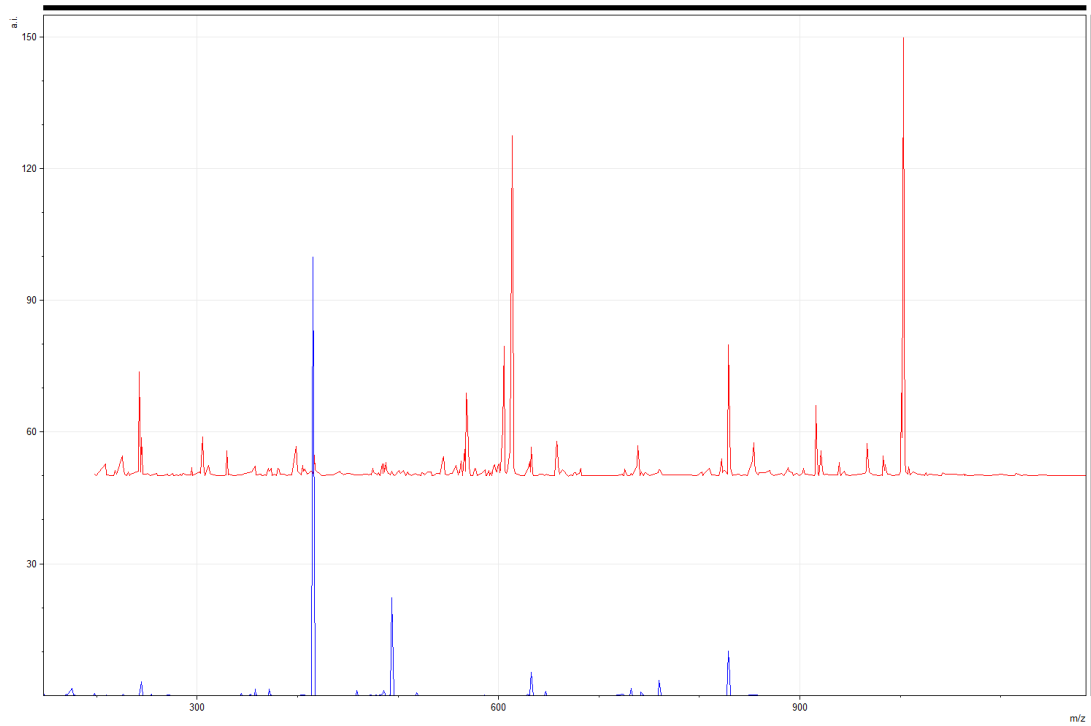
## 8. TEMLSESK



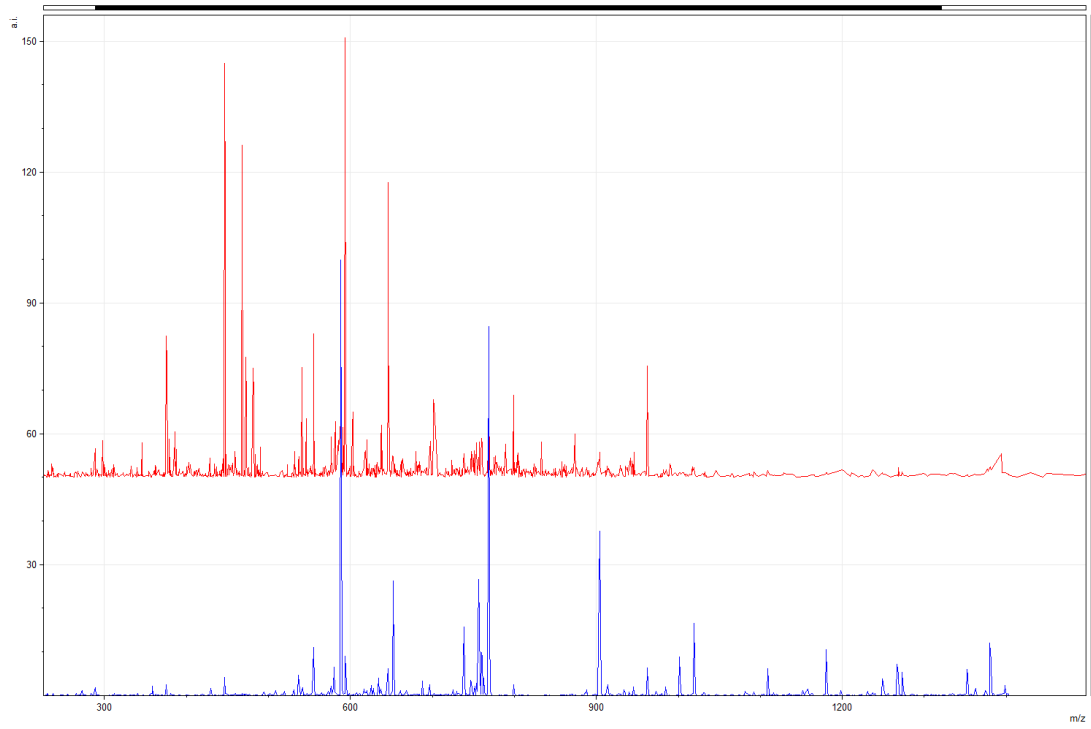
9. RGAEDEAAWRSWR



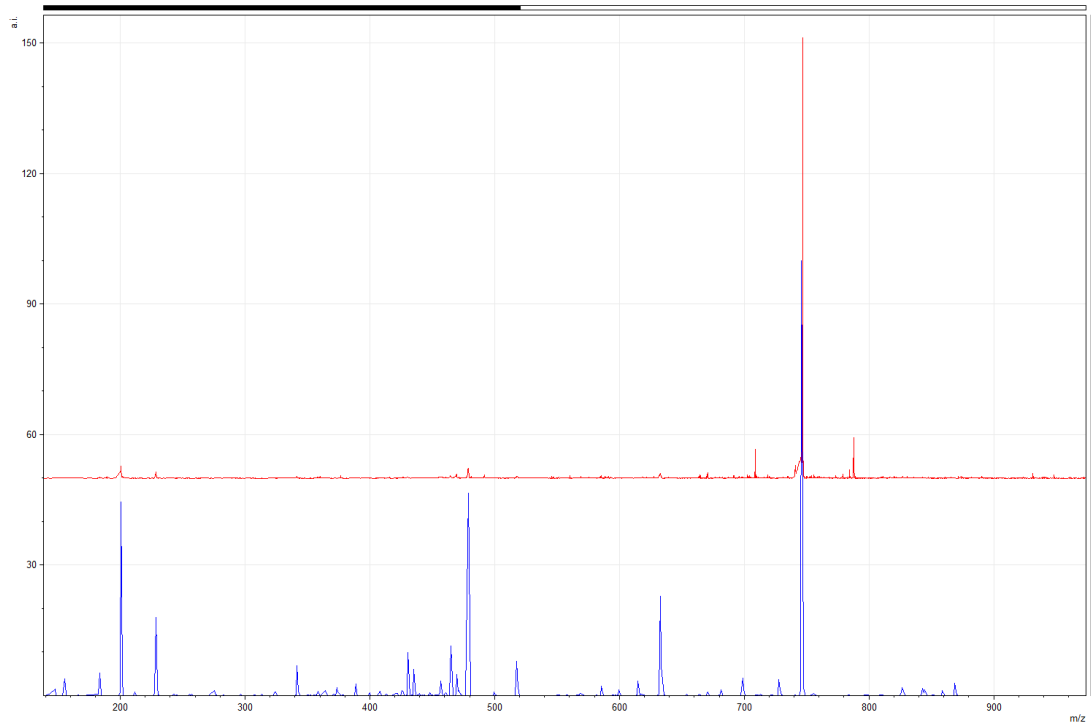
10. SSPVFQIPK



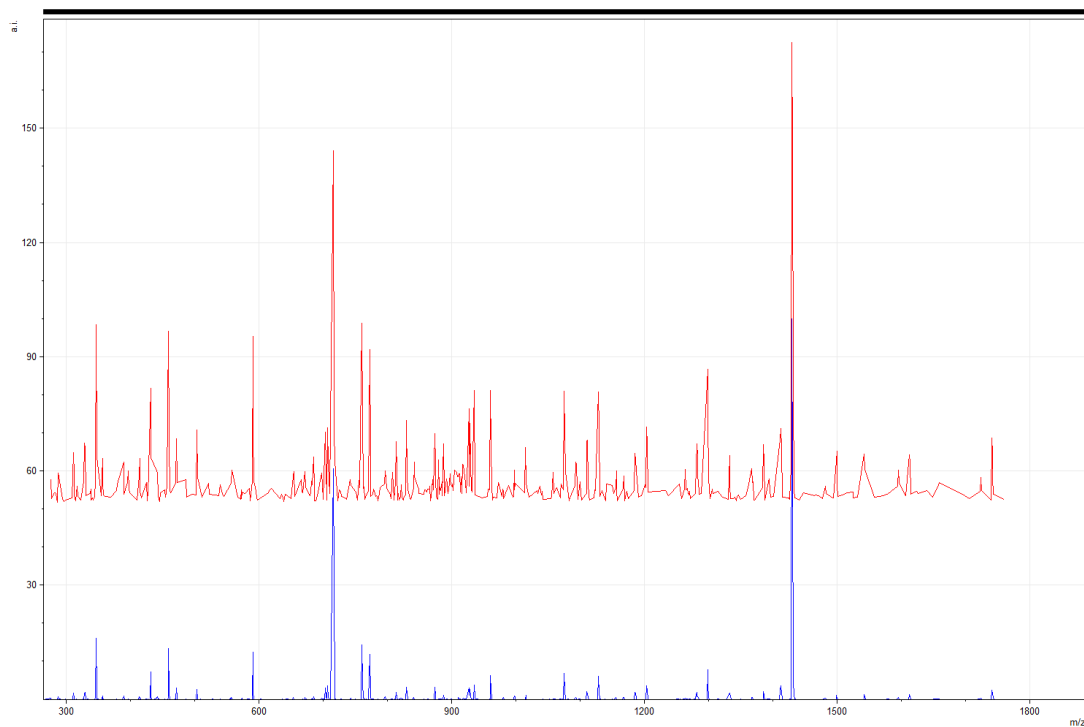
## 11. YTDRDFYFASIR



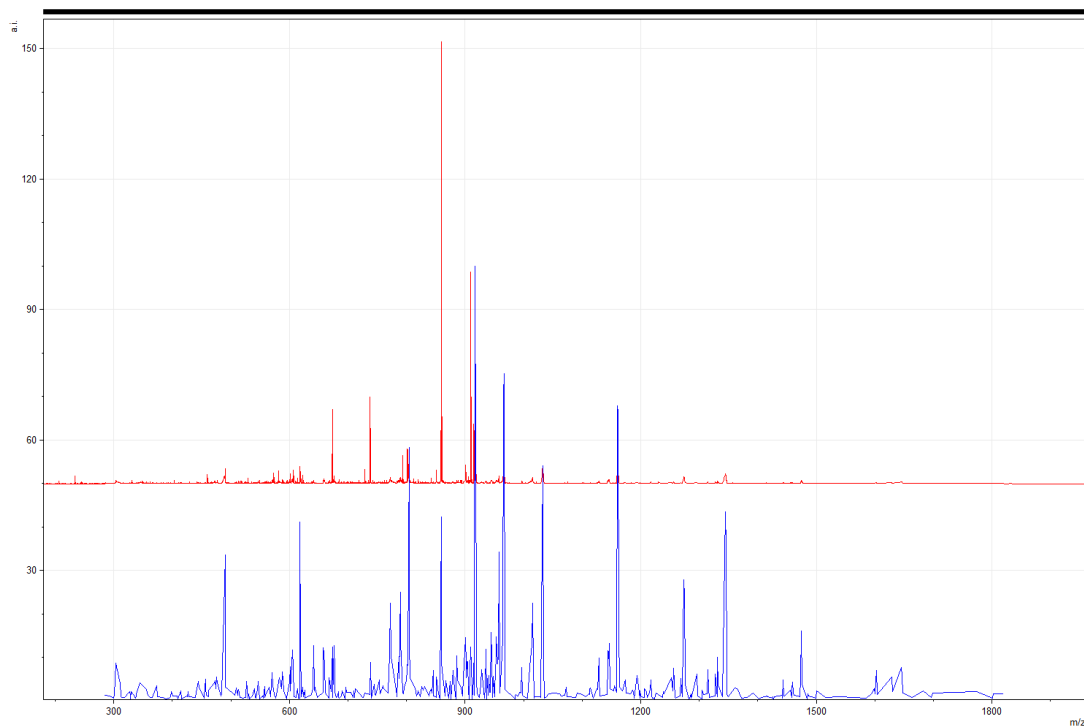
## 12. NILDELKK



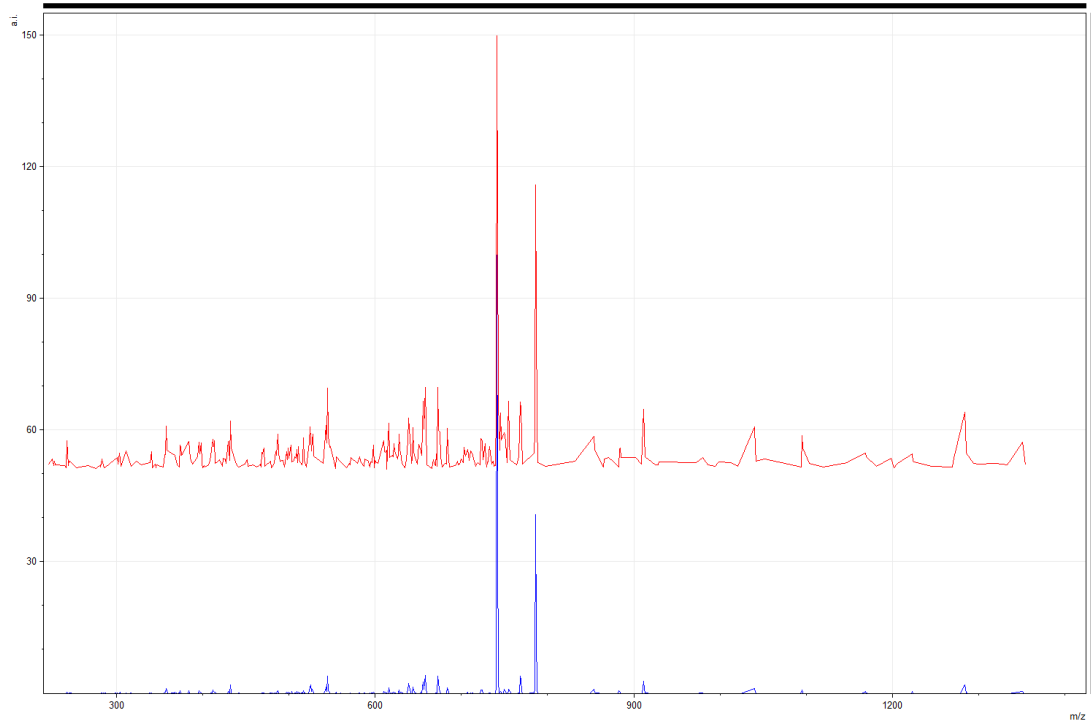
13. NDDIPEQDSLGLSNLQK



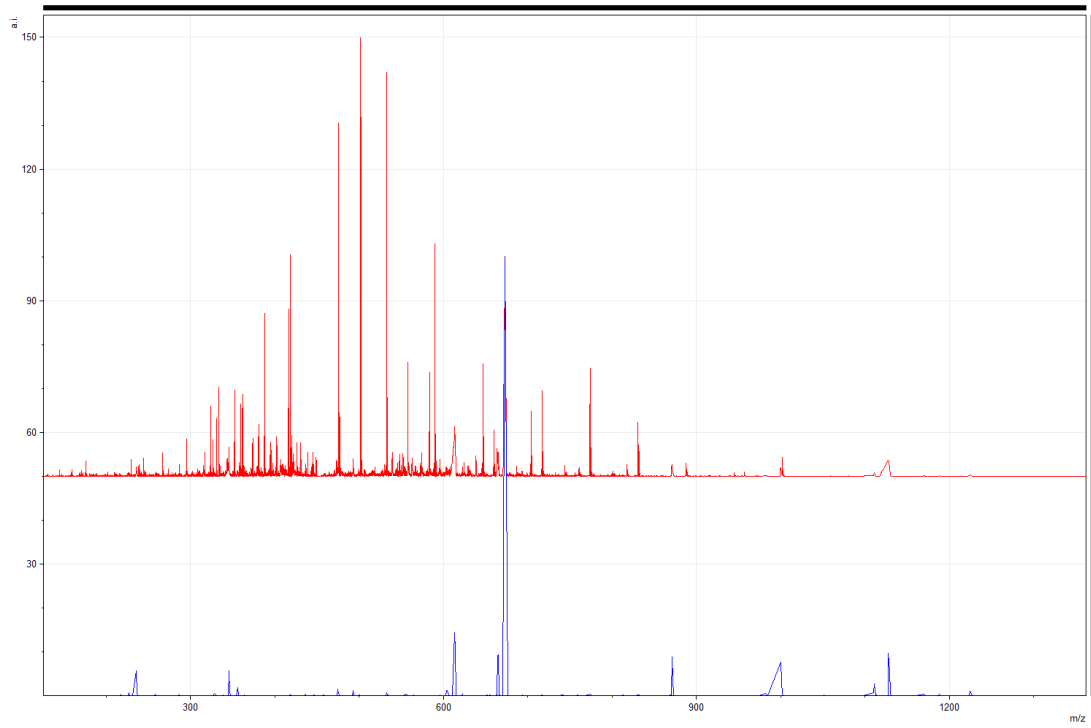
14. MTNQEAIQDLWQWRK



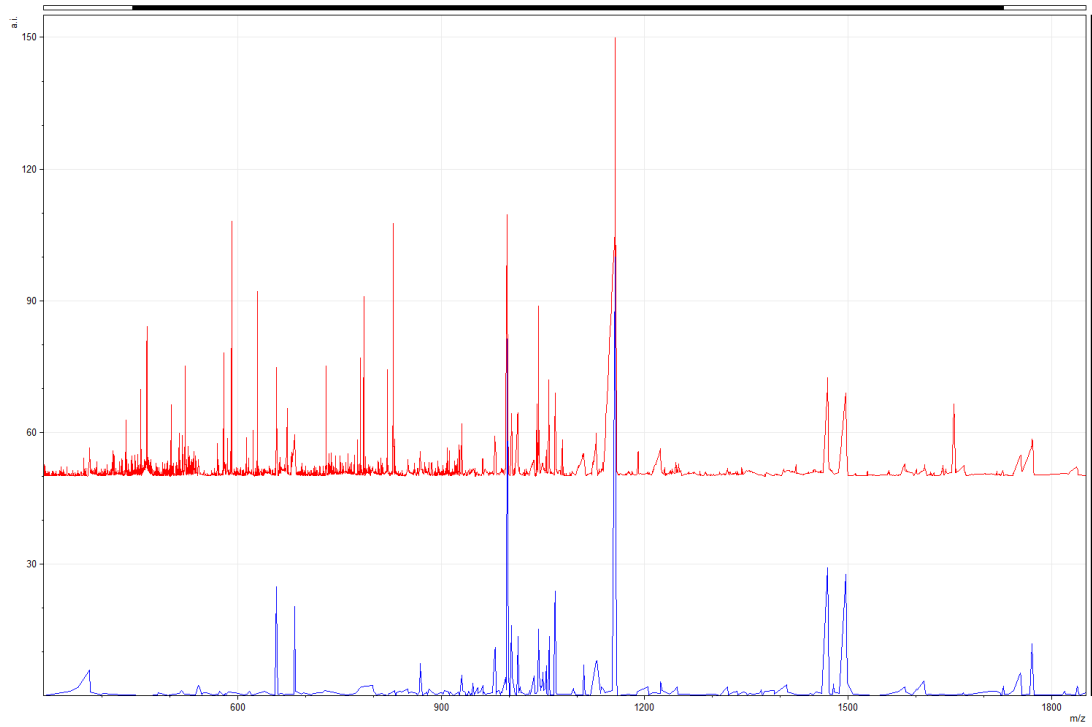
15. IQDEEGIPPDQQR



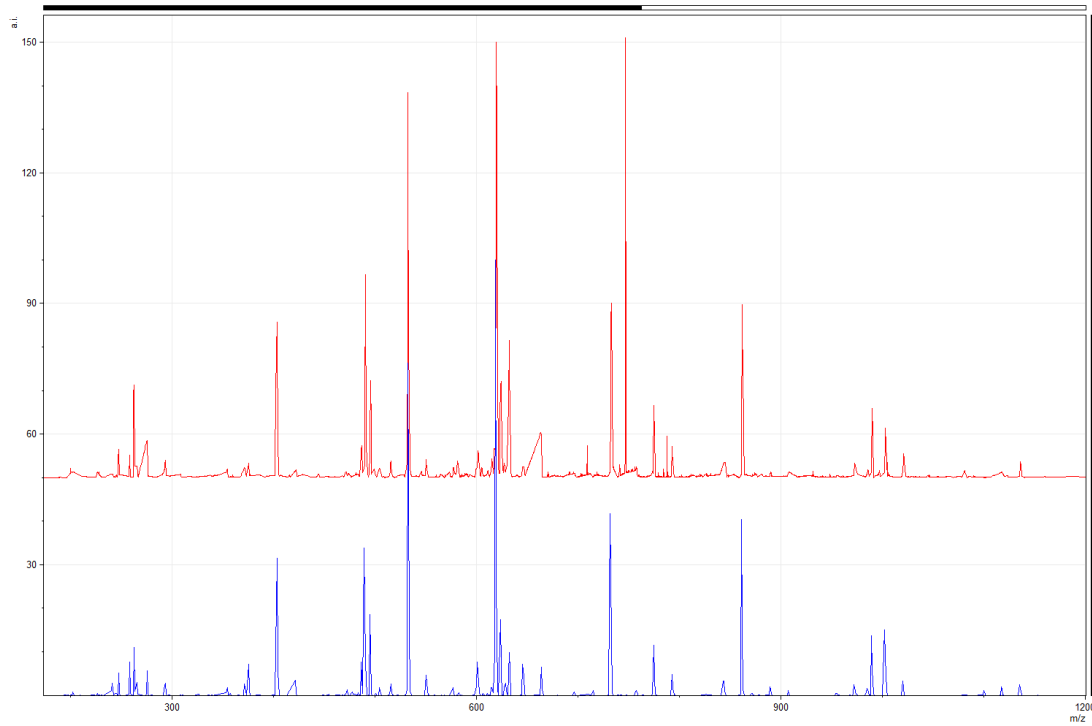
16. HPQEPIAGGGGER



17. GTRPEDSSVLIPTDNSTPHK



18. EYQEIENLDK



## Reference

1. Hein, M. Y.; Hubner, N. C.; Poser, I.; Cox, J.; Nagaraj, N.; Toyoda, Y.; Gak, I. A.; Weisswange, I.; Mansfeld, J.; Buchholz, F.; Hyman, A. A.; Mann, M., *Cell* **2015**, *163* (3), 712-23.