

Table S1: MALDI target identification

Supplementary Table 1.

Proteins & Peptides identified by LC-MALDI-TOF/TOF as part of the ImageID workflow.

Masses identified by LC-MALDI-TOF/TOF were then correlated with peptides identified by MALDI Imaging Mass Spectrometry.

Protein Report

Protein 1: Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
Accession: K2C1_HUMAN **Score:** 834.14
Database: SwissProt **MW [kDa]:** 66.00
Seq. Coverage [%]: 17.40 % **pl:** 8.82
No. of Peptides: 5

10	20	30	40	50	60	70	80	90	100	110	120
MSRQFSSRS	YRSGGGFSS	SAGIINYQRR	TTSSSTRRS	GGGGRFSSC	GGGGSFGAG	GFGSRSLVNL	GGSKSISISV	ARGGGRSGSF	GGGYGGGGFG	GGGFGGGGFG	GGGIGGGGFG
130	140	150	160	170	180	190	200	210	220	230	240
GFGSGGGGFG	GGGFGGGGYG	GGYPVCPGP	GIQEVTTNQS	LLQPLNVEID	PEIQKVSRE	REIQKSLNNQ	FASFIDKVR	LEQQNQVLQT	KWELLQQVDT	STRTHNLEPY	FESFINNLRR
250	260	270	280	290	300	310	320	330	340	350	360
RVDQLKSDQS	RLDSELKNMQ	DMVEDYRNKY	EDEINKRTNA	ENEFVTIKKD	VDGAYMTKVD	LQAKLDNLQQ	EIDFLTALYQ	AELSQMOTQI	SETNVILSMD	NNRSLDLDSI	IAEVKAQYED
370	380	390	400	410	420	430	440	450	460	470	480
IAQKSKAEAE	SLYQSKYEEL	QITAGRHGDS	VRNSKIEISE	LNRVIQRLRS	EIDNVKKQIS	NLQQSISDAE	QRGENALKDA	KNKLNDLEDA	LQQAKEDLAR	LLRDYQELMN	TKLALDLEIA
490	500	510	520	530	540	550	560	570	580	590	600
TYRTLLEGEE	SRMSGECAPN	VSVSVSTSH	TISGGGSRGG	GGGGYGSGGS	SYSGGGSYG	SGGGGGGGRG	SYSGGSSYG	SGGGSYGSGG	GGGGHGSYGS	GSSSGGYRGG	SGGGGGGSSG
610	620	630	640	650							
GRGSGGGSSG	GSIGGRGSSS	GGVKSSGGSS	SVKFEVSTTYS	GVTR							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
111	1	1475.7923	4.78	1	17.95	68.12		0	200-211	R.FLEQQNQVLQTK.W		CID
31	1	1308.6608	4.99	1	14.65	62.72		2	268-277	R.NKYEDEINKR.T		CID
121	1	1265.6501	10.22	1	18.70	76.14		0	278-288	R.TNAENEFVTIK.K		CID
40	2	2383.9526	0.33	1	15.70	343.04		0	519-549	R.GGGGGGYSGSGSSYSGGGSYSGGGGGGGR.G		CID
99	1	3312.3216	4.07	1	17.35	260.22		0	550-588	R.GSYSGSGSSYSGGGSYSGGGGGGHGSYSGGS:GYR.G		CID

Protein Report

Protein 2: keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens]
Accession: gi|119581085 **Score:** 325.57
Database: NCBIInr **MW [kDa]:** 63.30
Seq. Coverage [%]: 6.30 % **pl:** 5.00
No. of Peptides: 4

10	20	30	40	50	60	70	80	90	100	110	120
MSVRYSSSKH	YSSSRSGGGG	GGGCGGGGG	VSSLRISSSK	GSLGGGFSSG	GFSGGSFSG	SSGGGCFGGS	SGGYGGLGGF	GGGSFRGSYG	SSSFGGSYGG	SFGGGSFGGG	SFGGGSFGGG
130	140	150	160	170	180	190	200	210	220	230	240
GFGGGGFGGG	FGGGFGGDGG	LLSGNEKVTM	QNLNDRLAS	LDKVRALEES	NYELEGKIKE	WYEKHGNSHQ	GEPRDYSKY	KTIDDLKNQI	LNLITDNANI	LLQIDNARLA	ADDFRLKYEN
250	260	270	280	290	300	310	320	330	340	350	360
EVALRQSVEA	DINGLRRVLD	ELTLTKADLE	MQIESLTEEL	AYLKKNHEEE	MKDLRNVSTG	DVNVEMNAAP	GVDLTQLLNN	MRSQYEQLAE	QNRKDAAEAWF	NEKSKELTTE	IDNNIEQISS
370	380	390	400	410	420	430	440	450	460	470	480
YKSEITEIRR	NVQALEIEIQ	SQLALKQSLE	ASLAETEGRY	CVQLSQIQAQ	ISALEEQQLQ	IRAETECQNT	EYQQLLDIKI	RLENEIQTYR	SLLEGGSSSG	GGGRGGGSFG	GGYGGSSSGG
490	500	510	520	530	540	550	560	570	580	590	600
GSSGGGYGGG	HGGSSGGGYG	GGSSGGSSSG	GGYGGSSSGG	GHGSSSSGGY	GGGSSGGGGG	GYGGSSGGGG	SSSGGGYGGG	SSSGGHKSSS	SGSVGESSSK	GPRSAETSWD	TNKTRVIKTI
610	620	630									
IEEVAPDGRV	LSSMVESETK	KHYY									

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
141	1	1707.8014	17.11	1	21.25	118.95		0	41-59	K.GSLGGGFSSGGFSGGSFSR.G		CID
52	1	993.4991	-0.90	1	15.70	32.81		0	238-245	K.YENEVALR.Q		CID
38	3	1365.6576	13.37	1	15.55	99.34		0	323-333	R.SQYEQLAQNR.K		CID
35	3	1493.7592	16.66	1	15.25	74.47		1	323-334	R.SQYEQLAQNRK.D		CID

Protein 3: Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
Accession: K22E_HUMAN **Score:** 230.35
Database: SwissProt **MW [kDa]:** 65.40
Seq. Coverage [%]: 5.80 % **pl:** 8.85
No. of Peptides: 3

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MSCQISCKSR	GRGGGGGGFR	GFSSGSVVVS	GGSRRTSTSF	SCLSRHGGGG	GGFGGGGFGS	RSILVGLGGTK	SISISVAGGG	GGFGAAGGFG	GRGGGFGGGS	SFGGGSGFSG	GGFGGGGFGG
130	140	150	160	170	180	190	200	210	220	230	240
GRFGGGGGPG	GVGGLGGPGG	FGPGGYPGGI	HEVSVNQSL	QPLNVKVDPE	IQNVKAQERE	QIKTLNNKFA	SFIDKVRFLE	QQNQVLQTKW	ELLQQMNVGT	RPINLEPIFQ	GYIDSLKRYL
250	260	270	280	290	300	310	320	330	340	350	360
DGLTAERTSQ	NSELNNMQDL	VEDYKKKYED	EINKRTAAEN	DFVTLKKDVD	NAYMIKVELQ	SKVDLLNQEI	EFLKVLDAE	ISQIHQSVTD	TNVILSMDNS	RNLDLDSIIA	EVKAQYEEIA
370	380	390	400	410	420	430	440	450	460	470	480
QRSKEEAEAL	YHSKYEELQV	TVGRHGDSLK	EIKIEISELN	RVIQRLQGEI	AHVKKQCKNV	QDAIADAEQR	GEHALKDARN	KLNDLEEALQ	QAKEDLARLL	RDYQELMNVK	LALDVEIATY
490	500	510	520	530	540	550	560	570	580	590	600
RKLLEGEECR	MSGDLSSNVT	VSVTSSTISS	NVASKAAFEG	SGGRGSSSGG	GYSSGSSSYG	SGGRQSGSRG	GSGGGGSISG	GGYGSGGGSG	GRYGSGGGSK	GGISGSGGYG	SGGGKHSSGG
610	620	630	640								
GSRGGSSSGG	GYGSGGGGSS	SVKGSSGEAF	GSSVTFSFR								

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
70	1	1320.5862	2.57	1	16.60	129.28		0	46-61	R.HGGGGGGFGGGGFGSR.S		CID
111	1	1475.7923	4.78	1	17.95	68.12		0	198-209	R.FLEQQNQVLQTK.W		CID
34	1	1107.5510	7.31	1	15.25	32.95		0	354-362	K.AQYEEIAQR.S		CID

Protein 4: hornerin [Homo sapiens]
Accession: gi|28557150
Database: NCBI nr
Seq. Coverage [%]: 7.30 %

Score: 171.95
MW [kDa]: 48.60
pI: 10.10
No. of Peptides: 2

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
GSGSGHSSSY	EQHGSRSGQS	SRGEQHGSSS	GSSSSYGQHG	SGSRQSLGHG	QHGSQSGQSP	SPSRGRHSG	SGQSSSYSPY	GSGSGWSSSR	GPYESGSGHS	SGLGHRERSS	GQSSGYGQHG
130	140	150	160	170	180	190	200	210	220	230	240
SSSGHSSTHG	QHGSTSGQSS	SCGQHGAASSG	QSSSHGQHGS	GSSQSSGYGR	QGSQSGQSPG	HSQRGSGSRQ	SPSYGRHSG	SGRSSSSGQH	GSLGESSGF	GHHESSSQS	SSYSQHSGGS
250	260	270	280	290	300	310	320	330	340	350	360
GHSSGYGQHG	SRSGQSSRGE	RHGSSSGSSS	HYGQHSGSR	QSSGHGRQGS	GSGQSPSRGR	HGSLGHSSS	HGQHSGSGSR	SSSRGPYESR	SGHSSVFGQH	ESGSGHSSAY	SQHSGSGSHF
370	380	390	400	410	420	430	440	450	460	470	480
CSQGQHGSTS	GQSSTFDQEG	SSTGQSSSYG	HRGSGSSQSS	GYGRHAGSG	QSLSHGRHGS	GSGQSSSYGQ	HGSGSQSSG	YSQHSGSGGQ	DGYSYCKGGS	NHDGGSSGSY	FLSFPSSTSP
490	500										
YEYVQEQR	QRCY	FYQ									

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
29	1	1947.8917	-5.09	1	14.05	58.67		0	45-64	R.QSLGHGQHSGSGQSPSPSR.G		CID
30	1	1584.7156	0.41	1	14.65	113.28		0	91-106	R.GPYESGSGHSSGLGHR.E		CID

Protein 5: Chain A, Crystal Structure Of Atbag1 In Complex With Hsp70

Accession: gi|508123773

Database: NCBI nr

Seq. Coverage [%]: 7.70 %

Score: 165.44

MW [kDa]: 41.50

pI: 6.39

No. of Peptides: 2

10	20	30	40	50	60	70	80	90	100	110	120
PAVGIDLGT	YSCVGVFQHG	KVEIANDQG	NRTPSYVAF	TDTERLIGDA	AKNQVAMNPT	NTVFDARLI	GRRFDDAVVQ	SDMKHWPFMV	VNDAGRPKVQ	VEYKGETKSF	YPEEVSSMVL
130	140	150	160	170	180	190	200	210	220	230	240
TKMKEIAEAY	LGKTVTNAV	TVPAYFND	SRQATKDAGTI	AGLNVLRIIN	EPTAAAIAYG	LDKKVGAERN	VLIFDLGGGT	FDVSILTIED	GIFEVKSTAG	DTHLGGEDFD	NRMVNHFAIE
250	260	270	280	290	300	310	320	330	340	350	360
FKRKHKKDIS	ENKRAVRLR	TACERAKRTL	SSSTQASIEI	DSLYEGIDFY	TSITRARFEE	LNADLFRGTL	DPVEKALRDA	KLDKSQIHDI	VLVGSTRIIP	KIQKLLQDFF	NGKELNKSIN
370	380										
PDEAVAYGAA	VQAAILS										

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
186	1	1487.7207	13.06	1	30.85	66.25		0	33-45	R.TTPSYVAFTDTER.L		CID
175	1	1691.7357	6.01	1	28.00	99.19		0	217-232	K.STAGDTHLGGEDFDNR.M		CID

Protein 6: unnamed protein product [Homo sapiens]

Accession: gi|28193108

Database: NCBI nr

Seq. Coverage [%]: 6.10 %

Score: 156.86

MW [kDa]: 49.30

pI: 5.20

No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
MGRGTVILH	LKEDQTEYLE	ERRIKEIVKK	HSQFIGYPIT	LFVEKERDKE	VSDDEAEKE	DKEEKEKEE	KESEDKPEIE	DVGSDEEEK	KDGDKKKKK	IKEYIDQEE	LNKTKPIWTR
130	140	150	160	170	180	190	200	210	220	230	240
NPDDITNEEY	GEFYKSLTND	WEDHLAVKHF	SVEGQLEFRA	LLFVPRRAPF	DLFENRKKKN	NIKLYVRRVF	IMDNCEELIP	EYLNFIKGVV	DSEDLPLNIS	REMLQQSKIL	KVIRKNLVKK
250	260	270	280	290	300	310	320	330	340	350	360
CLELFTLAE	DKENYKFFYE	QFSKNIKLGI	HEDSQNRKKL	SELLRYTSA	SGDEMVSLLD	YCTRMKENQK	HIYYITGETK	DQVANSFAVE	RLRKHGLEVI	YMIEPIDEYC	VQQLKEFEGK
370	380	390	400	410	420						
TLVSVTKLEGL	ELPEDEEEKK	KQEEKTKFE	NLCKIMKDIL	EKKVEKVCEY	SIS						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
12	1	1833.8061	13.50	1	12.85	129.24		0	121-135	R.NPDDITNEEYGEFYK.S		CID

Protein 7: Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4

Accession: K1C14_HUMAN

Database: SwissProt

Seq. Coverage [%]: 7.40 %

Score: 116.61

MW [kDa]: 51.50

pI: 4.94

No. of Peptides: 3

Modification(s): Carbamidomethyl

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MTTCSRQFTS	SSSMKGSCGI	GGGIGGGSSR	ISSVLGGSC	RAPSTYGGGL	SVSSSRFSSG	GACGLGGGYG	GGFSSSSSSF	GSGFGGGYGG	GLGAGLGGGF	GGGFAGGDGL	LVGSEKVTMQ
130	140	150	160	170	180	190	200	210	220	230	240
NLNDRLASYL	DKVRALEEAN	ADLEVKIRDW	YQRQRPAEIK	DYSPYFKTIE	DLRKNILTAT	VDNANVLLQI	DNARLAADDF	RTKYETELNL	RMSVEADING	LRRVLDELTL	ARADLEMQIE
250	260	270	280	290	300	310	320	330	340	350	360
SLKEELAYLK	KNHEEEMNAL	RGQVGGDVNV	EMDAAPGVDL	SRIINEMRDQ	YERMAEKNRK	DAEEWFFTKT	EELNREVATN	SELVQSGKSE	ISELRRTMQN	LEIELQSQLS	MKASLENSLE
370	380	390	400	410	420	430	440	450	460	470	480
ETKGRYCMQL	AQIQEMIGSV	EEQLAQLRCE	MEQQNQEYKI	LLDVKTRLEQ	EIATYRRLLE	GEDAHLSSSQ	FSSGSQSSRD	VTSSSRQIRT	KVMDVHDGKV	VSTHEQVLRT	KN

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
31	1	1107.4845	833.42	1	15.70	16.21		0	31-41	R.ISSVLGGSCR.A	Carbamidomethyl: 10	CID
78	1	1425.6974	0.36	1	16.90	46.32		0	42-56	R.APSTYGGGLSVSSSR.F		CID
72	1	1122.5820	2.70	1	16.60	54.08		0	408-416	R.LEQEIATYR.R		CID

Protein 8: RecName: Full=Laminin subunit alpha-2; AltName: Full=Laminin M chain; AltName: Full=Laminin-12 subunit alpha; AltName: Full=Laminin-2 subunit alpha; AltName: Full=Laminin-4 subunit alpha; AltName: Full=Merosin heavy chain; Flags: Precursor

Accession: gi|215274259 **Score:** 109.48

Database: NCBIInr **MW [kDa]:** 343.70

Seq. Coverage [%]: 1.90 % **pl:** 5.99

Modification(s): Carboxymethyl, Propionamide **No. of Peptides:** 0

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MPGAAGVLLL	LLLSGGLGGV	QAQRPOQQRQ	SQAHQQRGLF	PAVLNLAENA	LITTNATCGE	KGPEMYCKLV	EHVPGQPVRN	PQCRICNQNS	SNPNQRHPIT	NAIDGKNTWW	QSPSIKNGIE
130	140	150	160	170	180	190	200	210	220	230	240
YHYVTITLDL	QQVFQIAYVI	VKAANSRPRG	NWILERSLDD	VEYKPQYHA	VTDTTECLTY	NIYPRTGPPS	YAKDDEVICT	SFYSKIHPLE	NGEIHISLIN	GRPSADDPSP	ELLEFTSARY
250	260	270	280	290	300	310	320	330	340	350	360
IRLRFQIRIT	LNADLMMFAH	KDPREIDPIV	TRRYYSVKD	ISVGGMCICY	GHARACPLDP	ATNKSRCCE	HNTCGDSCDQ	CCPGFHQKPW	RAGTFLTKTE	CEACNCHGKA	EECYDENVA
370	380	390	400	410	420	430	440	450	460	470	480
RRNLSLNIRG	KYIGGGVCIN	CTQNTAGINC	ETCTDGFFRP	KGVSPPNYPRP	CQPCCHCDPIG	SLNEVCVKDE	KHARRGLAPG	SCHCKTGFGG	VSCDRCARGY	TGYPDCKACN	CSSGLGSKNED
490	500	510	520	530	540	550	560	570	580	590	600
PCFGPCICKE	NVEGGDCSRC	KSGFFNLQED	NWKGCDCEFC	SGVSNRCQSS	YWTYGKIQDM	SGWYLTDLPG	RIRVAPQQDD	LDSPQQISIS	NAEARQALPH	SYWWSAPAPY	LGNKLPAVGG
610	620	630	640	650	660	670	680	690	700	710	720
QLTFTISYDL	EEEEEDTERV	LQLMIILEGN	DLSISTAQDE	VYLHPSEEHT	NVLLKKEESF	TIHGTHFPVR	RKEFMTVLAN	LKRVLQITY	SFGMDAIFRL	SSVNLESASV	YPTDGSIAAA
730	740	750	760	770	780	790	800	810	820	830	840
VEVCQCPPGY	TGSSCESCW	RHRRVNGTIF	GGICEPCQCF	GHAESCDDVT	GECLNCKDHT	GGPYCDKCLP	GFYGEPTKGT	SEDCQPCACP	LNIPSNFNSP	TCHLDRSLGL	ICDGCVPVGYT
850	860	870	880	890	900	910	920	930	940	950	960
GPRCERCAEG	YFGQPSVPGG	SCQPCQNDN	LDFSIPGSCD	SLSGSLICK	PGTTGRYCEL	CADGYFGDAV	DAKNCQPCRC	NAGGSFSEVC	HSQTGQCECR	ANVQGRQCDK	CKAGTFGLQS
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
ARGCVCPCNCN	SFGSKSFDCE	ESGQCWCQPG	VTGKKCDRCA	HGYFNFQEGG	CTACECSHLG	NNCDPKTGRC	ICPNTIGEK	CSKCAPNTWG	HSITTGCKAC	NCSTVGSLDF	QCNVNTGQCNC
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
CHPKFSGAKC	TECSRGHWN	PRCNLCDCFL	PGTDATTCD	ETKKCSCSDQ	TGQCTCKVNV	EGIHCDRCRP	GKFGLDKPN	LGCSSCYCFG	TTTQCSEAKG	LIRTWVTLKA	EQTILPLVDE
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
ALQHTTTTKGI	VFQHPDIVAH	MDLMREDLHL	EPFYWLPEQ	FEGKKLMAYG	GKLKYAIYFE	AREETGFSTY	NPQVIIRGGT	PTHARIIVRH	MAAPLIGQLT	RHEIEMTEKE	WKYYGDDPRV
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
HRTVTREDFL	DILYDIHYIL	IKATYGNFMR	QSRISEISME	VAEQGRGTTM	TPPADLIEKC	DCPLGYSGLS	CEACLPGFYR	LRSQPGGRTP	GPTLGTVCVPC	QCNHSSSLCD	PETSIQNCQ
1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
HHTAGDFCER	CALGYYGIVK	GLPNDCCQCA	CPLISSSNNE	SPSCVAEGLD	DYRCTACPRG	YEGQYCERCA	PGYTGSPGNP	GGSCQCECED	PYGSLPVPCD	PVTGFCTCRP	GATGRKCDGC
1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680
KHWHAREGWE	CVFCGDECTG	LLGLDLARLE	QMVMSINLTG	PLPAPYKMLY	GLENMTQELK	HLLSPQRAPE	RLIQLAEGNL	NTLVTEMNEL	LTRATKVTD	GEQTGQDAER	TNTRAKSLGE
1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
FIKELARDAE	AVNEKAIKLN	ETLGTREDAF	ERNLEGLQKE	IDQMIKELRR	KNLETQKEIA	EDELVAEAL	LKKVKKLFG	SRGENEEMEK	DLREKLADYK	NKVDDAWDLL	REATDKIREA
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920
NRLFAVNQKN	MTALEKKKEA	VESGKRQIEN	TLKEGNLID	EANRLADEIN	SIIDYVEDIQ	TKLPPMSEEL	NDKIDDLSEQ	IKDRKLAQKV	SQAESHAQAL	NDSSAVLDGI	LDEAKNISFN
1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040
ATAAFKAYSN	IKDYIDEAEK	VAKEAKDLAH	EATKLATGPR	GLLKEDAKGC	LQKSFRILNE	AKKLANDVKE	NEDHLNGLKT	RIENADARNG	DLLRTLNDTL	GKLSAIPNDT	AAKLQAVKDK
2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160
ARQANDTAKD	VLAQITELHQ	NLDGLKKNYN	KLADSVAKTN	AVVKDPSKNK	IIADADATVK	NLEQEADRLI	DKLKPIKELE	DNLKKNISEI	KELINQARKQ	ANSIKVSVSS	GGDCIRTYKP
2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
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Protein 9: alpha globin chain, partial [Homo sapiens]

Accession: gi|546234980

Database: NCBIInr

Seq. Coverage [%]: 29.40 %

Score: 99.75

MW [kDa]: 5.70

pI: 7.78

No. of Peptides: 1

10	20	30	40	50	60
MVLYPADKTN	VKAAWGK	VGA	HAGEYGAEAL	ERMFLSFPTT	KTYFPDFDLS H

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
16	2	1529.7405	4.05	1	14.20	99.75		0	18-32	K.VGAHAGEYGAEALER.M		CID

Protein 10: Oncostatin-M OS=Homo sapiens GN=OSM PE=1 SV=2

Accession: ONCM_HUMAN

Database: SwissProt

Seq. Coverage [%]: 3.20 %

Score: 80.81

MW [kDa]: 28.50

pI: 11.75

No. of Peptides: 2

Modification(s): Deamidated

10	20	30	40	50	60	70	80	90	100	110	120
MGVLLTQRTL	LSIVLALLFP	SMASMAAIGS	CSKEYRVLLG	QLQKQTDLMQ	DTSRLDPYI	RIQGLDVPKL	REHCRERPGA	FPSEETLRGL	GRRGFLQTLN	ATLGCVLHRL	ADLEQRLPKA
130	140	150	160	170	180	190	200	210	220	230	240
QDLERSGLNI	EDLEKLQMAR	PNILGLRNNI	YCMAQLLDNS	DTAEPKAGR	GASQPPTPTP	ASDAFQRLKE	GCRFLHGYHR	FMHSVGRVFS	KWGESPQRSR	RHSPHQALRK	GVRRTSPSRK
250	260										
GKRLMTRGQL	PR										

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
67	2	870.5533	1200.94	1	17.35	36.69		0	62-69	R.IQGLDVPK.L		CID
37	1	870.5390	52.66	1	17.50	44.12		0	62-69	R.IQGLDVPK.L	Deamidated: 2	CID

Protein 11: unnamed protein product [Homo sapiens]

Accession: gi|194388808

Database: NCBIInr

Seq. Coverage [%]: 4.70 %

Score: 76.03

MW [kDa]: 23.20

pI: 9.69

No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
MGKVKVGNG	FGRIGRLVTR	AAFNSGKVDI	VAINDPFIDL	NYMVYMFQYD	STHGKFHGTV	KAENGKLVIN	GNPITIFQER	DPSKIKWGDA	GAEYVVESTG	VFTTMEKAGA	HLQGGAKRVI
130	140	150	160	170	180	190	200	210	220		
ISAPSADAPM	FVMGVNHEKY	DNSLKIISNA	SCTTNCLAPL	AKVIHDNFGI	VEGLMTTVHA	ITATLREAHW	HGLPCPHCQR	VSGGPDLPSP	KTCQI		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
17	1	1032.5970	2.07	1	14.95	76.03		1	4-13	K.VKVG VNGFGR.I		CID

Protein 12: Muellerian-inhibiting factor OS=Homo sapiens GN=AMH PE=1 SV=3

Accession: MIS_HUMAN

Database: SwissProt

Seq. Coverage [%]: 1.60 %

Score: 71.06

MW [kDa]: 59.20

pI: 7.93

No. of Peptides: 2

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MRDLPLTSLA	LVLSALGALL	GTEALRAEEP	AVGTSGLIFR	EDLDWPPGSP	QEPLCLVALG	GDSNGSSSPL	RVVGALSAYE	QAFLGAVQRA	RWGPRDLATF	GVCNTGDRQA	ALPSLRRLLGA
130	140	150	160	170	180	190	200	210	220	230	240
WLRDPGGQRL	VVLHLEEVTV	EPTPSLRFQE	PPPGGAGPPE	LALLVLYPGP	GPEVTVTRAG	LPGAQSLCPS	RDTRYLVLA	DRPAGAWRGS	GLALTLOPRG	EDSRLSTARL	QALLFGDDHR
250	260	270	280	290	300	310	320	330	340	350	360
CFTRMTPALL	LLPRSEPAPL	PAHQQLDTVP	FPPPRPSAEL	EESPPSADPF	LETLTRLVRA	LRVPPARASA	PRLALDPDAL	AGFPQGLVNI	SDPAALERLL	DGEEPLLLLL	RPTAATTGDP
370	380	390	400	410	420	430	440	450	460	470	480
APLHDPTSAP	WATALARRVA	AELQAAAAEL	RSLPGLPPAT	APLLARLLAL	CPGGPGGLGD	PLRALLLLKA	LQGLRVEWRG	RDPRGPGRAG	RSAGATAADG	PCALRELSVD	LRAERSVLIP
490	500	510	520	530	540	550	560	570			
ETYQANNCQG	VCGWPQSDRN	PRYGNHVLL	LKMQVRGAAL	ARPPCCVPTA	YAGKLLISLS	EERISAHHPV	NMVATECGCR				

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
81	2	856.5277	1195.84	1	17.35	32.45		0	109-116	R.QAALPSLR.R		CID
104	1	1011.6412	34.99	1	17.80	38.61		1	109-117	R.QAALPSLRR.L		CID

Protein 13: PREDICTED: radial spoke head 1 homolog isoform X1 [Homo sapiens]

Accession: gi|530419415

Database: NCBIInr

Seq. Coverage [%]: 4.80 %

Score: 66.66

MW [kDa]: 30.80

pI: 4.27

No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
MSDLGSEELE	EEGENDIGGI	YKFKNGARYI	GEYVRNKKHG	QGTFIYPDGS	RYEGEWANDL	RHGHGVYYYI	NNDTYTGEWF	AHQRHGQGTY	LYAETGSKYV	GTWVNGQQEG	TAEIHLNHR
130	140	150	160	170	180	190	200	210	220	230	240
YQGKFLNKNP	VGPGKYVFDV	GCEQHGEYRL	TDMERGEEEE	EEELVTVVPK	WKATQITELA	LWTPTLPKPK	TSTDGPGQDA	PGAESAGEPG	EEAQALLEGF	EGEMDMRPGD	EDADVLREES
250	260	270	280								
REYDQEEFRY	DMDEGNINSE	EEETRQSDLQ	D								

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
19	1	1434.6867	7.39	1	14.95	66.66		0	39-51	K.HGQGTFIYPDGSR.Y		CID

Protein 14:	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Homo sapiens GN=PREX2 PE=2 SV=1	
Accession:	PREX2_HUMAN	Score: 64.74
Database:	SwissProt	MW [kDa]: 182.50
Seq. Coverage [%]:	1.40 %	pl: 7.60
		No. of Peptides: 2
Modification(s):	Carbamyl, Oxidation, Deamidated	

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MSDSRGDSR	AESAKDLEKQ	LRLRVCVLS	LQKTERDVVG	TLEFLVSAFL	HRMNQCAASK	VDKNVTEETV	KMLFSNIEDI	LAVHKEFLKV	VEECLHPEPN	AQQEVGTCFL	HFKDKFRIYD
130	140	150	160	170	180	190	200	210	220	230	240
EYCSNHEKAQ	KLLELNLKIR	TIRTFLLNCM	LLGGRKNTDV	PLEGYLVTP	QRICKYPLIL	KELLKRTPRK	HSDYAAMEA	LQAMKAVCSN	INEAKRQMEK	LEVLEEWQSH	IEGWEGSNIT
250	260	270	280	290	300	310	320	330	340	350	360
DTCTEMLMCG	VLLKISSGNI	QERVFFLFDN	LLVYCKRKR	RLKNSKASTD	GHRYLFRGRI	NTEVMEVENV	DDGTADFHSS	GHIVVNGWKI	HNTAKNKWFV	CMAKTPEEKH	EWFEAILKER
370	380	390	400	410	420	430	440	450	460	470	480
ERRKGLKLGM	EQDTWVMISE	QGEKLYKMMC	RQGNLIKDRK	RKLTTFPKCF	LGSEFVSWLL	EIGEIHRRPE	GVHLGQALLE	NGIIHHVTDK	HQFKPEQMLY	RFRYDDGTFY	PRNEMQDVIS
490	500	510	520	530	540	550	560	570	580	590	600
KGVRLYCRLH	SLFTPVIRDK	DYHLRTYKSV	VMANKLIDWL	IAQGDCRTRE	EAMIFGVGLC	DNGFMHHVLE	KSEFKDEPLL	FRFFSDEEME	GSNMKHLRMK	HDLKVVENVI	AKSLIKSNE
610	620	630	640	650	660	670	680	690	700	710	720
GSYGFGLGDK	NKVPIIKLVE	KGSNAEMAGM	EVGKKIFAIN	GDLVFMRFN	EVDCLFLKSL	NSRKPLRLV	STKPRETVKI	PDSADGLGFQ	IRGFGPSVH	AVGRGTVA	AGLHPQCII
730	740	750	760	770	780	790	800	810	820	830	840
KVNGINVSKE	THASVIAHVT	ACRKYRRTK	QDSIQWVYNS	IESAQEDLQK	SHSKPPGDEA	GDAFDCKVEE	VIDKFNTMAI	IDGKKEHVS	TVDNVHLEYG	VVYEYDSTAG	IKCNVVEKMI
850	860	870	880	890	900	910	920	930	940	950	960
EPKGFSLTA	KILEALAKSD	EHFVNCTSL	NSLNEVPTD	LQSKFSALCS	ERIEHLCQRI	SSYKFSRVL	KNRAWPTFKQ	AKSKISPLHS	SDFCPTNCHV	NVMEVSYPKT	STSLGSAFGV
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
QLDSRKHNHSH	DKENKSEGG	KLSPMVYIQH	TITMTAAPSG	LSLGQQDGHG	LRYLKLEEDL	ETQDIYQKLL	GKLQTALKEV	EMCVCQIDDL	LSSITYSPKL	ERKTSEGIIP	TDSNEKGER
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
NSKRVCFNVA	GDEQEDSGHD	TISNRDSYSD	CNSNRNSIAS	FTSICSSQCS	SYFHSDEMDS	GDELPLSVRI	SHDKQDKIHS	CLEHLFSQVD	SITNLLKGQA	VVRAFDQTKY	LTPGRGLQEF
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
QQEMEPLKSC	PKRLRLHIQ	DPWNLPSVR	TLAQNIRKFV	EEVKCRLLLA	LLEYSDETQ	LRRDMVFCQT	LVATVCAFSE	QLMAALNQMF	DNSKENEMET	WEASRRWLDQ	IANAGVLFHF
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
QSLSPNLTD	EQAMLEDTLV	ALFDLEKVSF	YFKPSEEEPL	VANVPLTYQA	EGSRQALKVY	FYIDSYHFEQ	LPQRLKNGGG	FKIHPVLFAQ	ALESMEGYYY	RDNVSVEEFQ	AQINAASLEK
1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
VKQYNQKLRA	FYLDKSNSP	NSTSKAAYVD	KLMRPLNALD	ELYRLVASFI	RSKRTAACAN	TACSASGVGL	LSVSSELNCR	LGACHIIMCS	SGVHRCTLSV	TLEQAAILAR	SHGLPPRYIM
1570	1580	1590	1600	1610							
QATDVMRKQG	ARVQNTAKNL	GVRDRTPQSA	PRLYKLCEPP	PPAGEE							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
151	1	1724.8605	537.10	1	30.55	38.87		1	141-155	R.TIRTFLLNCMLLGGK	Oxidation: 10	CID
52	1	993.4991	-12.21	1	15.70	25.87		1	1443-1449	K.QYNQKLRA	Carbamyl: 5; Deamidated: 1	CID

Protein Report

Protein 15:	MAX gene-associated protein OS=Homo sapiens GN=MGA PE=1 SV=3		
Accession:	MGAP_HUMAN	Score:	57.27
Database:	SwissProt	MW [kDa]:	331.60
Seq. Coverage [%]:	0.80 %	pI:	6.35
		No. of Peptides:	2

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MEEKQIIILA	NQDGGTVAGA	APTFFVILKQ	PGNGKTDQGI	LVTNQDACAL	ASSVSSPVKS	KGKICLPADC	TVGGITVTLD	NNSMWNEFYH	RSTEMILTKQ	GRRMFPYCRY	WITGLDSNLK
130	140	150	160	170	180	190	200	210	220	230	240
YILVMDISPV	DNHRYKWNDR	WWEPSGKAEP	HVLGRVFTHP	ESPSTGHYWM	HQPVSFYKLK	LTNNTLDQEG	HIILHSMHRY	LPRLHLVPAE	KAVEVIQLNG	PGVHTFTFPQ	TEFFAVTAYQ
250	260	270	280	290	300	310	320	330	340	350	360
NIQITQLKID	YNPFAKGRD	DGLNNKPQRD	GKQKNSSDQE	GNNISSSSGH	RVRLTEGQGS	EIQPGDLPL	SRGHETSGKG	LEKTSINIKR	DFLGFMDTDS	ALSEVPQLKQ	EISECLIASS
370	380	390	400	410	420	430	440	450	460	470	480
FEDDSRVASP	LDQNGS FNVV	IKEEPLDDYD	YELGECPEGV	TVKQEETDEE	TDVYSNSDD	PILEKQLKRH	NKVDNPEADH	LSSKWLPSSP	SGVAKAKMFK	LDTGKMPVVY	LEPCAVTRST
490	500	510	520	530	540	550	560	570	580	590	600
VKISELPDNM	LSTSRKDKSS	MLAELEYLPT	YIENSNETAF	CLGKESENGL	RKHSPDLRVV	QKYPILLKEPQ	WKYPDISDSI	STERILDDSK	DSVGDLSLGG	EDLGRKRTTM	LKIATAAKVV
610	620	630	640	650	660	670	680	690	700	710	720
NANQNASPNV	PGKRGRPRKL	KLCKAGRPPK	NTGKSLISTK	NTPVSPGSTF	PDVKPDLEDV	DGVLFVSFES	KEALDIHAVD	GTTESSSLQ	ASTTNDSSGYR	ARISQLEKEL	IEDLKTIRHK
730	740	750	760	770	780	790	800	810	820	830	840
QVIHPGLQEV	GLKLNSVDPT	MSIDLKYLGV	QLPLAPATSF	PFWNLTGTNP	ASPDAGFPFV	SRTGKTNDFT	KIKGWRGKFH	SASASRNEG	NSESLKNRS	AFCSDKLDEY	LENEGKLMET
850	860	870	880	890	900	910	920	930	940	950	960
SMGFSSNAPT	SPVVYQLPTK	STSYVRTLDS	VLKQSTISF	STSYSLKPHS	VPPVSRKAKS	QNRQATFSGR	TKSSYKSILP	YPVSPKQKYS	HVILGDKVTK	NSSGIISENQ	ANNFVPTLD
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
ENIFPKQISL	RQAQQQQQQQ	QGSRRPGLSK	SQVKLMDLED	CALWEGKPRT	YITEERADVS	LTLLTQAAS	LTKPIHTII	RKRAPPCCND	FCRLGCVCS	LALRKQPAH	CRRPDCMFGC
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
TCLKRKVVIV	KGSKTKHFQ	RKAAHRDPVF	YDTLGEEARE	EEGIREEEE	QLKEKKKRRK	LEYTICETEP	EQPVRHYPLW	VKVEGEVDPE	PVYIPTPSVI	EPMKPLLLPQ	PEVLSPTVKG
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
KLLTGKISPR	SYTPKPNPVI	REEDKDPVYL	YFESMMTCAR	VRVYERKKED	QRQPSSSSSP	SPSFQQQTSC	HSSPENHNNA	KEPDSEQQPL	KQLTCDLEDD	SDKLQEKSWK	SSCNEGESS
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
TSYMHQRSPG	GPTKLIIEIS	DCNWEEDRNK	ILSILSQHIN	SNMPQSLKVG	SFIIELASQR	KSRGEKNPPV	YSSRVKISMP	SCQDQDDMAE	KSGSETPDGP	LSPGKMEDIS	PVQTDALDSV
1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
RERLHGKGL	PFYAGLSPAG	KLVAIKRKPS	SSTSGLIQVA	SNAKVAASRK	PRTLLPSTSN	SKMASSSGTA	TNRPGKNLKA	FVPAKRPIAA	RPSPGGVFTQ	FVMSKVGALQ	QKIPGVSTPQ
1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680
TLAGTQKFSI	RPSPVMVTP	VVSSEPVQVC	SPVTAAVTTT	TPQVFLENTT	AVTPMTAISD	VETKETTYSS	GATTGTGVEV	SETNTSTSVT	STQSTATVNL	TKTTGITTPV	ASVAFPKSLV
1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
ASPSTITLPIV	ASTASTSLVV	VTAASSSMV	TTPTSSLGVS	PIILSGINGS	PPVSQRPENA	AQIPVATPQV	SPNTVKRAGP	RLHPNGQIV	QLLPLHLRGL	SNTQPNLQPV	MFRNPGSVMG
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920
IRLPAPSKPS	ETPPSSSTSS	AFSVMNPVIQ	AVGSSAVNV	ITQAPSLSS	GASFVSQAGT	LTLRISPPEP	QSFASKTGSE	TKITYSSGGQ	PVGTASLIPL	QSGSFALLQL	PGQKVPSSI
1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040
LQHVASLQMK	RESQNPQKD	ETNSIKREQE	TKKVLQSEGE	AVDPEANVIK	QNSGAATSEE	TLNDSLEDGR	DHLDEECLPE	EGCATVKPSE	HSCITGSHTD	QDYKDVNEEY	GARNRKSSKE
2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
12	1	1833.8061	-71.63	1	12.85	20.30		2	483-498	K.ISELPDNMLSTSRKDK.S		CID
54	1	1027.5137	-66.69	1	16.90	36.97		1	2474-2481	K.KLEYIYAK.Q		CID

Protein 16: hCG2039963 [Homo sapiens]

Accession: gi|119606679

Database: NCBIInr

Seq. Coverage [%]: 22.50 %

Score: 54.57

MW [kDa]: 7.90

pI: 10.79

No. of Peptides: 1

Modification(s): Carbamidomethyl, Carboxymethyl, Deamidated

10	20	30	40	50	60	70	80	90
AGAFGCSVAT	RGPGGLTRQQ	DSCMGIGDHG	SAAGARLSSR	PADDGVSLCR	AGWRAMVPSW	ITAINLCLFP	GSSDSPASSS	

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
124	1	1819.8843	624.03	1	22.75	54.57		0	19-36	R.QQDSCMGIGDHGSAAGAR.L	Carbamidomethyl: 5; Deamidated: 2	CID

Protein 17: PREDICTED: nuclear respiratory factor 1 isoform X3 [Homo sapiens]

Accession: gi|530385993

Database: NCBIInr

Seq. Coverage [%]: 2.50 %

Score: 52.48

MW [kDa]: 51.30

pI: 5.18

No. of Peptides: 1

Modification(s): Deamidated

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MEEHGVQTQTE	HMATIEAHAV	AQQVQQVHVA	TYTEHSMLSA	DEDSPPSPED	TSYDDSDILN	STAADDEVTAH	LAAAGPVGMA	AAAAVATGKK	RKRPHVFESN	PSIRKRQQTR	LLRKLRLATLD
130	140	150	160	170	180	190	200	210	220	230	240
EYTTTRVGQQA	IVLCISPSKP	NPVFKVFGAA	PLENVVRKYK	SMILEDLESA	LAEHAPAPQE	VNSELPPLTI	DGIPVSVDKM	TQAQLRAFIP	EMLKYSTGRG	KPGWGKESCK	PIWWPEDIPW
250	260	270	280	290	300	310	320	330	340	350	360
ANVRSDVRTE	EQKQRVSWTQ	ALRTIVKNCY	KQHGRELLY	AFEDQQTQTQ	ATATHSIAHL	VPSQTVVQTF	SNPDGTVSLI	QVGTGATVAT	LADASELPTT	VTVAQVNYSA	VADGEVEQNW
370	380	390	400	410	420	430	440	450	460	470	480
ATLQGGEMTI	QTTQASEATQ	AVASLAEAAV	AASQEMQQGA	TVTMAINSEA	AAHAVATLAE	ATLQGGGQIV	LSGETAAAVG	ALTGVQDANA	PHRVFHLALP	TALAWGPPEI	LKSTSVSAGQ
490											
H											

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
71	1	1439.8188	739.44	1	30.85	52.48		0	93-104	K.RPHVFESNPSIR.K		CID

Protein 18: Fibronectin type III domain-containing protein 1 OS=Homo sapiens GN=FNDC1 PE=1 SV=4
Accession: FNDC1_HUMAN **Score:** 50.64
Database: SwissProt **MW [kDa]:** 205.40
Seq. Coverage [%]: 0.90 % **pI:** 9.79
No. of Peptides: 0

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MAPEAGATLR	APRRLSWAAL	LLLAALLPVA	SSAAASVDHP	LKPRHVKLLS	TKMGLKVTPD	PPKDATSRPV	EHYNIAYGKS	LKSLKYIKVN	AETYSFLIED	VEPGVVYFVL	LTAENHSGVS
130	140	150	160	170	180	190	200	210	220	230	240
RPVYRAESPP	GGEWIEIDGF	PIKGPFPNE	TVTEKEVPNK	PLRVRVRSSD	DRLSVAWKAP	RLSGAKSPRR	SRGFLLGYGE	SGRKMNYVPL	TRDERTHEIK	KLASESVYVV	SLQSMNSQGR
250	260	270	280	290	300	310	320	330	340	350	360
SQPVYRAALT	KRKISEEDEL	DVPDDISVRV	MSSQSVLVSW	VDPVLEKQKK	VVASRQYTVR	YREKGELARW	DYKQIANRRV	LIENLIPDTV	YFAVRISQG	ERDQKSTSV	FQRTPEASPT
370	380	390	400	410	420	430	440	450	460	470	480
TAPENLVNWP	VNGKPTVVAA	SWDALPETEG	KVKEYILSYA	PALKPFGAKS	LTPYDGTSTA	LVDGLQPGER	YLFKIRATNR	RGLGPHSKAF	IVAMPTTSTA	DVEQNTEDNG	KPEKPEPSSP
490	500	510	520	530	540	550	560	570	580	590	600
SPRAPASSQH	PSVPASPQGR	NAKDLLLLDK	NKILANGGAP	RKPQLRAKKA	EELDLQSTEI	TGEEELGSRE	DSPMSPSDTQ	DQKRTLPPPS	RHGHSVVAPG	RTAVRARMPA	LPRREGVDKP
610	620	630	640	650	660	670	680	690	700	710	720
GFSLATQPRP	GAPPSASASP	AHHASTQGTS	HRPSLPASLN	DNDLVDSDSD	ERAVGSLHPK	GAFAPQPRPAL	SPSRQSPSSV	LRDRSSVHPG	AKPASPARRT	PHSGAAEEDS	SASAPPSRLS
730	740	750	760	770	780	790	800	810	820	830	840
PPHGGSSRLI	PTQPHLSSPL	SKGGKDGEDA	PATNSNAPSR	STMSSSVSSH	LSSRTQVSEG	AEASDGESHG	DGDREDGGRQ	AEATAQTLRA	RPASGHFHLL	RHKPFAANGR	SPSRFSIGRG
850	860	870	880	890	900	910	920	930	940	950	960
PRLQPSSSPQ	STVPSRAHPR	VPSHSDSHPK	LSSGIHGDEE	DEKPLPATVV	NDHVPSSSRQ	PISRGWEDLR	RSPQRGASLH	RKEPIPENPK	STGADTHPQG	KYSSLASKAQ	DVQQSTDADT
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
EGHSPKAQPG	STDRHASPAR	PPAARSQQHP	SVPRRMTPGR	APQQQPPPVV	ATSQHHPGPQ	SRDAGRSPSQ	PRLSLTQAGR	PRPTSQGRSH	SSSDPYTASS	RGMLPTALQN	QDEDAQGSYD
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
DDSTEVEAQD	VRAPAAHARA	KEAAASLPKH	QQVESPTGAG	AGGDHRSQRG	HAASPARPSR	PGGPQSRARV	PSRAAPGKSE	PPSKRPLSSK	SQQSVSAEDD	EEEDAGFFKG	GKEDLLSSSV
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
PKWPSSSTPR	GGKDADGSLA	KEEREPAIAL	APRGGSLAPV	KRPLPPPPGS	SPRASHVPSR	LPPRSAAATVS	PVAGTHPWPQ	YTTRAPPGHF	STTPMLSLRQ	RMMHARFRNP	LSRQPAPPSY
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
RQGYNGRPNV	EGKVLPGSNG	KPNGQRIING	PQGTKWVVDL	DRGLVLNAEG	RYLQDSHGPN	LRIKLGGDGR	TIVDLEGTVP	VSPDGLPLFG	QGRHGTPLAN	AQDKPILSLG	GKPLVGLLEVI
1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560
KKTTHPPTTT	MQPTTTTTPPL	PTTTTPRPTT	ATTRRTTTTR	RTTTRRPTTT	VRTTTRTTTT	TTPTPTTPIP	TCPPGTLERH	DDDGNLIMSS	NGIPECYAE	DEFSGLETDT	AVPTEEAYVI
1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680
YDEDEYEFETS	RPPTTTEPST	TATTPRVIPE	EGAISFPPEE	EFDLAGRKRF	VAPYVTVYLNK	DPSAPCSLTD	ALDHFQVDSL	DEIIPNDLKK	SDLPPQHAPR	NITVVAVEGC	HSFVIDVDWK
1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800
ATPGDVVTGY	LVYSASYEDF	IRNKWSTQAS	SVTHLPIENL	KPNTRYFFKV	QAQNPFGYGP	ISPSVSFVTE	SDNPLLVVRP	PGGEPIWIPF	AFKHDPSTYT	CHGRQYVKRT	WYRKFGVVVL
1810	1820	1830	1840	1850	1860	1870	1880	1890	1900		
CNSLRKYIYL	SDNLKDTFYS	IGDSWGRGED	HCQFVDSHLD	GRTGPQSYVE	ALPTIQGYR	QYRQEPVRFG	NIGFGTPYYY	VGWYECGVSI	PGKW		

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
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Protein Report

Protein 19: COL1A1 and PDGFB fusion transcript [Homo sapiens]
Accession: gi|3288487 **Score:** 50.41
Database: NCBIInr **MW [kDa]:** 37.00
Seq. Coverage [%]: 5.10 % **pl:** 5.09
No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
ALLVPLELVV	PPETVVSIVP	PALLALLAPL	VLNANLVKA	NLVMLVPKAM	LVPLGLPDPL	DPLAPLVMLV	LLEPKVLAAA	LVPLVLLVSL	VLLAESVLLA	PLEMLDPLAL	LVLLAKKAAK
130	140	150	160	170	180	190	200	210	220	230	240
VPVVRLLALD	VLVKLVPVLP	LALLARKDPL	VLMVLLVLLV	LPGLKVLLDS	VVWSACLVRE	EREASLVFLA	PLVNLANKVP	LEQVVNVVPP	VPWAPLDWLD	PLVNLVVRGL	LLPKVPLDET
250	260	270	280	290	300	310	320	330	340	350	360
VLLAPRVTVV	RPAPLDPLVL	WCSGAPGPVG	PAGKSGDRGE	TGPAGPAGPV	GPVGARGPAG	PQGPRGDKGE	TGEQGDRGIK	GHRGFSGLQG	PPGPPGDPIP	EELYEMLSDH	SIRSF

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
114	1	1546.8081	7.02	1	17.80	50.41		0	279-296	R.GETGPAGPAGPVGPVGAR.G		CID

Protein 20: unnamed protein product [Homo sapiens]
Accession: gi|7022948 **Score:** 47.85
Database: NCBIInr **MW [kDa]:** 49.00
Seq. Coverage [%]: 4.00 % **pl:** 9.90
No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
MKNALIPRIK	NACLQTSSLA	VRVNSLVCLG	KILEYLDKWF	VLDLILPFLQ	QIPSKEPAVL	MGILGIYKCT	FTHKKLGITK	EQLAGKVLPH	LIPLSIENNL	NLNQFNSFIS	VIKEMLNRL
130	140	150	160	170	180	190	200	210	220	230	240
SEHKTKLEQL	HIMQEQQKSL	DIGNQMNVE	EMKVTNIGNQ	QIDKVFNNIG	ADLLTGSESE	NKEDGLQNKH	KRASLTLEEK	QKLAKEQEQA	QKLKSQQPLK	PQVHTPVATV	KQTKDLTDTL
250	260	270	280	290	300	310	320	330	340	350	360
MDNMSLTSL	SVSTPKSSAS	STFASVPSMG	IGMMFSTPTD	NTKRNLTNGL	NANMGFQTS	FNMPVNTNQ	FYSSPSTVGV	TKMTLGTPPT	LPNFNALSVP	PAGAKQTQQR	PTDMSALNNL
370	380	390	400	410	420	430	440	450			
FGPQKPKVSM	NQLSQQKPNQ	WLNQFVPPQG	SPTMGSSVMG	TQMNVIQSA	FGMQGNPFFN	PQNFAPPTT	MTNSSASND	LKDLEF			

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
75	1	1907.9394	2.55	1	29.95	47.85		0	165-182	K.VFNNIGADLLTGSESENK.E		CID

Protein 21: Tetratricopeptide repeat protein 34 OS=Homo sapiens GN=TTC34 PE=2 SV=2

Accession: TTC34_HUMAN

Database: SwissProt

Seq. Coverage [%]: 1.60 %

Score: 46.12

MW [kDa]: 60.90

pI: 7.22

No. of Peptides: 0

10	20	30	40	50	60	70	80	90	100	110	120
MLQSRPRAGP	SRAQGRREAA	ETGGPTTQEG	VACGVHQLAT	LLMELDSEDE	ASRLAADAL	YRLGRLEETH	KALLVALSRR	PQAAPVLARL	ALLQLRRGFF	YDANQLVKKL	VQSGDTACLQ
130	140	150	160	170	180	190	200	210	220	230	240
PTLDVFCHEP	RQLLQGHCHA	RALAILRARP	GGADGRVHTK	EATAYLSLAI	FAAGSQASES	LLARARCYGF	LGQKKTAMFD	FNTVLRAEPG	NVQALCGRAL	VHLALDQLQE	AVDDIVSALK
250	260	270	280	290	300	310	320	330	340	350	360
LGPPTVVPPEL	RSIKPEAQAL	ITQGLYSHCR	ALLSQLPDTG	APLEDKDTQG	LLAVGEALIK	IDSGQPHWHL	LLADILMAQG	SYEEAGTHLE	KALHRAPTSE	AARARLGLLQ	LKKGDVPGAA
370	380	390	400	410	420	430	440	450	460	470	480
RDLQSLAEVD	APDLSCILLHL	LEASERQSLA	QAAAEAGTL	LDAGQPRQAL	GYCSLSVLAS	GSSACHLRRLR	ATCLAELQEF	GRALRDLHDV	LQEALGDGDL	PRRAEDFCRQ	GRLLLSLGDE
490	500	510	520	530	540	550	560	570			
AAAAGAFQAQ	LKLAPSLAQN	SLCRQPGRAP	TARMFLLRGQ	CCLEEQRHAE	AWTAVESGLL	VDPDHRGLKR	LKARIRREAS	SGCWLQ			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
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Protein 22: fibronectin type III domain containing 3B, isoform CRA_d [Homo sapiens]

Accession: gi|119598879

Database: NCBIInr

Seq. Coverage [%]: 7.40 %

Score: 45.53

MW [kDa]: 45.30

pI: 8.61

No. of Peptides: 1

Modification(s): Carbamyl, Deamidated

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MYVTMMMTDQ	IPLLELPPLLN	GEVAMMPHLV	NGDAAQQVIL	VQVNPGETFT	IRAEDGTLQC	IQGPAEVPMM	SPNGSIPPIH	VPPGYISQVI	EDSTGVRRVV	VTPQSPECYP	PSYPSAMSPT
130	140	150	160	170	180	190	200	210	220	230	240
HHLPPYLTHH	PHFIHNSHTA	YYPPVTGPGD	MPPQFFPQHH	LPHTIYGEQE	IIPFYGMSSY	ITREDQYSKP	PHKKLKDRQI	DRQNRLNSPP	SSIIKSSCTT	VYNGYGKGHS	GGSGGGGSGS
250	260	270	280	290	300	310	320	330	340	350	360
GPGIKKTERR	ARSSPKSND	DLQEYELEVK	RVQDILSGIE	KPQVRTRPTD	KSKSMILTPV	YAMYNVKGGS	CSEPVSFTH	SCAPECPFPF	KLAHRSSSL	TLQWKAPIDN	GSKITNYLLE
370	380	390	400	410							
WDENVLYRMP	PLLFMSPEAL	GRYLRSVLI	LKATVCQLVD	PVHFWS							

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
67	1	2717.0836	-37.53	1	16.45	45.53		1	216-245	K.SSCTTVYNGYGKGHSGGSGGGSGSGPGIK.K	Carbamyl: 12; Deamidated: 8	CID

Protein 23: unnamed protein product [Homo sapiens]

Accession: gi|47077801

Database: NCBIInr

Seq. Coverage [%]: 1.90 %

Score: 41.19

MW [kDa]: 84.40

pI: 6.41

No. of Peptides: 1

Protein Report

10	20	30	40	50	60	70	80	90	100	110	120
MAYHEKPVLP	PPLIILSHIV	SLFCCICKRR	KKDKTSDGPK	LFLTEEDQKK	LHDFEEQCVE	MYFNEKDDKF	HSGSEERIRV	TFERVEQMCI	QIKEVGDRVN	YIKRSIQSLD	SQIGHLQDLS
130	140	150	160	170	180	190	200	210	220	230	240
ALTVDTLTKL	TAQKASEASK	VHNEITRELS	ISKHLAQNLI	DDGPVRPSVW	KKHGVVNTLS	SSLPQGDLES	NNPFHCNILM	KDDKDPQCNI	FGQDLPAPVQ	RKEFNPEAG	SSSGALFPSA
250	260	270	280	290	300	310	320	330	340	350	360
VSPPELRQRL	HGVELLKIFN	KNQKLGSST	SIPHLSSPPT	KFFVSTPSQP	SCKSHLETGT	KDQETVCSKA	TEGDNTEFGA	FVGHRDSMDL	QRFKETSNKI	KILSNMNTSE	NTLKRVSsla
370	380	390	400	410	420	430	440	450	460	470	480
GFIDCHRTSI	PVHSKQAEKI	SRRPSTEDTH	EVDSKAALIP	DWLQDRPSNR	EMPSEEGTLN	GLTSPFKPAM	DTNYYYSAVE	RNNLMRLSQS	IPFTPVPPRG	EPVTVYRLEE	SSPNILNNSM
490	500	510	520	530	540	550	560	570	580	590	600
SSWSQLGLCA	KIEFLSKEEM	GGGLRRRAVKV	QCTWSEHDIL	KSGHLYIIS	FLPEVVNTWS	SIYKEDTVLH	LCLREIQQQR	AAQKLTFAFN	QMKPKSIPYS	PRFLEVFLLY	CHSAGQWFAV
610	620	630	640	650	660	670	680	690	700	710	720
EECMTGEFRK	YNNNNGDEII	PTNTLEEIML	AFSHWTYEYT	RGELLVLDLQ	GVGENLTDPs	VIKAEEKRSC	DMVFGPANLG	EDAIKNFRAK	HHCNSCCRKL	KLPDLKRNDY	TPDKIIFPQD
730	740	750									
EPSDLNLQPG	NSTKESESTN	SVRLML									

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
80	1	1567.7542	1248.55	1	30.55	41.19		1	492-505	K.IEFLSKEEMGGGLR.R		CID

Protein 24: unnamed protein product [Homo sapiens]

Accession: gi|14041882

Database: NCBItr

Seq. Coverage [%]: 5.40 %

Score: 38.59

MW [kDa]: 19.50

pI: 11.90

No. of Peptides: 0

Modification(s): Propionamide

10	20	30	40	50	60	70	80	90	100	110	120
MGAGGRMRG	APARLLLPLL	PWLLLLLAPE	ARGAPGCPLS	IRSCKCSGER	PKGLSGGVPG	PARRRVVCSG	GDLPEPPEPG	LLPNCTVTLL	LSNNKITGLR	NGSFLGLSLI	EKDLRNNII
130	140	150	160	170	180	190					
STVQPGAFLG	LGELKRLDLS	NNRIGCLTSE	TFQGLPRLLR	LNISGNIFSS	LQPGVFDELP	ALKVV					

Protein Report

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
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Protein 25: tRNA wybutosine-synthesizing protein 1 homolog B OS=Homo sapiens GN=TYW1B PE=2 SV=2
Accession: TYW1B_HUMAN **Score:** 36.05
Database: SwissProt **MW [kDa]:** 76.90
Seq. Coverage [%]: 1.30 % **pI:** 5.84
No. of Peptides: 1

Modification(s): Oxidation

10	20	30	40	50	60	70	80	90	100	110	120
MDPSADTWDL	SSPLISLWIN	RFYIYLGFV	SISLWICVQI	VIEMQGFATV	LAEAVTSLDL	PVAIINLKEY	DPDDHLIEEV	TSKNVCVFLV	ATYTDGLPTE	SAEFCKWLE	EASIDFRFGK
130	140	150	160	170	180	190	200	210	220	230	240
TYLKGMRDAV	FGLGNSAYAS	HFNVKGKND	KWLWMLGVHR	VMSRGECD	VVSKKHGSIE	ANFRAWKTKF	ISQLQALQKG	ERKKSCGGHC	KKGKCESHQH	GSEEREESQ	EQDELHHRDT
250	260	270	280	290	300	310	320	330	340	350	360
KEEPPFESS	EEFEGGEDHQ	SLNSIVDVED	LGKIMDHVKK	EKREKEQQEE	KSGLFRNMGR	NEDGERRAMI	TPALREALTK	QVDAPRERSL	LQTHILWNE	HRCMETTPSL	ACANKCVFCW
370	380	390	400	410	420	430	440	450	460	470	480
WHHNNPVGTE	WLWKMDQPEM	ILKEAIENHQ	NMIKQFKGVP	GVKAERFEEG	MTVKHCALSL	VGEPIIMYPEI	NRFLKLLHQC	KISSFLVTNA	QFPAEIRNLE	PVTQLYVSVD	ASTKDSLKKI
490	500	510	520	530	540	550	560	570	580	590	600
DRPLFKDFWQ	QFLDSLKALA	VKQRTVYRL	MLVKAWNVD	LQAYQLVSL	GNPDFIEVKG	VTYCRESSAS	SLTMAHVPWH	EEVVQFVREL	VDLIPEYEIA	CEHEHSNCLL	IAHRKFKIGG
610	620	630	640	650	660	670					
EWWTWIDYNR	FQELIQEYED	SGGSKTFSAK	DYMARTPHWA	LFGANERSFD	PKDTRHQRKN	KSKAISGC					

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
29	1	1044.5290	-66.32	1	15.55	36.05		1	307-315	R.RAMITPALR.E	Oxidation: 3	CID

Protein Report

Protein 26: Chain A, Solution Structure Of The Conserved C-Terminal Dimerization Domain Of Borealin
Accession: gi|242556145 **Score:** 34.82
Database: NCBIInr **MW [kDa]:** 8.10
Seq. Coverage [%]: 19.70 % **pl:** 9.99
No. of Peptides: 1

10	20	30	40	50	60	70	80
GSAGERIYNI	SCNGSPLADS	KEIFLTVPVG	GGESLRLLAS	DIQRHSIAQL	DPEALGNIKK	LSNRLAQICS	SIRTHK

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
36	1	1605.8640	2.78	1	15.25	34.82		0	45-59	R.HSIAQLDPEALGNIK.K		CID

Table S2: Densitometry assessments for Western blot from figure 3A.

Relative Protein Amounts Cell Lines			
	CDCA8	Actin	relative density
OVCAR3	10550.7	28657.71	0.368162761
OVCAR4	9258.459	27857.42	0.332351656
CAOV3	10755.12	26297.83	0.408973485
LP9	30.823	27848	0.00110683
	FND3B	Actin	relative density
OVCAR3	38829.69	28657.71	1.354947469
OVCAR4	40168.94	27857.42	1.441947563
CAOV3	39380.64	26297.83	1.497486295
LP9	39891.94	27848	1.43248816
	KRT14	Actin	relative density
OVCAR3	17086.87	28657.71	0.596240014
OVCAR4	16536.63	27857.42	0.593616788
CAOV3	17339.58	26297.83	0.659354011
LP9	54.903	27848	0.001971524
	HNRN	Actin	relative density
OVCAR3	19246.28	28657.71	0.671591635
OVCAR4	18884.45	27857.42	0.677896674
CAOV3	19791.4	26297.83	0.752586791
LP9	52.108	27848	0.001871157

Table S3: Western Blot Densitometry

	K14	actin	relative density	reduction
UT	4661.569	35919.26	0.129779101	1
NT	4208.861	36190.67	0.116296843	0.896113796
gs1	764.82	36706.79	0.020835925	0.160549154
gs2	506.799	37027.26	0.013687187	0.105465262
gs3	5567.933	36776.11	0.151400823	1.166604035

	cdca8	actin	relative density	reduction
NT	15806.21	32181.73	0.491154686	1
gs1	2245.719	33138.97	0.067766703	0.137974257
gs2	23505.47	33924.44	0.69287725	1.41071086
gs3	18845.23	32780.68	0.57488827	1.170483121

	HNRN	actin	relative density	reduction
UT	11245.81	11013.34	1.021108038	1
NT	10797.92	12764.22	0.845952713	0.828465433
gs1	846.648	11741.75	0.072105764	0.070615215
gs2	297.778	4245.548	0.070138884	0.068688994
gs3	846.648	12130.02	0.069797718	0.068354881

Figure S1: Western Blot screening following CRISPR transfection and selection.

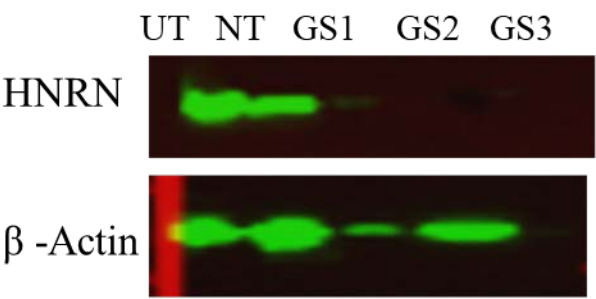
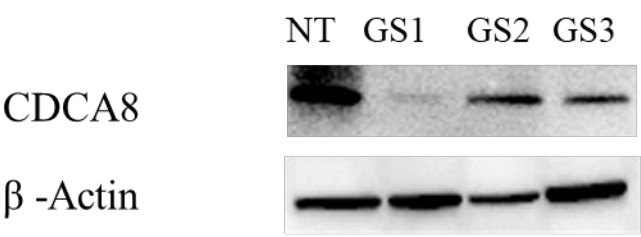
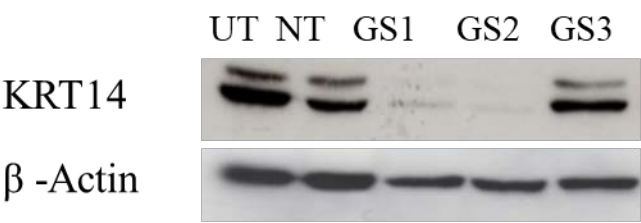


Table S4: Patient sample details for TMA analyses

Variables	
Total patient number	292
Age	12 to 76
Median	46
FIGO Grade and Stage	
I-I	15
I-Ia	9
I-Ib	3
I-Ic	1
I-II	2
I-IIa	3
I-IIb	2
I-IIIb	1
I-IIIc	1
I-IV	1
II-I	8
II-IA	10
II-IB	4
II-IC	3
II-II	6
II-IIA	2
II-IIC	1
II-IIIC	10
II-IV	4
III-I	10
III-IA	20
III-IB	13
III-IC	6
III-II	12
III-IIA	10
III-IIB	4
III-III	1
III-IIIc	12
III-IV	6
Normal/Benign	18
Ungraded/Unstaged	94
Histological Subtype	
Low Grade Serous	27
High Grade Serous	54
Papillary	44
Adenocarcinoma	4
Mucinous	14
Endometrioid	14
Clear cells	19
Normal	10
Fallopian Tube	8
GCT	34
Mixed	64

Figure S2: KRT14 and H&E staining of USBiomax TMAs

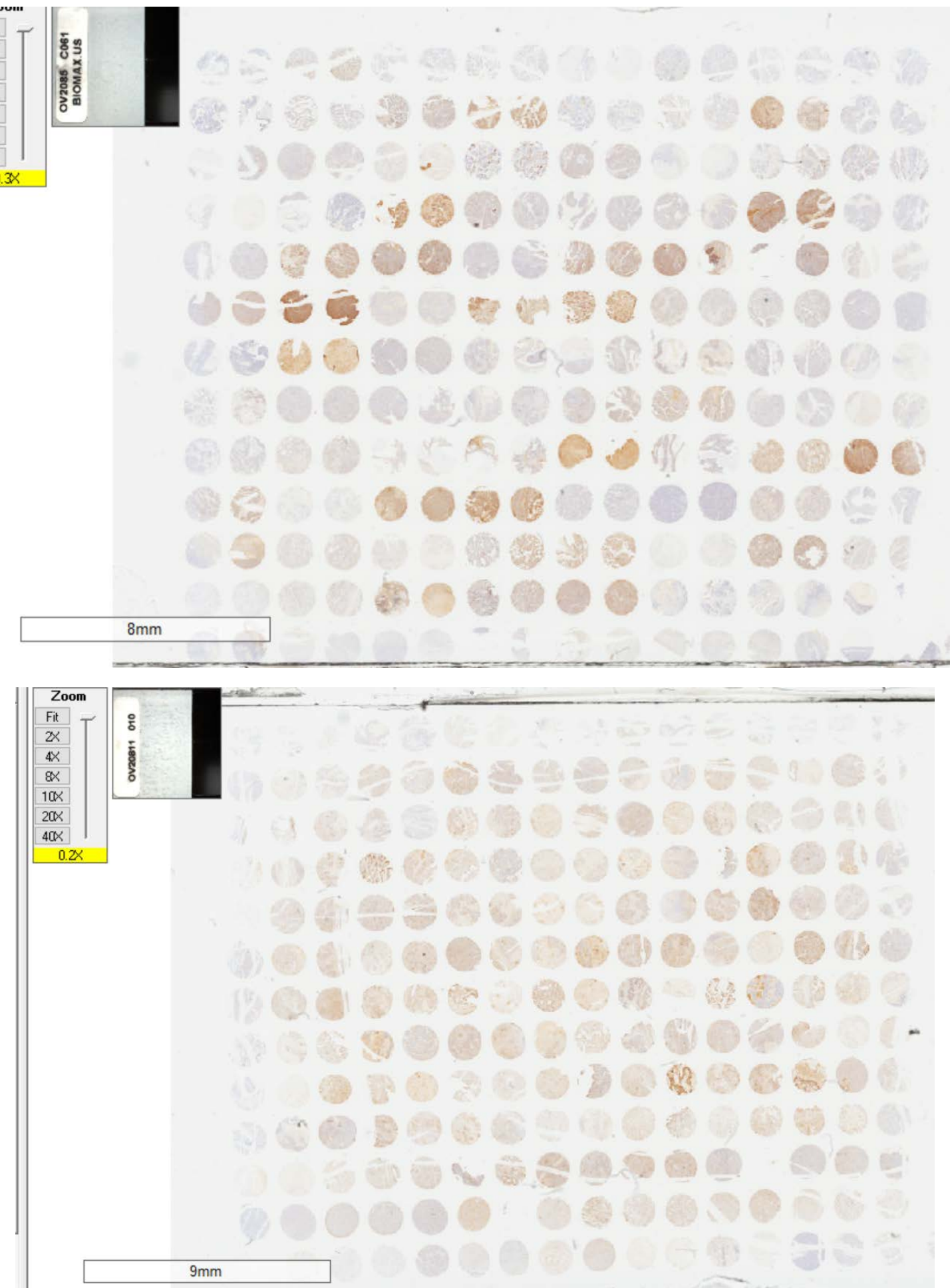


Figure S3: KRT14 antibody specificity on wild type, overexpressing and K14 knockout cells – OVCAR4

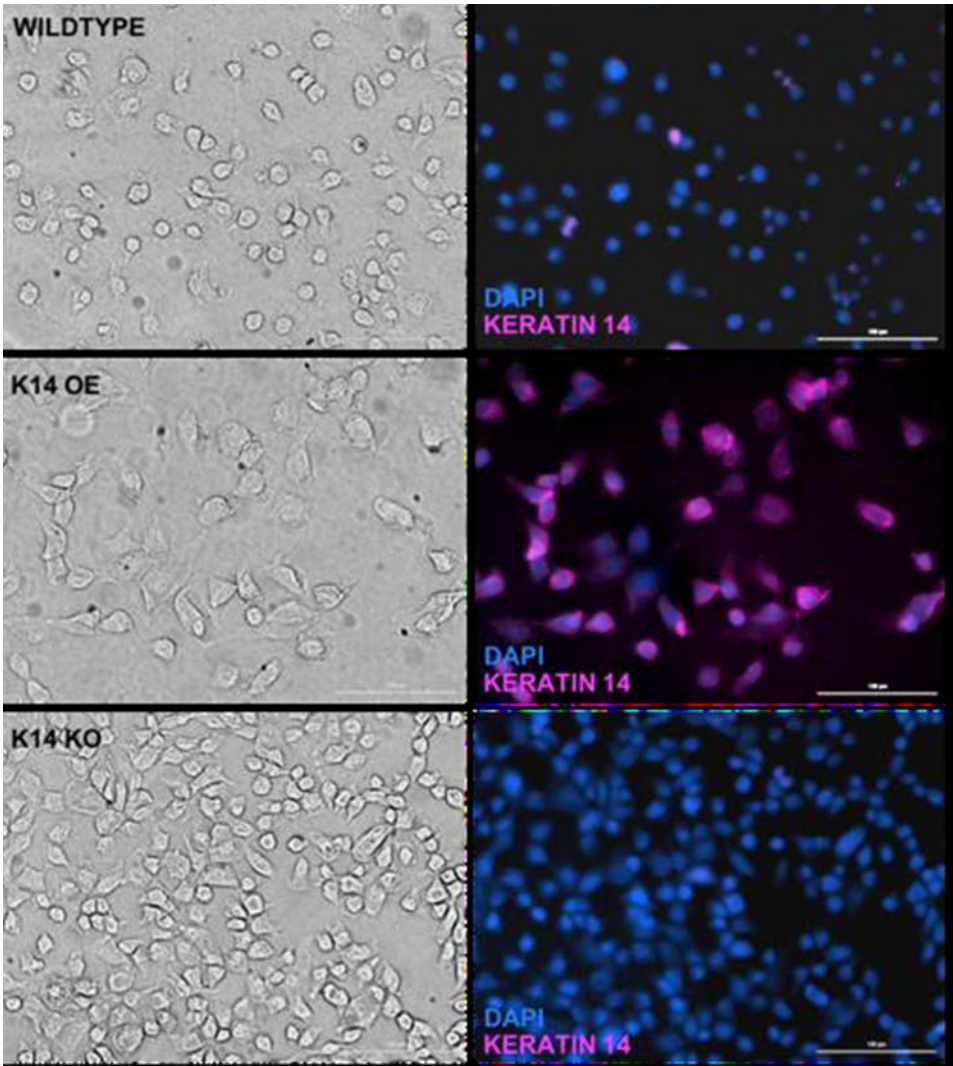
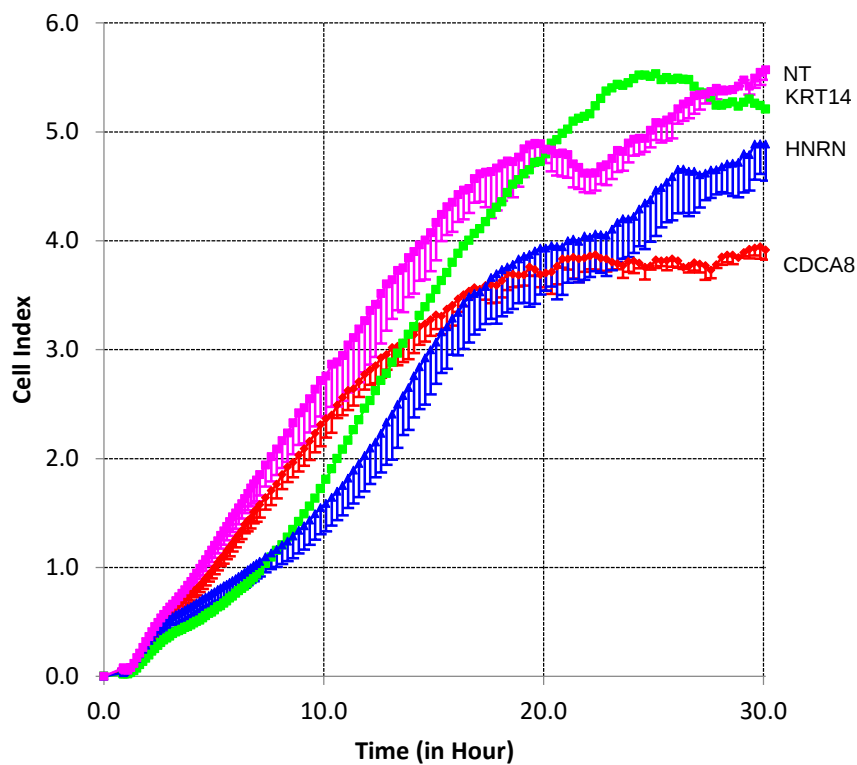


Figure S4: xCELLigence Proliferation and invasion - CaOV3

PROLIFERATION



Invasion

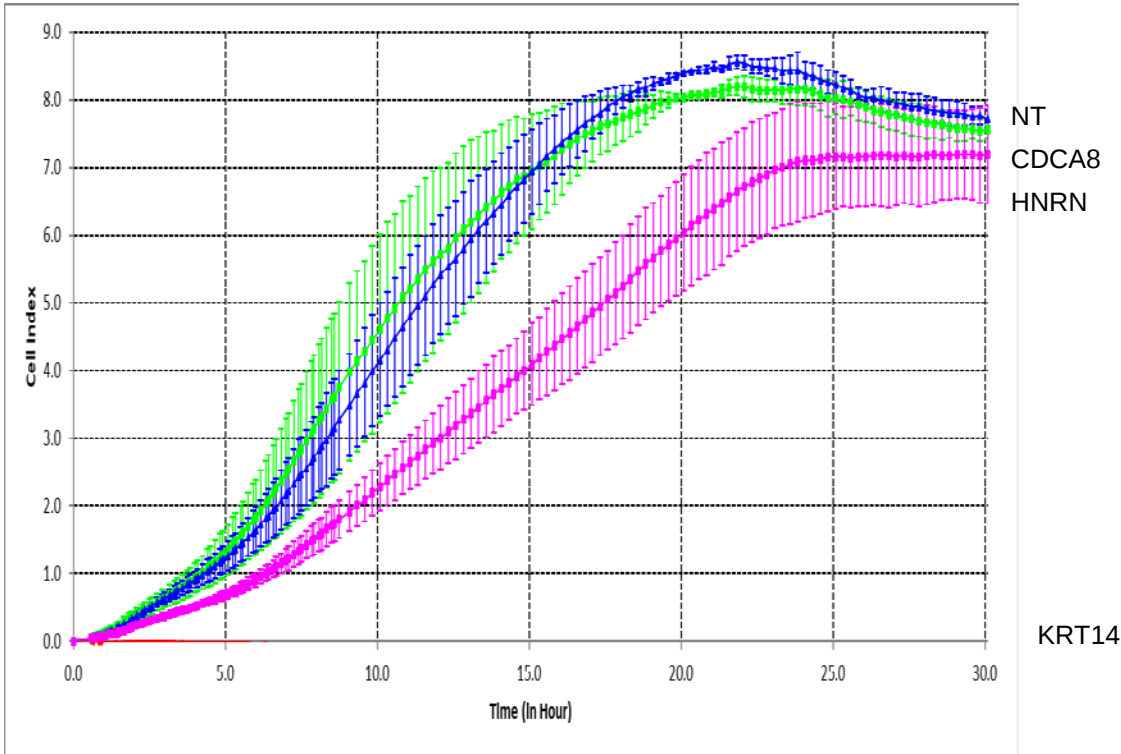


Table S5: CRISPR sgRNA sequences to target candidates.

Gene name	Exon number	sgRNA sequence (25 mer)
HRNR	1	ACGTATCATACTCCCCATGC
HRNR	1	GGAGTATGATACGTTGAACA
HRNR	2	GCGGCCCCGAAGCGTGATGGG
HRNR	2	GTCGGACACGGCTAGGAGAG
HRNR	2	TTTGGTCGATCTTCCAGCAG
CDCA8	1	CTGAAAGACTTCGACCGTGA
CDCA8	3	TTACTGTTGCCGCCTCTTCC
CDCA8	3	AGCCCTTGGAGGAAACAAAC
KRT14	1	TCATCCTCCCGCTTCTCCTC
KRT14	1	TGGTGGCCTTGGTGCTGGCT
KRT14	2	GCAGATTCTCACAGCCACAG
FNDC3B	1	GATGACCGACCAAATCCCTC
FNDC3B	2	GCTACCTCTCCGTTCAGCAA
FNDC3B	2	ATGATGCCCCACTTGGTGAA
FNDC3B	2	GACTTTCACAATAAGAGCAG
FNDC3B	2	GGAACACTTCAGTGCATTCA