

## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



### Project Info

**Name:** 200115-hikeshi-wt **Date:** Jan 15, 2020

### Sample Info & Protocols

**Name:** 200116-Hikeshi-C4S  
**Date:** Jan 16, 2020

### Search Result Info

<b>Search Result:</b>	LC-MALDI_OtherMammals_Mascot_2020-01-17 11:09:35		
<b>Location:</b>	/200115-hikeshi-wt/200116-Hikeshi-C4S/200116-Hikeshi-C4S		
<b>Search Method:</b>	LC-MALDI_OtherMammals	<b>Version:</b>	
<b>Search Engine(s):</b>	Mascot, 2.6.2	<b>Ident. Compound(s):</b>	5/1564
<b>Database(s):</b>	SwissProt, SwissProt_2019_07.fasta		
<b>Note:</b>			

## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



### Results

Protein 1: Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4

Accession:	FLNA_HUMAN	Score:	76.2
Database:	SwissProt	Seq. Coverage [%]:	0.9
MW [kDa] / pI:	280.6 / 5.7	No. of Peptides:	2

## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



10	20	30	40	50	60	70	80	90	100
MSSSHSRAGQ	SAAGAAPGGG	VDTRDAEMPA	TEKDLAEDAP	WKKIQQNTFT	RWCNEHLKCV	SKRIANLQTD	LSDGLRLIAL	LEVLSQKKMH	RKHNRPTFR
110	120	130	140	150	160	170	180	190	200
QMQLNNSVA	LEFLDRESIK	LVSIDSKAIV	DGNLKLILGL	IWTLILHYSI	SMPMWDEED	EEAKKQTPKQ	RLLGWIQNKL	PQLPITNFSR	DWQSGRALGA
210	220	230	240	250	260	270	280	290	300
LVDSCAPGLC	PDWDSWDASK	PVTNAREAMQ	QADDWLGIPO	VITPEEIVDP	NVDEHSVMY	LSQFPKAKLK	PGAPLRPKLN	PKKARAYGPG	IEPTGNMVKK
310	320	330	340	350	360	370	380	390	400
RAEFTVETRS	AGQGEVLVYV	EDPAGHQEEA	KVTANNDKNR	TFSVWYVPEV	TGTHKVTVLF	AGQHIKSPF	EVYVDKSQGD	ASKVTAQGGP	LEPSGNIANK
410	420	430	440	450	460	470	480	490	500
TTYFEIFTAG	AGTGEVEVVI	QDPMGQKGT	EPQLEARGDS	TYRCSYQPTM	EGVHTVHVTF	AGVPIRSPY	TVTGVQACNP	SACRAVGRGL	QPKGVRVKET
510	520	530	540	550	560	570	580	590	600
ADFKVYTKGA	GSGELKVTVK	GPKGEERVQ	KDLGDGVYGF	EYYPMVPGTY	IVTITWGGQN	IGRSPFEVKV	GTECGNQKVR	AWGPGLEGGV	VGKSADFVVE
610	620	630	640	650	660	670	680	690	700
AIGDDVGTLG	FSVEGPSQAK	IECDDKGDGS	CDVRYWPQEA	GEYAVHVLN	SEDIRLSPFM	ADIRDAPQDF	HPDRVKARGP	GLEKTGVAVN	KPAEFTVDAK
710	720	730	740	750	760	770	780	790	800
HGGKAPLRVQ	VQDNEGCPVE	ALVKDNGNGT	YSCSYVPRKP	VKHTAMVSWG	GVSIPNSPFR	VNVGAGSHPN	KVKVYGPQVA	KTGLKAHEPT	YFTVDCAEAG
810	820	830	840	850	860	870	880	890	900
QGDVSIKIC	APGVVGPAEA	DIDFDIIRND	NDTFTVKYTP	RGAGSYTIMV	LFADQATPTS	PIRVKVEPSH	DASKVKAEGP	GLSRTGVELG	KPTHFTVNAK
910	920	930	940	950	960	970	980	990	1000
AAGKGKLDVQ	FSGLTKGDAV	RDVDIIDHHD	NTYTVKYTPV	QQGPVGVNVT	YGGDPIPKSP	FSVAVSPSLD	LSKIKVSGLG	EKVDVGKDQE	FTVKSAGAGG
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
QGKVASKIVG	PSGAAPVCKV	EPGLGADNSV	VRFLPREEGP	YEVEVTYDGV	PVPGSPFPLE	AVAPTQPSKV	KAFGPGLQGG	SAGSPARFTI	DTKGAGTGGL
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
GLTVEGPCEA	QLECLDNGDG	TCSVSYVPT	PGDYNINILF	ADTHIPGSPF	KAHVVPFCDA	SKVKCSGPG	ERATAGEVGQ	FQVDCSSAGS	AELTIEICSE
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
AGLPAEVIYQ	DHGDGTHIT	YIPLCPGAYT	VTIKYGGQPV	PNFPSKLQVE	PAVDTSQVQC	YGPQIEGQGV	FREATTEFSV	DARALQTQGG	PHVKARVANP

## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



### MS/MS Peptide Matches

Cmpd.	m/z meas.	z	$\Delta$ m/z [ppm]	$\Delta$ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
1090	1226.6485	1	-3.50	-0.0043	37.83	45.91	1	0.0	0	R.AWGPGLEGGVVGK.S		581-593	CID
267	1108.6142	1	2.95	0.0033	25.17	30.3	1	0.0	0	R.ALTQTGGPHVK.A		1284-1294	CID

### Protein 2: RNA-binding protein 10 OS=Homo sapiens OX=9606 GN=RBM10 PE=1 SV=3

**Accession:** RBM10\_HUMAN  
**Database:** SwissProt  
**MW [kDa] / pI:** 103.5 / 5.7

**Score:** 69.7  
**Seq. Coverage [%]:** 1.6  
**No. of Peptides:** 1

## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



10	20	30	40	50	60	70	80	90	100
MEYERRGGRG	DRTGRYGATD	RSQDDGGENR	SRDHDYRDMD	YRSYPREYGS	QEGKHDYDDS	SEEQSAEDSY	EASPGSETQR	RRRRRRHRHSP	TGPPGFPRDG
110	120	130	140	150	160	170	180	190	200
DYRDQDYRTE	QGEHEEEEEED	EEEEKASNI	VMLRMLPQAA	TEDDIRGQLQ	SHGVQAREVR	LMRNKSSGQS	RGFAFVEFSH	LQDATRWMEA	NQHSNLNLGQ
210	220	230	240	250	260	270	280	290	300
KVSMHYSDPK	PKINEDWLCN	KCGVQNFKRR	EKCFKCGVPK	SEAEQKLPLG	TRLDQQTLPL	GGRELSQGLL	PLPQPYQAQG	VLASQALSQG	SEPSSENAND
310	320	330	340	350	360	370	380	390	400
TIILRNLNPH	STMSILGAL	APYAVLSSSN	VRVIKDKQTQ	LNRGFAFIQL	STIVEAAQLL	QILQALHPPL	TIDGKTINVE	FAKGSKRDMA	SNEGSRISAA
410	420	430	440	450	460	470	480	490	500
SVASTAIAAA	QWASQASQG	GEGTWATSEE	PPVDYSYYQQ	DEGYGNSQGT	ESSLYAHGYL	KGTKGPGITG	TKGDPTGAGP	EASLEPGADS	VSMQAFSRAQ
510	520	530	540	550	560	570	580	590	600
PGAAPGIYQQ	SAEASSSQGT	AANSQSYTIM	SPAVLKSELQ	SPTHSSALP	PATSPTAQES	YSQYPVPDVS	TYQYDETSYG	YYDPQTGLYY	DPNSQYYNA
610	620	630	640	650	660	670	680	690	700
QSQQYLYWDG	ERRTYVPALE	QSADGHKETG	APSKEGKEKK	EKHKTAKTAQQ	IAKDMERWAR	SLNKQKENFK	NSFQPISSLR	DDERRESATA	DAGYATLEKK
710	720	730	740	750	760	770	780	790	800
GALAERQHTS	MDLPKLASDD	RPSPPRGLVA	AYSGESDSEE	EQERGGPERE	EKLTDWQKLA	CLLCRRQFPS	KEALIRHQQL	SGLHKQNLEI	HRRRAHSENE
810	820	830	840	850	860	870	880	890	900
LEALEKNDME	QMKYRDRAAE	RREKYGIPEP	PEPKRRKYGG	ISTASVDFEQ	PTRDGLGSDN	IGSRMLQAMG	WKEGSGGLGRK	KQGIVTPIEA	QTRVRGSGLG
910	920	930	940						
ARGSSYGVT	TESYKETLHK	TMVTRFNEAQ							

## MS/MS Peptide Matches

Cmpd.	m/z meas.	z	$\Delta$ m/z [ppm]	$\Delta$ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
1299	1620.7583	1	-24.80	-0.0402	39.83	69.72	1	0.0	1	R.MLQAMGWKEGSGGLGR.K		865-879	CID

# Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



## Protein 3: Protein phosphatase 1B OS=Homo sapiens OX=9606 GN=PPM1B PE=1 SV=1

Accession: PPM1B\_HUMAN Score: 37.9  
Database: SwissProt Seq. Coverage [%]: 1.9  
MW [kDa] / pI: 52.6 / 5.0 No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100
MGAFLDKPKT	EKHNAHGAGN	GLRYGLSSMQ	GWRVEMEDAH	TAVVGIPHGL	EDWSFFAVYD	GHAGSRVANY	CSTHLLLEHIT	TNEDFRAAGK	SGSALELSVE
110	120	130	140	150	160	170	180	190	200
NVKNIGIRTGF	LKIDEYMRNF	SDLRNGMDRS	GSTAVGVMIS	PKHIYFINGC	DSRAVLYRNG	QVCFSTQDHK	PCNPREKERI	QNAGGSVMIQ	RVNGSLAVSR
210	220	230	240	250	260	270	280	290	300
ALGDYDYKCV	DGKGPTQLV	SPEPEVYEIL	RAEDEFIIL	ACDGIWDVMS	NEELCEYVKS	RLEVSDDLN	VCNWVDTCL	HKGSRDNMSI	VLVCFSNAPK
310	320	330	340	350	360	370	380	390	400
VSDEAVKDS	ELDKHLESRV	EEIMEKSGEE	GMPDLAHVMR	ILSAENIPNL	PPGGGLAGKR	NVIEAVYSRL	NPHRESDGAS	DEAEESGSQG	KLVEALRQMR
410	420	430	440	450	460	470	480		
INHRGNRYQL	LEEMLTSYRL	AKVEGEESPA	EPAATATSSN	SDAGNPVTMQ	ESHTESEGL	AELDSSNEDA	GTRKMSGEKI		

### MS/MS Peptide Matches

Cmpd.	m/z meas.	z	$\Delta$ m/z [ppm]	$\Delta$ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
1012	1050.5371	1	-19.74	-0.0207	35.83	37.87	1	0.0	0	R.NVIEAVYSR.L		361-369	CID

## Protein 4: Probable tRNA (uracil-O(2)-)-methyltransferase OS=Homo sapiens OX=9606 GN=TRMT44 PE=1 SV=2

Accession: TRM44\_HUMAN Score: 32.9  
Database: SwissProt Seq. Coverage [%]: 1.1  
MW [kDa] / pI: 84.6 / 7.0 No. of Peptides: 1

## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



10	20	30	40	50	60	70	80	90	100
MAEVGRTGIS	YPGALLPQGF	WAAVEVWLER	PQVANKRLCG	ARLEARWSAA	LPCAEARGPG	TSAGSEQKER	GPGPGQGSPG	GGPGPRSLSG	PEQGTACCEL
110	120	130	140	150	160	170	180	190	200
EEAQGGCQQE	EAQREAA <sup>SV</sup> P	LRDSGHPGHA	EGREGDFPAA	DLDLWEDFS	QSLARGNSEL	LAFLTSSGAG	SQPEAQRELD	VVLRTVIPKT	SPHCPLTTPR
210	220	230	240	250	260	270	280	290	300
REIVVQDVLN	GTITFLPLEE	DDEGNLKVVM	SNVYQIQLSH	SKEEWFISVL	IFCPERWHS	GIVYPKPTWL	GEELLAKLAK	WSVENKKSDF	KSTLSLISIM
310	320	330	340	350	360	370	380	390	400
KYSKAYQELK	EKYKEMVKVW	PEVTDPEKFF	YEDVAIAAYL	LILWEEERAE	RRLTARQSFV	DLGCGNGLLV	HILSSEGHPG	RGIDVRRRKI	WDMYGPQTQL
410	420	430	440	450	460	470	480	490	500
EEDAITPNDK	TLFPDWDWLI	GNHSD <sup>EL</sup> TPW	IPVIAARSSY	NCRFFVLPC	FFDFIGRYSR	RQSKKTQYRE	YLDIFIKEVGF	TCGFHVDEDC	LRIPSTKRVC
510	520	530	540	550	560	570	580	590	600
LVGKSRTYPS	SREASVDEKR	TQYIKSRRGC	PVSPPGWELS	PSPRWVAAGS	AGHCDGQAL	DARVGCVTRA	WAAEHGAGPQ	AEGPWLPGFH	PREKAERVRN
610	620	630	640	650	660	670	680	690	700
CAALPRDFID	QVVLQVANLL	LGGKQLNTRS	SRNGSLKTWN	GGESLSLAEV	ANELDTETLR	RLKRECGGLQ	TLLRNSHQVF	QVVNGRVHIR	DWREETLWKT
710	720	730	740	750	760				
KQPEAKQRL	SEACKTRLCW	FFMHHPDGCA	LSTDCCPFAH	GPAELRPPT	TPRKIS				

## MS/MS Peptide Matches

Cmpd.	m/z meas.	z	$\Delta$ m/z [ppm]	$\Delta$ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
673	842.4784	1	6.36	0.0054	31.67	32.87	1	0.0	0	R.EAASVPLR.D		115-122	CID

Protein 5: Centrosome-associated protein 350 OS=Homo sapiens OX=9606 GN=CEP350 PE=1 SV=1

Accession: CE350\_HUMAN  
 Database: SwissProt  
 MW [kDa] / pI: 350.7 / 6.0  
 Modification(s): Phospho

Score: 32.2  
 Seq. Coverage [%]: 0.0  
 No. of Peptides: 0



## Protein Report

LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35



10	20	30	40	50	60	70	80	90	100
MRSSKSKEVP	LPNPRNSQSK	DTVQADITTS	WDALSQTKAA	LRHIENKLEV	APTSTAVCDS	VMDTKKSSTS	ATRKISRKDG	RYLDDSWVNA	PISKSTKSRK
110	120	130	140	150	160	170	180	190	200
EKSRSPLRAT	TLESNVKKN	RVEFREPLVS	YREIHGAPSN	FSSSHLESKH	VYCVDVNEEK	TESGNWMIGS	REERNIRSCD	FESSQSSVIN	DTVVRFLNDR
210	220	230	240	250	260	270	280	290	300
PAIDALQNSE	CLIRMGASMR	TEEEMP	NRTK	GSENNLKLSV	NNMAHDTDPK	ALRLTDSSPS	STSTSNSQRL	DILKRRQHDV	KLEKLKERIR
310	320	330	340	350	360	370	380	390	400
GRGQKLGHID	HPVMVNVNDN	SVTAKVRKVA	TAPPAPAYKG	FNPSETKIRT	PDGKVVQAE	FQMSRELYR	DLALHFADDI	SIKEKPAEKS	KEKKVVKPVR
410	420	430	440	450	460	470	480	490	500
KVQKVAQLSS	TECRTGSSHL	ISTSSWRDQ	KLVKILGPA	PRMEPKEQRT	ASSDRGGRER	TAKSGGHIGR	AESDPRLDVL	HRHLQNSER	SRSKSRSENN
510	520	530	540	550	560	570	580	590	600
IKKLASSLPD	NKQEENTALN	KDFLPIEIRG	ILDDLQLDST	AHTAKQDTVE	LQNQKSSAPV	HAPRSHSPVK	RKPKKITANE	DPPVISKRRH	YDTDEVQRQYI
610	620	630	640	650	660	670	680	690	700
VRQQEERKRK	QNEEKKAQKE	ATEQKNRLQ	ELYRKQKEAF	TKVKVPPSE	PSATRLQET	YSKLLLEKTL	LEEPSHQHVT	QETQAKPGYQ	PSGESDKENK
710	720	730	740	750	760	770	780	790	800
VQERPPSASS	SSDMSLSEPP	QPLARKDLME	STWMQPERLS	PQVHHSQPQP	FAGTAGSLLS	HLLSLEHVGI	LHKDFESILP	TRKNHNMASR	PLTFTPQPYV
810	820	830	840	850	860	870	880	890	900
TSPAAYTDAL	LKPSASQYKS	KLDRIEALKA	TAASLSSRIE	SEAKKLAGAS	INYGSAWNTE	YDVQQAPQED	GPWTKAVTPP	VKDDNEDVFS	ARIQKMLGSC
910	920	930	940	950	960	970	980	990	1000
VSHATFDDDL	PGVG	NLSEFK	KLPEMIRPQS	AISSFRVRSP	GPKPEGLLAQ	LCKRQTDSSS	SDMQACSQDK	AKISLGSSID	SVSEGPLLSE
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
DGQPLLKVAE	ILKEKEFCPG	ERNSEPIKE	FQKEAEKFLP	LFGHIGGTQS	KGPWEELAKG	SPHSVINIFT	KSYQLYGKGF	EDKLDRGTST	SRPL
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
LSGVSYEDDF	VSSPGTGTST	EKKSTLEPHS	TLSPQEDHSN	RKSAYDPSSV	DVTSQHSSGA	QSAASSRSST	SSKGKKGKKE	KTEWLDSTFG	NVQNSLLDEE
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
KAERGSHQGK	KSGTSSKLSV	KDFEQTLDTD	STLEDLSGHS	VSVSSDKGRS	QKTPTSPLSP	SSQKSLQFDV	AGTSSERSKS	SVMPTITGF	KPNAPLTDLN



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LC-MALDI\_OtherMammals\_Mascot\_2020-01-17 11:09:35

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