

Protein Report

LC-MALDI_OtherMammals_Mascot_2020-01-15 19:00:42



Project Info

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

Sample Info & Protocols

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

Search Result Info

Search Result:	LC-MALDI_OtherMammals_Mascot_2020-01-15 19:00:42	
Location:	/200115-hikeshi-wt/200115-hikeshi-wt/200115-hikeshi-wt	
Search Method:	LC-MALDI_OtherMammals	Version:
Search Engine(s):	Mascot, 2.6.2	Ident. Compound(s): 6/300
Database(s):	SwissProt, SwissProt_2019_07.fasta	
Note:		

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Results

Protein 1: Protein Hikeshi OS=Homo sapiens OX=9606 GN=HIKESHI PE=1 SV=2

Accession: HIKES_HUMAN Score: 207.4
Database: SwissProt Seq. Coverage [%]: 16.2
MW [kDa] / pI: 21.6 / 5.3 No. of Peptides: 3

10	20	30	40	50	60	70	80	90	100
MFGCLVAGRL	VQTAAQQVAE	DKFVFDLPDY	ESINHVVVFM	LGTIPFPEGM	GGSVYFSYPD	SNGMPVWQLL	GFVTNGKPSA	IFKISGLKSG	EGSQHPFGAM
110	120	130	140	150	160	170	180	190	200
NIVRTPSVAQ	IGISVELLDS	MAQQTPVGNA	AVSSVDSFTQ	FTQKMLDNFY	NFASSFAVSQ	AQMTSPSEM	FIPANVVLKW	YENFQRRLAQ	NPLFWKT

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
158	1686.7879	1	-8.16	-0.0138	38.17	92.92	1	0.0	0	K.SGEGSQHPFGAMNIVR.T		89-104	CID
112	1042.4743	1	0.19	0.0002	34.67	51.29	1	0.0	0	K.WYENFQR.R		180-186	CID
218	1116.6077	1	-11.05	-0.0123	43.17	63.21	1	0.0	0	R.LAQNPLFWK.T		188-196	CID

Protein 2: Fermitin family homolog 1 OS=Homo sapiens OX=9606 GN=FERMT1 PE=1 SV=1

Accession: FERM1_HUMAN Score: 31.5
Database: SwissProt Seq. Coverage [%]: 1.9
MW [kDa] / pI: 77.4 / 5.9 No. of Peptides: 1

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10	20	30	40	50	60	70	80	90	100
MLSSTDFTF	SWELVVRVDH	PNEEQQKQDVT	LRVSGDLHVG	GVMLKLVEQI	NISQDWSDF	LWWEQKHCWL	LKTHWTLDKY	GVQADAKLLF	TPQHMLRLR
110	120	130	140	150	160	170	180	190	200
LPNLKQVRLR	VSFSAVVFKA	VSDICKILNI	RRSEELSLK	PSGDYFKKKK	KKDKNNKEPI	IEDILNLESS	PTASGSSVSP	GLYSKTMTP	YDPINGTPAS
210	220	230	240	250	260	270	280	290	300
STMTWFSDSP	LTEQNCILA	FSQPPQSPEA	LADMYQPRSL	VDKAKLNAGW	LDSSRSIMEQ	GIQEDQLLL	RFKYYSFFDL	NPKYDAVRIN	QLYEQARWAI
310	320	330	340	350	360	370	380	390	400
LLEEIDCTEE	EMLIFAALQY	HISKLSLSAE	TQDFAGESEV	DEIEAALSNL	EVTLEGGKAD	SLLEDITDIP	KLADNLKLF	PKLLPKAFK	QYWFIFKDT
410	420	430	440	450	460	470	480	490	500
IAYFKNKELE	QGEPEKLNL	RGCEVVPDVN	VAGRKFGLK	LIPVADGMNE	MYLRCDHENQ	YAQWMAACML	ASKGKTADS	SYQPEVLN	SFLRMKRN
510	520	530	540	550	560	570	580	590	600
ASQVASSLEN	MDMNPECFVS	PRCAKRHKSK	QLAARILEAH	QNVAQMPLE	AKLRFIQAWQ	SLPEFGLTY	LVRFKGSKD	DILGVSYNRL	IKIDAATGIP
610	620	630	640	650	660	670	680		
VTTWRFTNIK	QWNVNWETRQ	VVIEFDQNVF	TAFTCLSADC	KIVHEYIGGY	IFLSTRSKDQ	NETLDEDLFH	KLTGGQD		

MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
50	1400.7292	1	-17.16	-0.0240	28.83	31.48	1	0.0	0	K.IDAATGIPVTTWR.F		593-605	CID

Protein 3: Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=5

Accession: RRBP1_HUMAN
 Database: SwissProt
 MW [kDa] / pI: 152.4 / 8.7

Score: 27.3
 Seq. Coverage [%]: 0.7
 No. of Peptides: 1

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10	20	30	40	50	60	70	80	90	100
MDIYDTQTLG	VVVFGGFMV	SAIGIFLVST	FSMKETSYEE	ALANQRKEMA	KTHHQKVEKK	KKEKTVEKKG	KTKKKKEEKN	GKIPDHPAP	NVTVLLREPV
110	120	130	140	150	160	170	180	190	200
RAPAVAVAPT	PVQPPPIIVAP	VATVPAMPQE	KLASSPKDKK	KKEKKVAKVE	PAVSSVVNSI	QVLTSKAAIL	ETAPKEVPMV	VVPPVGAIGN	TPATGTTQGK
210	220	230	240	250	260	270	280	290	300
KAEGTQNSK	KAEGAPNQGR	KAEGTPNQGK	KTEGTPNQGK	KAEGTPNQGK	KAEGTPNQGK	KAEGAQNQGK	KVDTPNQGK	KVEGAPTQGR	KAEGAQNQAK
310	320	330	340	350	360	370	380	390	400
KVEGAQNQGK	KAEGAQNQGK	KGEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KVEGAQNQGK
410	420	430	440	450	460	470	480	490	500
KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK	KVEGAQNQGK	KAEGAQNQGK	KAEGAQNQGK
510	520	530	540	550	560	570	580	590	600
KAEGAQNQGG	KGEGAQNQGK	KTEGAQGGKA	ERSPNQGGKG	EGAPIQGGKA	DSVANQGTKV	EGITNQGGKA	EGSPSEGKKA	EGSPNQGGKA	DAAANQGGKT
610	620	630	640	650	660	670	680	690	700
ESASVQGRNT	DVAQSPEAPK	QEAPAKKSG	SKKKGEPGPP	DADGPLYLPY	KTIVSTVSGM	VFNEGEAQL	IEILSEKAGI	IQDTWHKATQ	KGDPVALIKR
710	720	730	740	750	760	770	780	790	800
QLEEKEKLLA	TEQEDAAVAK	SKLRELNKEM	AAEKAKAAAG	EAKVKKQLVA	REQEITAVQA	RMQASYREHV	KEVQQLQGI	RTLQEQLENG	PNTQLARLQQ
810	820	830	840	850	860	870	880	890	900
ENSILRDALN	QATSQVESKQ	NAELAKLRQE	LSKVSKEKLV	KSEAVRQDEQ	QRKALEAKAA	AFEKQVLQLQ	ASHRESEAL	QKRLDEVSR	LCHTQSSHAS
910	920	930	940	950	960	970	980	990	1000
LRADAEKAQE	QQQQMAELHS	KLQSSEAEVR	SKCEELSGH	GQLQEARAEN	SQLTERIRSI	EALLEAGQAR	DAQDVQASQA	EADQQQTRLK	ELESQVSGLE
1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
KEATELREAV	EQQKVKNNDL	REKNWKAMEA	LATAEQACKE	KLKSLTQAKE	ESEKQLCLIE	AQTMEALLAL	LPELSVLAQQ	NYTEWLQDLK	EKGPTLLKHP
1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
PAPAEPSDL	ASKLREAEET	QSTLQAECDQ	YRSILAETEG	MLRDLQKSVE	EEEQVWRAKV	GAAEEELQKS	RVTVKHLEEI	VEKLKGELES	SDQVREHTSH
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
LEAELEKMA	AASAECONYA	KEVAGLRQLL	LESQSQLDAA	KSEAQKQSDE	LALVRQQLSE	MKSHVEDGDI	AGAPASSPEA	PPAEQDPVQL	KTQLEWTEAI

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MS/MS Peptide Matches

Cmpd.	m/z meas.	z	Δ m/z [ppm]	Δ m/z [Da]	Rt [min]	Score	No. of Cmpds.	Site [%]	P	Sequence	Modification	Range	Type
180	1142.7105	1	18.65	0.0213	41.00	27.28	1	0.0	1	R.AATRLQELLK.T		1366-1375	CID