Result of identification of HA-FLCN IP p130 by PMF analysis

The MW of the peptide fragments obtained by MALDI-TOF/MS analysis.

AP-1 : 584.39	AP-11 : 1285.65	AP-21 : 3174.56
AP-2 : 709.41	AP-12 : 1522.80	
AP-3 : 940.41	AP-13 : 1540.75	
AP-4 : 994.54	AP-14 : 1638.65	
AP-5 : 1011.50	AP-15 : 1648.33	
AP-6 : 1202.64	AP-16 : 1664.74	
AP-7 : 1203.75	AP-17 : 1874.98	
AP-8 : 1218.66	AP-18 : 2034.02	
AP-9 : 1241.12	AP-19 : 2050.07	
AP-10 : 1259.77	AP-20 : 2456.20	

Cys modification:carboxymetylation

Identificaion to BC001956+BAB85547
Digestion by (Enzyme) : **LysC**
(MW : **130630.18** Da)

peptide	observed	theoretical	delta	corresponding sequence	Head	Tail	comment
AP-1	584.39	584.34	+0.05	[K]KPPDK[I]	732	736	
AP-2	709.41	709.36	+0.05	[K]QYRDK[L]	665	669	
AP-3	940.41	940.38	+0.03	[K]QNNEFCK[C]	880	886	
AP-4	994.54	994.52	+0.02	[R]STGMVVEKK[P]	724	732	1Met-ox
AP-5	1011.50	1011.49	+0.01	[K]LRTCFDAK[L]	670	677	
AP-6	1202.64	1202.58	+0.06	[K]HSSQSVDMLAK[T]	485	495	0Met-ox
AP-7	1203.75	1203.64	+0.11	[K]RRNEDISVSK[L]	65	74	
AP-8	1218.66	1218.57	+0.09	[K]HSSQSVDMLAK[T]	485	495	1Met-ox
AP-11	1285.65	1285.58	+0.07	[K]NHLCYRFMK[E]	429	437	1Met-ox
AP-12	1522.80	1522.76	+0.04	[K]IVPASFSCEAAQTK[V]	737	750	1AAM-Cys
AP-13	1540.75	1540.74	+0.01	[K]EERGAIDQHQETK[Q]	786	798	
AP-14	1638.65	1638.67	-0.02	[K]ESEEIRTPNCNCK[Y]	599	611	
AP-16	1664.74	1664.73	+0.01	[K]ESEEIRTPNCNCK[Y]	599	611	2AAM-Cys
AP-17	1874.98	1874.98	0.00	[K]WTVQVASSQRRVTDNK[L]	1057	1072	
AP-18	2034.02	2034.00	+0.02	[K]GEIEESEYVLVTMHRNK[S]	576	592	0Met-ox
AP-19	2050.07	2049.99	+0.08	[K]GEIEESEYVLVTMHRNK[S]	576	592	1Met-ox
AP-20	2456.20	2456.19	+0.01	[K]TCFPQQDQRDTLSILVPHGDK[E]	898	918	
AP-21	3174.56	3174.48	+0.08	[K]YCSHPLLGQNVENISQQEREDIQNSSK[E]	612	638	

1	**11**	**21**	**31**	**41**	**51**	**61**	**71**
MAPTLFQKLF	SKRTGLGAPG	RDARDPDCGF	SWPLPEFDPS	QIRLIVYQDC	ERRGRNVLFD	SSVKRRNEDI	SVSKLCSDAQ
81	**91**	**101**	**111**	**121**	**131**	**141**	**151**
VKVFGKCCQL	KPGGDSSSSL	DSSVTSSSDI	KDQCLKYQGS	RCSSDANMLG	EMMFGSVAMS	YKGSTLKIHQ	IRSPPQLMLS
161	**171**	**181**	**191**	**201**	**211**	**221**	**231**
KVFTARTGSS	ICGSLNTLQD	SLEFINQDNN	TLKADNNTVI	NGLLGNIGLS	QFCSPRRAFS	EQGPLRLIRS	ASFFAVHSNP
241	**251**	**261**	**271**	**281**	**291**	**301**	**311**

MDMPGRELNE DRDSGIARSA SLSSLLITPF PSPNSSLTRS CASSYQRRWR RSQTTSLENG VFPRWSIEES FNLSDESCGP

321 331 341 351 361 371 381 391

NPGIVRKKKI AIGVIFSLSK DEDENNKFNE FFFSHFPLFE SHMNKLKSAI EQAMKMSRRS ADASQRSLAY NRIVDALNEF

401 411 421 431 441 451 461 471

RTTICNLYTM PRIGEPVWLT MMSGTPEKNH LCYRFMKEFT FLMENASKNQ FLPALITAVL TNHLAWVPTV MPNGQPPIKI

481 491 501 511 521 531 541 551

FLEKHSSQSV DMLAKTHPYN PLWAQLGDLY GAIGSPVRLA RTVVVGKRQD MVQRLLYFLT YFIRCSELQE THLLENGEDE

561 571 581 591 601 611 621 631

AIVMPGTVIT TTLEKGEIEE SEYVLVTMHR NKSSLLFKES EEIRTPNCNC KYCSHPLLGQ NVENISQQER EDIQNSSKEL

641 651 661 671 681 691 701 711

LGISDECRMI SPSDCQEENA VDVKQYRDKL RTCFDAKLET VVCTGSVPVD KCALSESGLE STEETWQSEK LLDSDSHTGK

721 731 741 751 761 771 781 791

AMRSTGMVVE KKPPDKIVPA SFSCEAAQTK VTFLIGDSMS PDSDTELRSQ AVVDQITRHH TKPLKEERGA IDQHQETKQT

801 811 821 831 841 851 861 871

TKDQSGESDT QNMVSEEPCE LPCWNHSDPE SMSLFDEYFN DDSIETRTID DVPFKTSTDS KDHCCMLEFS KILCTKNNKQ

881 891 901 911 921 931 941 951

NNEFCKCIET VPQDSCKTCF PQQDQRDTLS ILVPHGDKES SDKKIAVGTE WDIPRNESSD SALGDSESED TGHDMTRQVS

961 971 981 991 1001 1011 1021 1031

SYYGGEQEDW AEEDEIPFPG SKLIEVSAVQ PNIANFGRSL LGGYCSSYVP DFVLQGIGSD ERFRQCLMSD LSHAVQHPVL

1041 1051 1061 1071 1081 1091 1101 1111

DEPIAEAVCI IADMDKWTVQ VASSQRRVTD NKLGKEVLVS SLVSNLLHST LQLYKHNLSP NFCVMHLEDR LQELYFKSKM

1121 1131 1141 1151 1161

LSEYLRGQMR VHVKELGVVL GIESSDLPLL AAVASTHSPY VAQILL