Result of identification of HA-FNIP1 IP p90 by PMF analysis

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

AP-1 : 515.28	AP-11 : 1242.70	AP-21 : 2541.39
AP-2 : 617.30	AP-12 : 1296.67	
AP-3 : 973.45	AP-13 : 1308.69	
AP-4 : 989.40	AP-14 : 1559.76	
AP-5 : 1039.49	AP-15 : 1632.88	
AP-6 : 1076.54	AP-16 : 1748.87	
AP-7 : 1082.03	AP-17 : 1759.77	
AP-8 : 1151.54	AP-18 : 1764.85	
AP-9 : 1190.70	AP-19 : 1950.00	
AP-10 : 1224.64	AP-20 : 2278.17	

Cys modification:carbamidomethylation

Identificaion to **gi|72219|pir||HHHU86 heat shock protein 90-alpha - human**
Digestion by (Enzyme) : **Lys-C**
(MW : **84660.09** Da)

peptide	observed	theoretical	delta	corresponding sequence	Head	Tail	comment
AP-1	515.28	515.37	-0.09	[K]VIRK[N]	411	414	
AP-2	617.30	617.35	-0.05	[K]DILEK[K]	577	581	
AP-3	973.45	973.42	+0.03	[K]DYCTRMK[E]	479	485	0Met-ox
AP-4	989.40	989.41	-0.01	[K]DYCTRMK[E]	479	485	1Met-ox
AP-6	1076.54	1076.54	0.00	[K]KFYEQFSK[N]	436	443	
AP-8	1151.54	1151.56	-0.02	[K]YIDQEELNK[T]	284	292	
AP-9	1190.70	1190.69	+0.01	[K]ELHINLIPNK[Q]	75	84	
AP-10	1224.64	1224.63	+0.01	[K]HIYYITGETK[D]	490	499	
AP-11	1242.70	1242.71	-0.01	[K]ADLINNLGTIAK[S]	101	112	
AP-12	1296.67	1296.67	0.00	[K]LGIHEDSQNRK[K]	447	457	
AP-13	1308.69	1308.68	+0.01	[K]IRYESLTDPSK[L]	59	69	
AP-14	1559.76	1559.73	+0.03	[K]SLTNDWEDHLAVK[H]	315	327	1Trp -> fKyn
AP-15	1632.88	1632.88	0.00	[K]DQVANSAFVERLRK[H]	500	513	
AP-16	1748.87	1748.92	-0.05	[K]QDRTLTIVDTGIGMTK[A]	85	100	0Met-ox
AP-17	1759.77	1759.81	-0.04	[K]AQALRDNSTMGYMAAK[K]	616	631	2Met-ox
AP-18	1764.85	1764.91	-0.06	[K]QDRTLTIVDTGIGMTK[A]	85	100	1Met-ox
AP-19	1950.00	1950.02	-0.02	[K]EIFLRELISNSSDALDK[I]	42	58	
AP-20	2278.17	2278.12	+0.05	[K]LSELLRYYTSASGDEMVSLK[D]	459	478	1Met-ox

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1	**11**	**21**	**31**	**41**	**51**	**61**	**71**
MPEETQTQDQ	PMEEEEVETF	AFQAEIAQLM	SLIINTFYSN	KEIFLRELIS	NSSDALDKIR	YESLTDPSKL	DSGKELHINL
81	**91**	**101**	**111**	**121**	**131**	**141**	**151**
IPNKQDRTLT	IVDTGIGMTK	ADLINNLGTI	AKSGTKAFME	ALQAGADISM	IGQFGVGFYS	AYLVAEKVTV	ITKHNDDEQY
161	**171**	**181**	**191**	**201**	**211**	**221**	**231**
AWESSAGGSF	TVRTDTGEPM	GRGTKVILHL	KEDQTEYLEE	RRIKEIVKKH	SQFIGYPITL	FVEKERDKEV	SDDEAEEKED
241	**251**	**261**	**271**	**281**	**291**	**301**	**311**

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KEEEKEKEEK ESEDKPEIED VGSDEEEEKK DGDKKKKKKI KEKYIDQEEL NKTKPIWTRN PDDITNEEYG EFYKSLTNDW
321        331        341        351        361        371        381        391
EDHLAVKHFS VEGQLEFRAL LFVPRRAPFD LFENRKKKNN IKLYVRRVFI MDNCEELIPE YLNFIRGVVD SEDLPLNISR
401        411        421        431        441        451        461        471
EMLQQSKILK VIRKNLVKKC LELFTELAED KENYKKFYEQ FSKNIKLGIH EDSQNRKKLS ELLRYYTSAS GDEMVSLKDY
481        491        501        511        521        531        541        551
CTRMKENQKH IYYITGETKD QVANSAFVER LRKHGLEVIY MIEPIDEYCV QQLKEFEGKT LVSVTKEGLE LPEDEEEKKK
561        571        581        591        601        611        621        631
QEEKKTKFEN LCKIMKDILE KKVEKVVVSN RLVTSPCCIV TSTYGWTANM ERIMKAQALR DNSTMGYMAA KKHLEINPDH
641        651        661        671        681        691        701        711
SIIETLRQKA EADKNDKSVK DLVILLYETA LLSSGFSLED PQTHANRIYR MIKLGLGIDE DDPTADDTSA AVTEEMPPLE
721        731
GDDDTSRMEE VD
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heat shock protein 90-alpha - human

ACCESSION HHHU86