

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

AP-1 : 701.389	AP-11 : 2420.327
AP-2 : 916.521	AP-12 : 2468.492
AP-3 : 1021.511	AP-13 : 2602.302
AP-4 : 1117.605	
AP-5 : 1227.712	
AP-6 : 1437.715	
AP-7 : 1487.809	
AP-8 : 1579.835	
AP-9 : 1804.061	
AP-10 : 2320.330	

Cys modification: carbamidomethylation

Identificaion to [gi|22907034|ref|NP_659434.2| folliculin isoform 1 \[Homo sapiens\]](#)

Digestion by (Enzyme) : **Lys-C**

(MW : **64473.66** Da)

peptide	observed	theoretical	delta	corresponding sequence	Head	Tail	comment
AP-1	701.389	701.394	-0.005	[K]VDSRPK[E]	524	529	
AP-3	1021.511	1021.510	+0.001	[K]ACGSRLTEK[L]	264	272	
AP-5	1227.712	1227.706	+0.006	[K]VRGIIDELQGK[A]	193	203	
AP-7	1487.809	1487.796	+0.013	[K]LLSILGASEEDNVK[L]	535	548	
AP-11	2420.327	2420.282	+0.045	[K]YEFVVTSGSPVAADRVGPTILNK[I]	463	485	
AP-13	2602.302	2602.322	-0.020	[K]IEAALTNQNLSVDVVDQCLVCLK[E]	486	508	

1	11	21	31	41	51	61	71
MNAIVALCHF	CELHGPRTLFL	CTEVLHAPLP	QGDGNEDSPG	QGEQAEEEEEG	GIQMNSRMRA	HSPAEGASVE	SSSPGPKKSD
81	91	101	111	121	131	141	151
MCEGCRSLAA	GHPGYISHDK	ETSIKYVSHQ	HPSHPQLFSI	VRQACVRSL	CEVCPGREGP	IFFGDEQHGF	VFSHTFFIKD
161	171	181	191	201	211	221	231
SLARGFQRWY	SIITIMMDRI	YLINSWPFL	GK VRGIIDEL	QGK ALKVFEA	EQFGCPQRAQ	RMNTAFTPFL	HQRNGNAARS
241	251	261	271	281	291	301	311
LTSLTSDDNL	WACLHTSAFW	LLK ACGSRLT	EKL LEGAPTE	DTLVQMEKLA	DLEEESESWD	NSEAESEEKA	PVLPESTEGR
321	331	341	351	361	371	381	391
ELTQGAESS	SLSGCGSWQP	RKLPVFKSLR	HMRQVLGAPS	FRMLAWHVLM	GNQVIWKS	VDLVQSAFEV	LRTMLPVGCV
401	411	421	431	441	451	461	471
RIIPYSSQYE	EAYRCNFLGL	SPHVQIPPHV	LSSEFAVIVE	VHAAARSTLH	PVGCEDDQSL	SK YEFVVTSG	SPVAADRVGP
481	491	501	511	521	531	541	551
TILNKIEAAL	TNQNLSVDVV	DQCLVCLK EE	WMNKVKVLFK	FTK VDSRPKE	DTQK LLSILG	ASEEDNVKLL	KFWMTGLSKT
561	571						
YKSHLMSTVR	SPTASESRN						

folliculin isoform 1 [Homo sapiens]

ACCESSION [NP_659434.2](#)