

Table 1. Recovered and identified (by MS) peptides generated by enzymatic digestion of rTF₁₋₂₄₃¹, rTF₁₋₂₆₃² and pTF³ with trypsin (fragment 1 to 30) and of rTF₁₋₂₄₃¹, rTF₁₋₂₆₃² and pTF³ with Glu-C (marked with *).

Fragment	Peptide sequence	Amino acids	Peptide length (aa)	Peptide mass (Da)
1	SGTTNTVAAYNLTWK ^{1,2,3}	1-15	15	1626.7
2	STNFK ^{1,2}	16-20	5	595.6
3	TILEWEPK ^{1,2,3}	21-28	8	1015.1
4	PVNQVYTVQISTK ^{1,2,3}	29-41	13	1476.6
5	SGDWK ³	42-46	5	591.6
6	SK ^{1,2,3}	47-48	2	233.2
7	CFYTTDTECDLTDEIVK ^{1,2,3}	49-65	17	1996.1
8	DVK ^{1,2,3}	66-68	3	360.4
9	QTYLAR ^{1,2,3}	69-74	6	750.8
10	*VFSYPAGNVE ^{1,2,3}	75-84	10	1082.1
	*STGSAGE ^{1,2}	85-92	7	607.5
	*PLYE ^{1,2}	93-96	4	624.0
	*NSPE ^{1,2}	97-100	4	549.0
	*FTPYLE ²	101-106	6	768.8
	*TNLGQPTIQSFE ^{1,2,3}	107-118	12	1334.4
	*QVGTK ^{2,3}	119-122	5	531.6
11	VNVTVEDER ^{1,2,3}	123-131	9	1060.1
12	TLVR	132-135	3	487.6
13	R ^{1,2,3}	136	1	174.0
14	NNTFLSLR ^{1,2,3}	137-144	8	964.0
15	DVFGK ^{1,2,3}	145-149	5	564.6
16	DLIYTLYYWK ^{1,2,3}	150-159	10	1377.6
17	SSSSGK	160-165	6	551.5
18	K	166	1	146.2
19	TAK	167-169	3	318.3
20	TNTNEFLIDVDK ^{1,2,3}	170-181	12	1408.5
21	GENYCFSVQAVIPSR ^{1,2,3}	182-196	15	1669.8
22	TVNR ¹	197-200	4	488.5
23	K ^{1,3}	201	1	146.2
24	STDSPVECMGQEK ^{1,3}	202-214	13	1410.5
25	GEFR ¹	215-218	4	507.5
26	EIFYIIGAVVVFVVIILVILAILSHK	219-244	26	2896.6
27	CR	245-246	2	295.0
28	K ^{2,3}	247	1	146.2
29	AGVGQSWK ^{2,3}	248-255	8	831.9
30	ENSPLNVS ^{2,3}	249-263	8	858.9