

Table 2a. Identified peptides of the larger limited proteolysis fragment of tANK (≈ 18.5 kDa)

Fragment no.	Observed mass, daltons*	Calculated mass, daltons	Peptide sequence	Sequence position
1	1,087.5281	1,086.4842	R.NYRDSYNR.T	26-33
2	1,402.7586	1,401.7504	K.DIEGSTALIWAVK.N	62-74
3	1,253.5830	1,252.6048	K.GSNVBTKDFSGK.T	88-99
4	1,370.7948	1,369.7453	R.NLEGETPLIVASK.Y	128-140
5	1,746.9964	1,745.9312	R.NLEGETPLIVASKYGR.S	128-143
6	951.5327	950.5185	K.YGRSEIVK.K	141-148
7	1,285.7499	1,284.7401	K.KLLELGADISAR.D	149-160
8	1,157.6640	1,156.6452	K.LLELGADISAR.D	150-160
9	1,089.6127	1,088.6342	R.IFGRQEVIK.I	173-181

Table 2b. Identified peptides of the small limited proteolysis fragment of tANK (≈ 10 kDa)

Fragment no.	Observed mass, daltons*	Calculated mass, daltons	Peptide sequence	Sequence position
1	1,370.8069	1,369.7453	R.NLEGETPLIVASK.Y	128-140
2	1,747.0270	1,745.9312	R.NLEGETPLIVASKYGR.S	128-143
3	1,285.8013	1,284.7401	K.KLLELGADISAR.D	149-160
4	1,157.6884	1,156.6452	K.LLELGADISAR.D	150-160
5	2,343.3569	2,342.2441	K.LLELGADISARDLTGLTAEASAR.I	150-172
6	1,204.6607	1,203.6095	R.DLTGLTAEASAR.I	161-172
7	1,089.6727	1,088.6342	R.IFGRQEVIK.I	173-181
8	920.5358	919.5239	K.IFTEVRR.A	182-188

*During ionization, the peptides get (in case of MALDI) singly protonated. Therefore, the masses get shifted by 1 Da, $[M+H]^+$.