

Supplementary Table

Table 1

Peptide fragments of sTF1-214 observed by tandem mass spectrometry.

Start – End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
6-10	524.27	523.26	523.26	0.00	0	N.TVAAY.N
6-15	583.82	1165.62	1165.61	0.01	0	N.TVAAYNLTWK.S
9-15	448.24	894.46	894.46	0.00	0	A.AYNLTWK.S
11-15	661.37	660.36	660.36	0.00	0	Y.NLTWK.S
21-32	727.39	1452.77	1452.76	0.01	1	K.TILEWEPKPVNQ.V
21-37	682.03	2043.07	2043.07	0.00	1	K.TILEWEPKPVNQVYTVQ.I
21-41	825.12	2472.33	2472.33	0.00	1	K.TILEWEPKPVNQVYTVQISTK.S
24-37	858.94	1715.86	1715.85	0.01	1	L.EWEPKPVNQVYTVQ.I
35-41	388.73	775.44	775.44	0.00	0	Y.TVQISTK.S
47-65 –	737.10	2208.28	2209.98	-1.69 [#]	1	K.SKCFYTTDTECDLTDEIVK.D
49-68 –	779.47	2335.40	2337.04	-1.64 [#]	1	K.CFYTTDTECDLTDEIVKDVK.Q
69-74	376.21	750.40	750.40	0.00	0	K.QTYLAR.V
74-114	1115.79	4459.13	4459.15	-0.02	1	A.RVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQP TIQ.S
75-86	635.80	1269.59	1269.59	0.00	0	R.VFSYPAGNVEST.G
75-86	646.79	1291.57	1291.57	0.00	0	R.VFSYPAGNVEST.G Sodiated (DE) [+21.98]
75-93	941.45	1880.89	1880.88	0.01	0	R.VFSYPAGNVESTGSAGEPL.Y
77-86	512.73	1023.45	1023.45	0.00	0	F.SYPAGNVEST.G
77-93	818.38	1634.75	1634.74	0.01	0	F.SYPAGNVESTGSAGEPL.Y
77-114	1353.31	4056.90	4056.91	-0.01	0	F.SYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQ.S
85-114	1080.85	3239.53	3239.51	0.02	0	E.STGSAGEPLYENSPEFTPYLETNLGQPTIQ.S
87-103	929.42	1856.82	1856.81	0.01	0	T.GSAGEPLYENSPEFTPY.L
87-114	1025.48	3073.43	3073.42	0.01	0	T.GSAGEPLYENSPEFTPYLETNLGQPTIQ.S Sodiated (DE) [+21.98]
97-114	1018.01	2034.00	2033.99	0.01	0	N.SPEFTPYLETNLGQPTIQ.S
104-114	1213.64	1212.63	1212.63	0.00	0	Y.LETNLGQPTIQ.S
104-122	1045.54	2089.07	2089.07	0.00	0	Y.LETNLGQPTIQSFEQVGTK.V
115-122	448.23	894.45	894.44	0.01	0	Q.SFEQVGTK.V
115-123	497.76	993.51	993.51	0.00	0	Q.SFEQVGTKV.N
123-131	530.77	1059.52	1059.52	0.00	0	K.VNVTVEDER.T
150-154	624.32	623.32	623.32	0.00	0	K.DLIYT.L
150-155	737.41	736.40	736.40	0.00	0	K.DLIYTL.Y
170-181	704.85	1407.69	1407.69	0.00	0	K.TNTNEFLIDVDK.G
170-185	936.44	1870.86	1870.86	0.00	1	K.TNTNEFLIDVDKGENY.C
172-185	828.89	1655.77	1655.77	0.00	1	N.TNEFLIDVDKGENY.C
202-210	637.22	1272.43	1272.43	0.00	0	K.STDSPVECM.G Glutathione (C) [+305.07]
202-212	729.76	1457.51	1457.51	0.00	0	K.STDSPVECMGQ.E Glutathione (C) [+305.07]
202-214	572.56	1714.65	1714.65	0.00	0	K.STDSPVECMGQEK.- Glutathione (C) [+305.07]

LTQFT or QTOF (#) instruments were used to determine peptide masses after double digestion of sTF with trypsin. The values refer to the initial and last amino acids of the tryptic peptides (Start-End), their masses per charge (m/z; Observed), the experimentally obtained and calculated peptide molecular weights (Mr (expt), Mr (calc)), the difference between experimental and calculated masses (Delta), and the number of missed tryptic cleavages (Miss). In the last row the identified sequences are given. The calculated values refer to the free thiol forms of the cysteines. # The disulfide bonded peptides were only observed using QTOF.