Supplementary Table II. Purified wild-type CgA (10 µM/reaction) was digested with 0.3 µM of CTSL for 15 min at 30 ºC and was analyzed by LC-MS/MS. Peptides generated in pancreastatin, (IIA) vasostatin (IIB), WE14 (IIC), GE25 (IID) and chromacin (IIE) region were listed in the following Tables.

IIA. Peptides generated in the pancreastatin region of CgA by CTSL.

Observed mass	Calculated mass	Residues of CgA	Sequence	C.I. %
1047.5297	1047.5428	249-258	R_KGESRSEALA_V	99.977
1125.5963	1125.6051	236-245	V_LNPHPSLGYK_E	100
1246.6415	1246.6613	290-300	E_EMAVVPQGLFR_G	98.901
1261.627	1261.6495	246-256	K_EIRKGESRSEA_L	99.719
1375.6854	1375.7039	289-300	E_EEMAVVPQGLFR_G	99.984
1445.7471	1445.7706	246-258	K_EIRKGESRSEALA_V	99.262
1504.7227	1504.7465	288-300	E_EEEMAVVPQGLFR_G	100
1762.8403	1762.8315	286-300	K_EEEEEMAVVPQGLFR_G	99.6
3225.387	3225.5117	273-300	D_PEGKGEQEHSQQKEEEEEMAVVPQGLFR_G	100

IIB. Peptides generated in the vasostatin region of CgA.

Observed mass	Calculated mass	Residues of CgA	Sequence	C.I. %
1071.5062	1071.5217	75-83	H_QQKKHSGFE_D	99.787
1072.6119	1072.611	41-49	E_TLRGDERIL_S	99.718
1133.5239	1133.5433	92-101	E_NQSSQAELKE_A	100
1133.5299	1133.5433	91-100	L_ENQSSQAELK__E	99.999
1474.7225	1474.7384	88-100	S_EVLENQSSQAELK_E	100
1780.8912	1780.9202	69-83	G_AKERAHQQKKHSGFE_D	99.961
1837.9149	1837.9415	68-83	Q_GAKERAHQQKKHSGFE_D	100
1918.8783	1918.924	84-100	E_DELSEVLENQSSQAELK_E	100
1948.943	1948.9736	67-83	L_QGAKERAHQQKKHSGFE_D	99.327
2047.9384	2047.9666	84-101	E_DELSEVLENQSSQAELKE_A	100
2282.092	2282.1272	68-87	Q_GAKERAHQQKKHSGFEDELS_E	100

IIC. Peptides generated in the WE14 region of CgA by CTSL.

Observed mass	Calculated mass	Residues of CgA	Sequence	C.I.%
1176.6328	1176.6293	326-335	S_KMDQLAKELT_A	100
1216.6766	1216.6896	332-341	A_KELTAEKRLE_G	99.992
1263.6355	1263.6614	325-335	W_SKMDQLAKELT_A	99.999
1350.6274	1350.6437	316-325	S_KEWEDSKRWS_K	99.899
1464.7164	1464.7264	320-331	E_DSKRWSKMDQLA__K	99.79
1478.7225	1478.7386	316-326	S_KEWEDSKRWSK_M	99.988
1852.849	1852.8646	316-329	S_KEWEDSKRWSKMDQ_L	99.938
1902.9889	1903.0317	326-341	S_KMDQLAKELTAEKRLE_G	99.974
2036.9614	2036.9858	316-331	S_KEWEDSKRWSKMDQLA_K	100

IID. Peptides generated in the GE25 region of CgA by CTSL.

Observed mass	Calculated mass	Residues of CgA	Sequence	C.I. %
1418.6465	1418.6659	375-386	R_GWRPSSREDSLE_A	99.94
1574.7511	1574.767	374-386	R_RGWRPSSREDSLE__A	99.409
1997.9578	1998.0039	375-392	R_GWRPSSREDSLEAGLPLQ_V	99.342
2409.2031	2409.2744	374-394	R_RGWRPSSREDSLEAGLPLQVR_G	99.98

IIE. Peptides generated in the chromacin region of CgA.

Observed mass	Calculated mass	Residues of CgA	Sequence	C.I. %
1674.8568	1674.8656	185-200	D_SEGLSQGLVDREKGLS_A	99.8
2175.0298	2175.02	174-194	S_QKYPGPQAEGDSEGLSQGLVD_R	100
2628.2312	2628.2537	174-198	S_QKYPGPQAEGDSEGLSQGLVDREKG_L	100
2845.3347	2845.3962	174-200	S_QKYPGPQAEGDSEGLSQGLVDREKGLS_A	100