

10	20	30	40	50
MAEELVLERC	DLELETNGRD	HHTADLCREK	LVVRRGQPFW	LTLLHFEGRNY
60	70	80	90	100
EASVDSLTFSS	VVTGPAPSQE	AGTKARFPLR	DAVEEGDWTG	TVVDQQDCTL
110	120	130	140	150
SLQLTTPANA	PIGLYRLSLE	ASTGYQGSSF	VLGHFILLFN	AWCPADAVYL
160	170	180	190	200
DSEEEERQ	EYVLTQQGFYQ	SAKFIKNIPW	NFGQFEDGIL	DICLILLDVN
210	220	230	240	250
PKFLKNAGRD	CSRSSPVYV	GRVVSGMVNC	NDDQGVLLGR	WDNNYGDGVS
260	270	280	290	300
PMSWIGSVDI	LRRWNHGCQ	RVKYGQCWVF	AAVACTVLRC	LGIPTRVVTN
310	320	330	340	350
YNSAHDQNSN	LLIEYFRNEF	GEIQGDKSEM	IWNFHCWVES	WMTRPDLQPG
360	370	380	390	400
YEGWQALDPT	PQEKSEGTYC	CGPVPVRAIK	EGDLSTKYDA	PFVFAEVNAD
410	420	430	440	450
VVDWIQQDDG	SVHKSINRSL	IVGLKISTKS	VGRDEREDIT	HTYKYPEGSS
460	470	480	490	500
EEREAFTRAN	HLNKLAEKEE	TGMAMRIRVG	QSMNMGSGFD	VFAHITNNTA
510	520	530	540	550
EEYVCRLLLC	ARTVSYNGIL	GPECGTKYLL	NLNLEPFSEK	SVPLCILYEK
560	570	580	590	600
YRDCLTESNL	IKVRALLVEP	VINSYLLAER	DLYLENPEIK	IRILGEPKQK
610	620	630	640	650
RKLVAEVSLO	NPLPVALEGC	TFTVEGAGLT	EEQKTVEIPD	PVEAGEEVKV
660	670	680		
RMDLLPLHMG	LHKLVNFES	DKLKAVKGFR	NVIIGPA	

Supplementary Figure S2.

Sequence coverage of TG2. The analysis of all identified peptides of human tissue transglutaminase (TG2) resulted in a sequence coverage of 79.6 % (UniProtKB accession No. P21980).