Endoplasmic reticulum-resident protein 57 (ERp57) oxidatively inactivates human transglutaminase 2

Michael C. Yi[†], Arek V. Melkonian^{†,§}, James A. Ousey[†] and Chaitan Khosla^{†,‡,⊥}

From the Departments of [†]Chemical Engineering and [‡]Chemistry, [§]School of Medicine, and [±]Stanford ChEM-H, Stanford University, Stanford, California 94305, United States

SUPPORTING INFORMATION

Supplemental Figures:

Figure S1: Specificity of antibodies used in this study.

Figure S2: Identification of reduced Cys370 and Cys371 in TG2.

Figure S3: Identification of the Cys370-Cys371 disulfide bond in TG2.

Figure S4: Identification of reduced domain a CXXC in ERp57.

Figure S5: Identification of reduced domain a' CXXC in ERp57.

Figure S6: Basal extracellular TG2 activity in HUVEC.

Figure S7: ERp57-targeted siRNA knockdown in HUVEC.

Figure S8: ERp57-targeted siRNA knockdown in HUVEC supplemented with exogenous 1 µM oxidized ERp57.

Supplemental Table:

Table S1: List of peptides analyzed by mass spectrometry.



Figure S1. Specificity of antibodies used in this study. HUVEC cultures were lysed with RIPA buffer and resolved by reducing SDS-PAGE. Antibody specificity was assessed by Western immunoblotting with the listed antibodies. Ladder represents molecular mass in kDa.



Figure S2. Identification of reduced Cys370 and Cys371 in TG2. *Top,* Isotopic distribution of ³⁶⁵SEGTYC(IAM)C(IAM)GPVPVR³⁷⁷. Bottom, Identity of the peptide confirmed by tandem mass spectrum (*MS/MS*) with each *y* fragment ion labeled.



Figure S3. Identification of the Cys370-Cys371 disulfide bond in TG2. *Top*, Isotopic distribution of 365 SEGTYC(IAA)C(IAA)GPVPVR 377 . *Bottom*, Identity of the peptide confirmed by tandem mass spectrum (*MS/MS*) with each *y* fragment ion labeled.



Figure S4. Identification of reduced domain a CXXC in ERp57. *Top,* Isotopic distribution of ³⁹ISDTGSAGLMLVEFFAPWC(IAM)GHC(IAM)K⁶¹. Bottom, Identity of the peptide confirmed by tandem mass spectrum (*MS/MS*) with each *y* fragment ion labeled.



Figure S5. Identification of reduced domain a' CXXC in ERp57. *Top,* Isotopic distribution of ³⁹⁶DVLIEFYAPWC(IAM)GHC(IAM)K⁴¹⁰. Bottom, Identity of the peptide confirmed by tandem mass spectrum (MS/MS) with each *y* fragment ions labeled.



Figure S6. Basal extracellular TG2 activity in HUVEC. 200 μ M 5BP was added for 3 h to control siRNA-transfected cells to assay for TG2 activity. 5BP incorporation (blue) is proportional to TG2 activity. Experimental conditions were performed in triplicate. During confocal microscopy analysis, three images were taken per replicate using a 20x objective and all images are presented. Images were post-processed and analyzed in FIJI. Images in Row 8 were used in Figure 8E. *Scale bar = 100 µm*.



Figure S7. ERp57-targeted siRNA knockdown in HUVEC. 200 μ M 5BP was added for 3 h to ERp57 siRNA-transfected cells to assay for TG2 activity. 5BP incorporation (blue) is proportional to TG2 activity. Experimental conditions were performed in triplicate. During confocal microscopy analysis, at least three images were taken per replicate using a 20x objective, and all images are presented. Images were post-processed and analyzed in FIJI. Images in Row 6 were used in Figure 8E. *Scale bar = 100 µm*.



Figure S8. ERp57-targeted siRNA knockdown in HUVEC supplemented with exogenous 1 μ M oxidized ERp57. 1 μ M oxidized ERp57 was pre-incubated with ERp57 siRNA-treated HUVEC cultures for 30 min. After, 200 μ M 5BP was added for 3 h to assay for TG2 activity. 5BP incorporation (blue) is proportional to TG2 activity. Experimental conditions were performed in triplicate. During confocal microscopy analysis, three images were taken per replicate using a 20x objective, and all images are presented. Images were post-processed and analyzed in FIJI. Images in Row 2 were used in Figure 8E. *Scale bar = 100 \mum.*

Protein	Peptide Sequence	Theoretical m/z	Observed m/z	Charge
TG2	SEGTYC(IAM)C(IAM)	741.3078	741.3282	2
Reduced	GPVPVR			
Cys370,				
Cys371				
TG2	SEGTYC(IAA)C(IAA)G	742.3136	742.3078	2
Oxidized	PVPVR			
Cys370,				
Cys371				
ERp57	ISDTGSAGLMLVEFFA	861.7182	861.7324	3
Reduced	PWC(IAM)GHC(IAM)			
Domain a	K			
ERp57	DVLIEFYAPWC(IAM)	632.2777	632.2917	3
Reduced	GHC(IAM)K			
Domain a'				

Table S1: Peptides derived from reduced/oxidized TG2 and reduced ERp57 that were detected by mass spectrometry.