

Figure S3. Mass spectrometric analysis of the secreted hEPO-Stab.

Unprocessed, full-length amino acid sequence of hEPO-Stab is shown: the amino acid sequence of STABILON (blue) and the signal peptide of hEPO (green) are highlighted and underlined. Peptides identified by mass spectrometry after endoprotease treatment are highlighted in red.

Signal peptide

Stabilon

hEPO sequence

hEpo-Stab protein sequence

1	<u>MGVHECPAWL</u>	<u>WLLLSLLSLP</u>	<u>LGLPVLGAPP</u>	RLICDSRVLE	RYLLEAKEAE	NITTGCAEHC	SLNENITVPD	TKVNFYAWKR
81	MEVGQQAVEV	WQGLALLSEA	VLRGQALLVN	SSQPWEPLQL	HVDKAVSGLR	SLTTLLRALG	AQKEAISPPD	AASAAPLRTI
161	TADTFRKLFR	VYSNFLRGKL	KLYTGEACRT	GDRASKDKKS	DGKDSQKK			

MS-identified tryptic peptides (secreted protein):

1	MGVHECPAWL	WLLLSLLSLP	LGLPVLGAPP	RLICDSRVLE	RYLLEAKEAE	NITTGCAEHC	SLNENITVPD	TKVNFYAWKR
81	MEVGQQAVEV	WQGLALLSEA	VLRGQALLVN	SSQPWEPLQL	HVDKAVSGLR	SLTTLLRALG	AQKEAISPPD	AASAAPLRTI
161	TADTFRKLFR	VYSNFLRGKL	KLYTGEACRT	GDRASKDKKS	DGKDSQKK			

MS-identified chymotryptic peptides (secreted protein):

1	MGVHECPAWL	WLLLSLLSLP	LGLPVLGAPP	RLICDSRVLE	RYLLEAKEAE	NITTGCAEHC	SLNENITVPD	TKVNFYAWKR
81	MEVGQQAVEV	WQGLALLSEA	VLRGQALLVN	SSQPWEPLQL	HVDKAVSGLR	SLTTLLRALG	AQKEAISPPD	AASAAPLRTI
161	TADTFRKLFR	VYSNFLRGKL	KLYTGEACRT	GDRASKDKKS	DGKDSQKK			