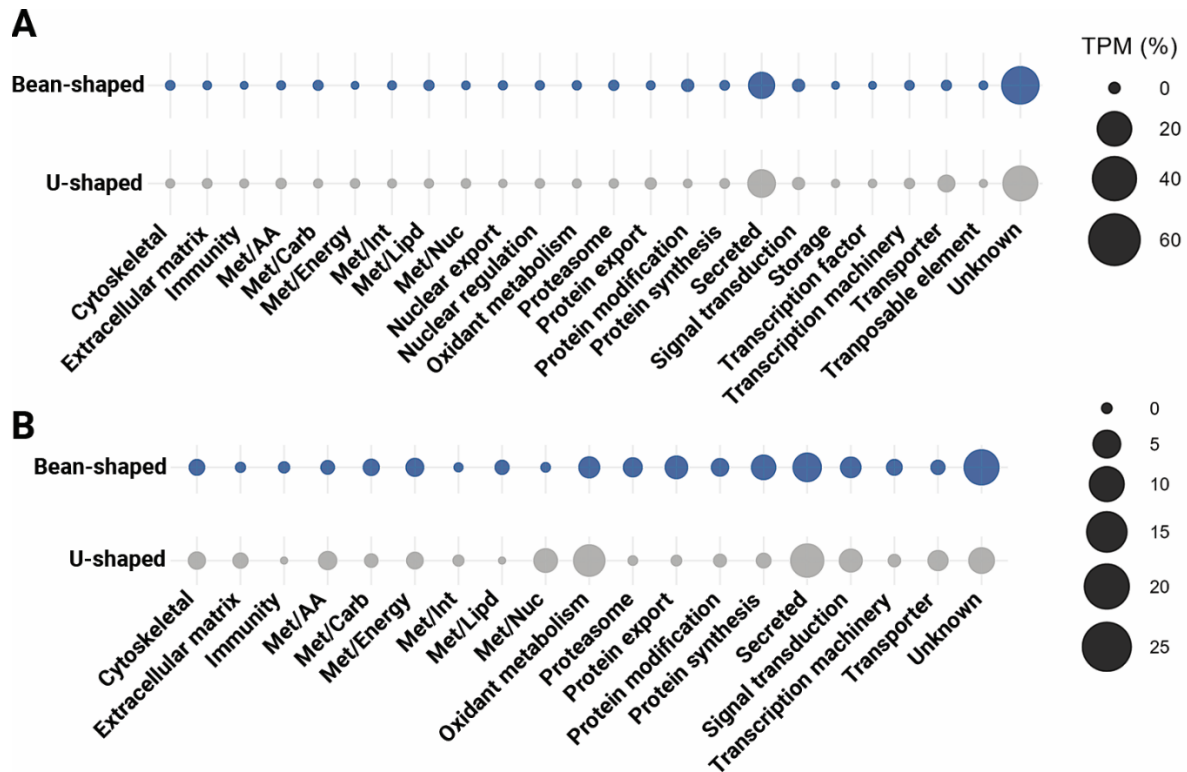**Supplementary Figure 1**: Silver-stained SDS-PAGE (10%) gel containing protein extracts from Bean-shaped (5 µg) and U-shaped (3 µg) salivary glands. The Protein Precision Plus Standard (Bio-Rad) was used as the molecular weight marker.

Supplementary Figure 2: Bubble plot representing the functional classification of the unique transcripts and proteins identified in the Bean- and U-shaped salivary glands of *P. humanus*. The size of the spheres represents the average **(A)** TPM of the CDS of each class or the **(B)** NSAF of the proteins identified by LC-MS/MS as percentages.

A

```
                         10        20        30        40
                .....|....|....|....|....|....|....|....|
seqSigP-12505   MADFKILLIAVLALFSLECQSAQVPKSATNLDLRLFVENS
XP_002432909.1  MADFKILLIAVLALFSLECQSAQVPKSATNLDLRLFVENS

                         50        60        70        80
                .....|....|....|....|....|....|....|....|
seqSigP-12505   ETVAKTLLSSLNDALDKVKPNVDVMVEELSPEAKTLVKEA
XP_002432909.1  ETVAKTLLSSLNDALDKVKPNVDVMVEELSPEAKTLVKEA

                         90       100       110       120
                .....|....|....|....|....|....|....|....|
seqSigP-12505   VKEGREKLAKEQERVNVVFDTLNKAMKDLEPTKSCADKFS
XP_002432909.1  VKEGREKLAKEQERVNVVFDTLNKAMKDLEPTKSCADKFS

                        130       140       150       160
                .....|....|....|....|....|....|....|....|
seqSigP-12505   GPGKKWAHETEKKFVEVYEKVMKKHGKVLENLKVGGEKVL
XP_002432909.1  GPGKKWAHETEKKFVEAYEKVMKKHGKVLENLKVGGEKVL

                        170       180       190       200
                .....|....|....|....|....|....|....|....|
seqSigP-12505   KNARQLFDEKVPKFVACWTPGKKDSKECVNKEVQSTLQEG
XP_002432909.1  KNARQLFDEKVPKFVACWTPGKKDSKECVNKEVQSTLQEG

                        210       220       230       240
                .....|....|....|....|....|....|....|....|
seqSigP-12505   LKLVSDLTTLMQTADADLPPVMEDMVGKLAPVALGAMTGM
XP_002432909.1  LKLVSDLTTLMQTADADLPPVMEDMLGKLAPVALGAMTGM

                        250
                .....|....|....|
seqSigP-12505   TDLMNKFSDCVANLK
XP_002432909.1  TDLMNKFSDCVANLK
```

B
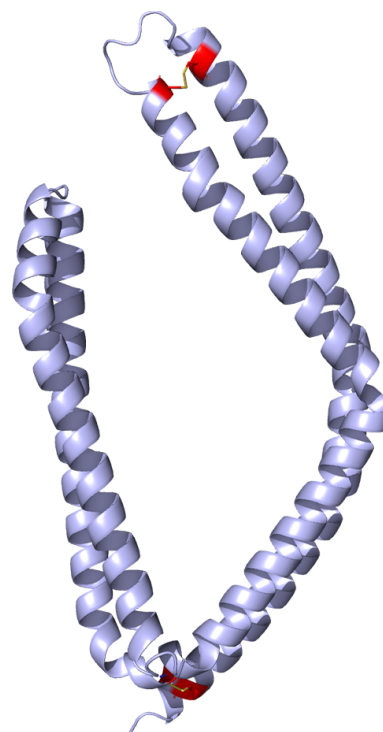
Supplementary Figure 3: Amino acid alignment of seqSigP-12505 and the *P. humanus* genomic entry XP_002432909.1. **(A)** The putative signal peptide is highlighted in red, while the cysteine residues forming the two disulfide bridges are marked in orange. Non-conserved residues between both sequences are depicted in blue. **(B)** Predicted structure of the mature seqSigP-12505 protein generated using AlphaFold2. Cysteine residues involved in disulfide bridge formation are highlighted in red. The figure was rendered and edited using PyMOL.

Supplementary File 1: Excel spreadsheet containing summary results and associated files of the transcriptome analysis.

Supplementary File 2: Excel spreadsheet containing summary results from the LC-MS analysis.