

# Supplementary Materials

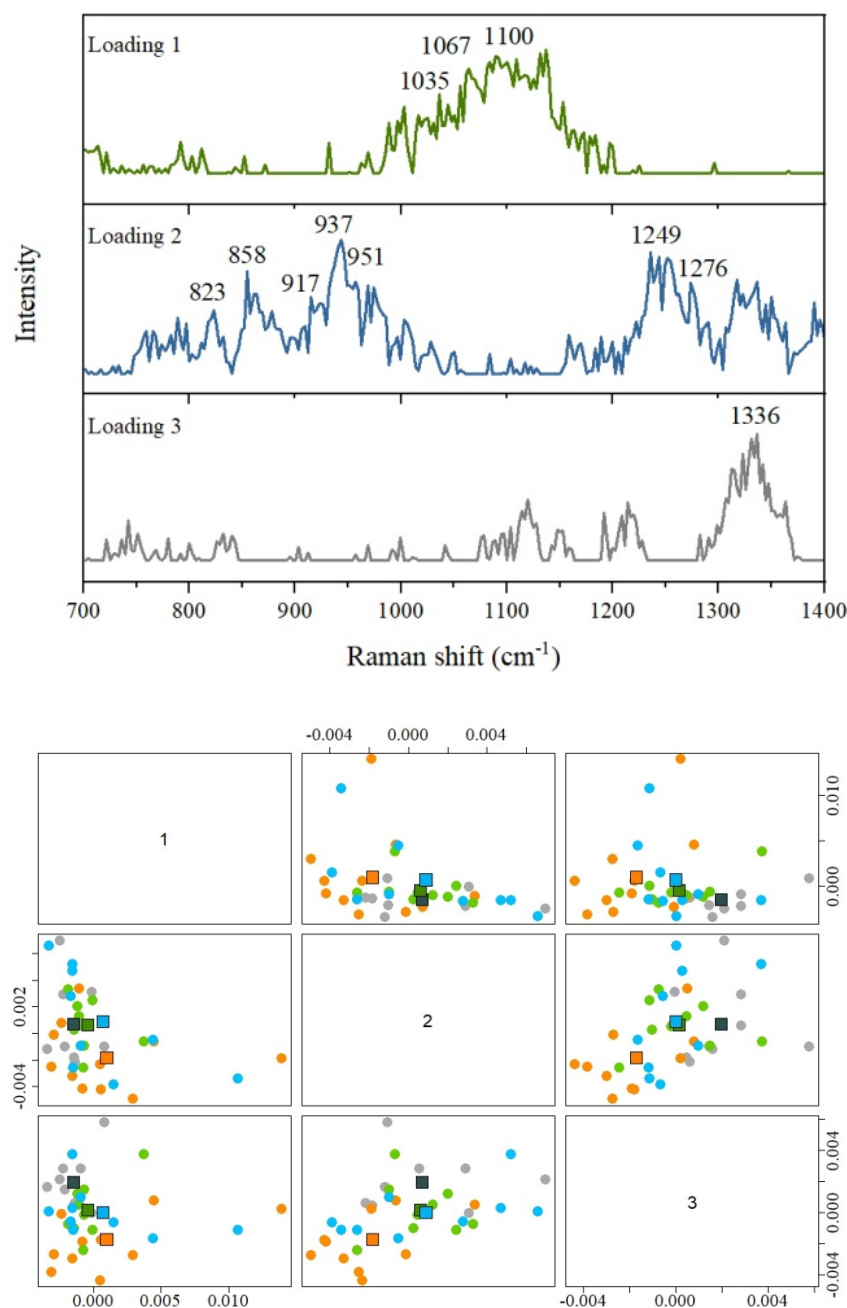
Table S1

Table S1. Collagen I Raman band assignments for the spectral region 700-1800  $\text{cm}^{-1}$

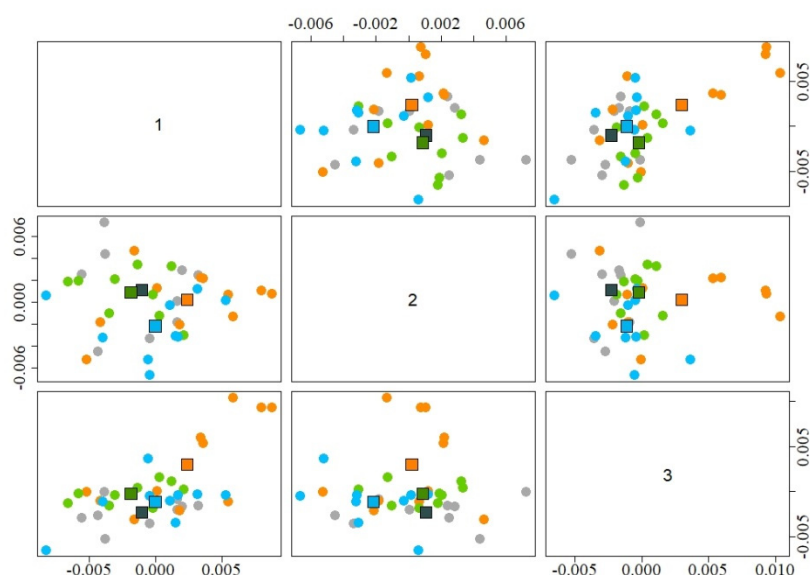
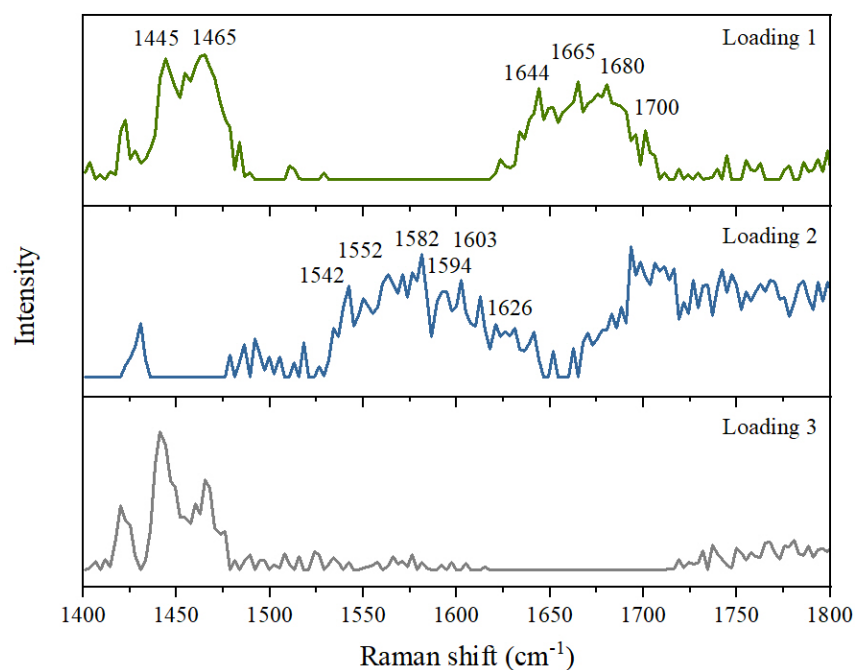
Position	Assignment	Reference
823 $\text{cm}^{-1}$	C-C stretching of collagen backbone	[49]
831 $\text{cm}^{-1}$	Out of plane C-H collective motion in tyrosine	[37], [41]
858 $\text{cm}^{-1}$	Proline, hydroxyproline and tyrosine C-C stretching of proline and hydroxyproline Side chain vibrations of proline and hydroxyproline C-C vibration of the collagen backbone	[45], [37] [49], [36] [35], [46]
917 $\text{cm}^{-1}$	C-C stretching of proline	[35] [42], [36]
934/937 $\text{cm}^{-1}$	C-C stretching of collagen backbone	[44], [36] [42], [45] [46], [35]
951 $\text{cm}^{-1}$	Tyrosine out of plane vibration	[48]
1008 $\text{cm}^{-1}$	Phenylalanine	[49], [36]
1035 $\text{cm}^{-1}$	C-N stretching in proline C-H in-plane bending mode of phenylalanine	[49] [37]
1067 $\text{cm}^{-1}$	C-N stretching in proline	[49]
1100 $\text{cm}^{-1}$	Deformation N-C-H in proline	[49] [37], [36]
1249 $\text{cm}^{-1}$	Amide III (C-N stretching of amide bond)	[49], [35] [46], [36]
1276 $\text{cm}^{-1}$	Amide III	[36], [38] [35], [47]
1314 $\text{cm}^{-1}$	$\text{CH}_3\text{CH}_2$ twisting-collagen	[38]
1320 $\text{cm}^{-1}$	$\text{CH}_3\text{CH}_2$ deformation of collagen ( $\text{CH}_3\text{CH}_2$ twisting in collagen)	[36], [47] [35]
1336 $\text{cm}^{-1}$	$\text{CH}_3\text{CH}_2$ deformation of collagen ( $\text{CH}_3\text{CH}_2$ wagging in collagen; $\text{CH}_2$ scissoring)	[37] [35]
1445 $\text{cm}^{-1}$	$\text{CH}_3\text{CH}_2$ deformation of collagen $\text{CH}_2$ bending and scissoring modes of collagen and phospholipids	[38]
1465 $\text{cm}^{-1}$	$\text{CH}_2/\text{CH}_3$ deformation of collagen and lipids $\text{CH}_2$ wagging	[38]
1544 $\text{cm}^{-1}$	Amide II	[38] [39]
1557 $\text{cm}^{-1}$	Amide II (Stretching C-N and deformation N-H)	[38]
1594 $\text{cm}^{-1}$	Phenylalanine	[38] [40]
1644 $\text{cm}^{-1}$	Amide I	[38]
1665 $\text{cm}^{-1}$	Amide I	[38] [36], [42]
1680 $\text{cm}^{-1}$	Amide I	[38]
1700 $\text{cm}^{-1}$	Amide I	[38] [35]

Figure S1 and Figure S2

Non-negative PCA analysis was performed on two intervals: (700-1400)  $\text{cm}^{-1}$  and (1400-1800)  $\text{cm}^{-1}$  separately because the prominent modes in the latter interval are several times more intensive than the majority of modes in the first interval. First three loading vectors and corresponding PCA score pair plots for both intervals are shown in the Figure S1 and Figure S2.



**Figure S1.** In the upper panel are presented PCA loading vectors 1-3 and in the lower panel score pair plots for the interval (700-1400  $\text{cm}^{-1}$ ). Circles represent score values for each spectra from the experimental groups: control (non-diabetic) - *dark grey*, L-arginine (L-arginine-treated non-diabetic) - *sky blue*, diabetic - *orange*, and diabetic L-arginine-treated rats - *green*. Mean values of the scores for each group are represented by squares and colored as the group they correspond to.



**Figure S2.** In the upper panel are presented PCA loading vectors 1-3 and in the lower panel score pair plots for the interval  $(1400-1800 \text{ cm}^{-1})$ . Circles represent score values for each spectra from the groups of samples: control (non-diabetic) - *dark grey*, L-arginine (L-arginine-treated non-diabetic) - *sky blue*, diabetic - *orange*, and diabetic L-arginine-treated rats - *green*. Mean values of the scores for each group are represented by squares and colored as the group they correspond to.

First loading vector in Figure S1 shows a broad peak with several superimposed peaks in the interval  $(1000-1200 \text{ cm}^{-1})$ . In the score plot for the first component the means are ordered as following: control < diabetes+L-arginine < L-arginine < diabetes, which means that the intensity of the peaks shown in loading component one increases in the same order.

In a similar way the intensities of the vibrational modes positioned at  $823 \text{ cm}^{-1}$ ,  $858 \text{ cm}^{-1}$ ,  $917 \text{ cm}^{-1}$ ,  $937 \text{ cm}^{-1}$ ,  $951 \text{ cm}^{-1}$ ,  $1249 \text{ cm}^{-1}$  and  $1276 \text{ cm}^{-1}$ , observed in the loading vector 2, increase in the order: diabetes < diabetes+L-arginine ~ control < L-arginine.

The intensity of the  $1336\text{ cm}^{-1}$  mode, observed in the loading vector 3 in Figure S1, increases in the order: diabetes < diabetes+L-arginine  $\sim$  L-arginine < control.

Features observed in the loading vector 1 in Figure S2 are positioned at  $1445\text{ cm}^{-1}$ ,  $1465\text{ cm}^{-1}$  ( $\text{CH}_2$  bending modes of proteins) and in the region  $1620\text{-}1700\text{ cm}^{-1}$  (amide I modes) have intensities which increase in the order: diabetes+L-arginine  $\sim$  control < L-arginine < diabetes.

By observing loading vector 2 and scores for component 2 (graphs in the middle column of lower panel) in Figure S2, it can be concluded that the modes positioned between  $1580\text{ cm}^{-1}$  and  $1630\text{ cm}^{-1}$  increase in the intensity in the order: L-arginine < diabetes < diabetes+L-arginine  $\sim$  control.