

## Supplementary Materials

**Table S1.** Peptide fingerprinting of GA from healthy person.

|                   |                   |                   |                   |                   |                    |
|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|
|                   |                   | 1                 | 7                 | <u>17</u>         | 27                 |
|                   |                   | <u>DAHKSE</u>     | <u>VAHRFKDLGE</u> | <u>ENFKALVLIA</u> | <u>FAQYLQQCPF</u>  |
| 37                | 47                | 57                | 67                | 77                | 87                 |
| <u>EDHVKLVNEV</u> | <u>TEFAKTCVAD</u> | <u>ESAENCDKSL</u> | <u>HTLFGDKLCT</u> | <u>VATLRETYGE</u> | <u>MADCCAKQEP</u>  |
| 97                | 107               | 117               | 127               | 137               | 147                |
| <u>ERNECFLQHK</u> | <u>DDNPNLPRLV</u> | <u>RPEVDVMCTA</u> | <u>FHDNEETFLK</u> | <u>KYLYEIARRH</u> | <u>PYFYAPPELLF</u> |
| 157               | 167               | 177               | 187               | 197               | 207                |
| <u>FAKRYKAAFT</u> | <u>ECCQAADKAA</u> | <u>CLLPKLDEL</u>  | <u>DEGKASSAKQ</u> | <u>RLKCASLOKF</u> | <u>GERAFKAWAV</u>  |
| 217               | 227               | 237               | 247               | 257               | 267                |
| <u>ARLSQRFPKA</u> | <u>EFAEVSKLVT</u> | <u>DLTKVHTECC</u> | <u>HGDLLCADD</u>  | <u>RADLAKYICE</u> | <u>NQDSISSKLK</u>  |
| 277               | 287               | 297               | 307               | 317               | 327                |
| <u>ECCEKPLLEK</u> | <u>SHCIAEVEND</u> | <u>EMPADLPSLA</u> | <u>ADFVESKDVC</u> | <u>KNYAEAKDVF</u> | <u>LGMFLYEYAR</u>  |
| 337               | 347               | 357               | 367               | 377               | 387                |
| <u>FAKRYKAAFT</u> | <u>LRLAKTYETT</u> | <u>LEKCCAAADP</u> | <u>HECYAKVFDE</u> | <u>FKPLVEEPQN</u> | <u>LIKONCELFE</u>  |
| 397               | 407               | 417               | 427               | 437               | 447                |
| <u>ARLSQRFPKA</u> | <u>LLVRYTKKVP</u> | <u>QVSTPTLVEV</u> | <u>SRNLGKVGSK</u> | <u>CKKHPEAKRM</u> | <u>PCAEDYLSV</u>   |
| 457               | 467               | 477               | 487               | 497               | 507                |
| <u>ECCEKPLLEK</u> | <u>TPVSDRVTKC</u> | <u>CTESLVNRRP</u> | <u>CFSALEVDET</u> | <u>YVPKEFNAET</u> | <u>FTFHADICTL</u>  |
| 517               | 527               | 537               | 547               | 557               | 567                |
| <u>RHPDYSVLL</u>  | <u>TALVELVKHK</u> | <u>PKATKEQLKA</u> | <u>VMDDFAAFVE</u> | <u>KCKKADDKET</u> | <u>CFAEEGKKLV</u>  |
| 577               | 585               |                   |                   |                   |                    |
| <u>AASQAALGL</u>  |                   |                   |                   |                   |                    |

Amino acid code letters in red are from tryptic digestion and letters underlined are from Glu-C digestion. Total sequence coverage is 88.2%.

**Table S2.** Peptide fingerprinting of GA from diabetic patient.

|                   |                   |                   |                   |                   |                    |
|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|
|                   |                   | 1                 | 7                 | <u>17</u>         | 27                 |
|                   |                   | <u>DAHKSE</u>     | <u>VAHRFKDLGE</u> | <u>ENFKALVLIA</u> | <u>FAQYLQQCPF</u>  |
| 37                | 47                | 57                | 67                | 77                | 87                 |
| <u>EDHVKLVNEV</u> | <u>TEFAKTCVAD</u> | <u>ESAENCDKSL</u> | <u>HTLFGDKLCT</u> | <u>VATLRETYGE</u> | <u>MADCCAKQEP</u>  |
| 97                | 107               | 117               | 127               | 137               | 147                |
| <u>ERNECFLQHK</u> | <u>DDNPNLPRLV</u> | <u>RPEVDVMCTA</u> | <u>FHDNEETFLK</u> | <u>KYLYEIARRH</u> | <u>PYFYAPPELLF</u> |
| 157               | 167               | 177               | 187               | 197               | 207                |
| <u>FAKRYKAAFT</u> | <u>ECCQAADKAA</u> | <u>CLLPKLDEL</u>  | <u>DEGKASSAKQ</u> | <u>RLKCASLOKF</u> | <u>GERAFKAWAV</u>  |
| 217               | 227               | 237               | 247               | 257               | 267                |
| <u>ARLSQRFPKA</u> | <u>EFAEVSKLVT</u> | <u>DLTKVHTECC</u> | <u>HGDLLCADD</u>  | <u>RADLAKYICE</u> | <u>NQDSISSKLK</u>  |
| 277               | 287               | 297               | 307               | 317               | 327                |
| <u>ECCEKPLLEK</u> | <u>SHCIAEVEND</u> | <u>EMPADLPSLA</u> | <u>ADFVESKDVC</u> | <u>KNYAEAKDVF</u> | <u>LGMFLYEYAR</u>  |
| 337               | 347               | 357               | 367               | 377               | 387                |
| <u>RHPDYSVLL</u>  | <u>LRLAKTYETT</u> | <u>LEKCCAAADP</u> | <u>HECYAKVFDE</u> | <u>FKPLVEEPQN</u> | <u>LIKONCELFE</u>  |
| 397               | 407               | 417               | 427               | 437               | 447                |
| <u>QLGEYKFQNA</u> | <u>LLVRYTKKVP</u> | <u>QVSTPTLVEV</u> | <u>SRNLGKVGSK</u> | <u>CKKHPEAKRM</u> | <u>PCAEDYLSV</u>   |
| 457               | 467               | 477               | 487               | 497               | 507                |
| <u>LNQLCVLHEK</u> | <u>TPVSDRVTKC</u> | <u>CTESLVNRRP</u> | <u>CFSALEVDET</u> | <u>YVPKEFNAET</u> | <u>FTFHADICTL</u>  |
| 517               | 527               | 537               | 547               | 557               | 567                |
| <u>SEKERQIKKQ</u> | <u>TALVELVKHK</u> | <u>PKATKEQLKA</u> | <u>VMDDFAAFVE</u> | <u>KCKKADDKET</u> | <u>CFAEEGKKLV</u>  |
| 577               | 585               |                   |                   |                   |                    |
| <u>AASQAALGL</u>  |                   |                   |                   |                   |                    |

Amino acid code letters in red are from tryptic digestion and letters underlined are from Glu-C digestion. Total sequence coverage is 77.6%.