

Table S1. Information of patients allergic to soybeans

| Sample | Gender | Ethnicity | Birth Date | Soybean allergen IgE levels (kU/I) |
|--------|--------|-----------|------------|------------------------------------|
| 1 | Female | Caucasian | 04/01/1979 | 5.484 |
| 2 | Female | American | 09/09/1992 | 72.333 |
| 3 | Female | American | 09/09/1992 | 38 |
| 4 | Male | Asian | 10/14/1993 | 12.088 |
| 5 | Female | American | 09/09/1992 | 47.7 |

Table S2. The molecular weight of soybean allergens (Amnuaycheewa & de Mejia, 2010; Pi, Sun, Fu, et al., 2021)

| Soybean allergens | Molecular weight (kDa) |
|--------------------------|--|
| Gly m 1 | 8.3 |
| Gly m 2 | 8 |
| Gly m 3 | 14 |
| Gly m 4 | 17 |
| Gly m 5 | α subunit: 57-76 α' subunit: 57-83 β subunit: 42-53 |
| Gly m 6 | G1 subunit: 56 G2 subunit: 54 G3 subunit: 54 G4 subunit: 64 G5 subunit: 59 |
| Gly m 7 | 76.2 |
| Gly m 8 | 28 |
| Gly m Bd 28K (P28) | 28 |
| Gly m Bd 30K (P34) | 30 |
| Kunitz trypsin inhibitor | 20 |

Table S3. The information of proteins

| Accession | Description | Coverage [%] | MW [kDa] |
|-----------|----------------------------------|--------------|----------|
| P0DO16 | Beta-conglycinin alpha subunit 1 | 54 | 70.3 |
| P11827 | Beta-conglycinin alpha' subunit | 51 | 72.2 |
| P04776 | Glycinin G1 | 51 | 55.7 |
| P25974 | Beta-conglycinin beta subunit 1 | 50 | 50.4 |
| F7J077 | Beta-conglycinin beta subunit 2 | 50 | 50.4 |
| P02858 | Glycinin G4 | 49 | 63.8 |
| P04347 | Glycinin G5 | 35 | 57.9 |
| P04405 | Glycinin G2 | 33 | 54.4 |
| P11828 | Glycinin G3 | 29 | 54.2 |

| | | | |
|------------|--|----|------|
| P26987 | Stress-induced protein SAM22 | 24 | 16.8 |
| A0A0R2FDV8 | DNA-binding protein HU | 13 | 10 |
| A0A0A1M9Z2 | 30S ribosomal protein S5 | 12 | 17.9 |
| A0A5E8NL87 | Elongation factor Tu | 11 | 43.4 |
| A0A375C1Q5 | Elongation factor Tu | 10 | 43.1 |
| A0A063XHU6 | 50S ribosomal protein L19 | 9 | 13.4 |
| A0A5E8NN63 | 6-phosphogluconate dehydrogenase (Decarboxylating) | 8 | 32.7 |
| A0A2K4ZCR6 | 50S ribosomal protein L15 | 8 | 15.6 |
| A0A5E8NNK3 | Pyruvate kinase | 7 | 50.4 |
| A0A375BT21 | 30S ribosomal protein S13 | 7 | 13.6 |
| A0A375BF93 | Iron-sulfur cluster assembly scaffold protein IscU | 7 | 14.1 |
| A0A063XB64 | 50S ribosomal protein L5 | 7 | 20.1 |
| A0A063XB29 | Elongation factor Tu | 7 | 43.6 |
| A0A375C644 | 2-dehydro-3-deoxy-phosphogluconate aldolase | 6 | 21.6 |
| I8IE20 | Calmodulin | 5 | 17 |
| A0A6I7CXS1 | Ribonuclease YeeF | 5 | 21.6 |
| A0A5E8NKS0 | ATP-dependent Clp protease ATP-binding subunit | 5 | 76.9 |
| A0A410ZVW4 | Chaperone protein DnaK | 4 | 65.9 |
| A0A375DUA1 | Response regulator in two-component regulatory system with CopS, regulation of copper resistance | 4 | 25.6 |
| A0A375BT57 | 50S ribosomal protein L2 | 4 | 30.1 |
| A0A375BBT8 | ATP synthase subunit beta | 4 | 50.8 |
| A0A2K4ZIL3 | 30S ribosomal protein S2 | 4 | 28.2 |
| I8U0Z5 | Molecular chaperones HSP70/HSC70, HSP70 superfamily | 3 | 69.7 |
| A0A375CH53 | Elongation factor G | 3 | 77.8 |
| A0A375CDG7 | Putative type I secretion system outer membrane efflux transmembrane protein | 3 | 53.4 |
| A0A375CA40 | Flagellin | 3 | 44.9 |
| A0A375BFG8 | Ketol-acid reductoisomerase (NADP(+)) | 3 | 36.6 |
| A0A164WWR4 | Trigger factor | 3 | 47.5 |
| I8U0C5 | Elongation factor 1-alpha | 2 | 50 |
| I8I9W5 | ATP synthase subunit alpha | 2 | 59.9 |
| A0A5E8NP70 | Glucose-6-phosphate 1-dehydrogenase | 2 | 55.1 |
| A0A5E8NKK6 | Glyceraldehyde-3-phosphate dehydrogenase | 2 | 35.7 |
| A0A375BVD9 | 60 kDa chaperonin | 2 | 57.4 |

| | | | |
|------------|--|---|-------|
| A0A375BUT8 | Putative ACYL-CoA DEHYDROGENASE OXIDOREDUCTASE | 2 | 65.3 |
| A0A375BER7 | Succinate-semialdehyde dehydrogenase I, NADP-dependent | 2 | 51.5 |
| A0A375BBA9 | Succinate--CoA ligase [ADP-forming] subunit beta | 2 | 41.2 |
| A0A375B8Y2 | ATP synthase subunit alpha | 2 | 55.4 |
| A0A375B8J0 | Adenosylhomocysteinase | 2 | 51.9 |
| A0A2K4ZPJ1 | Neopullulanase | 2 | 71.6 |
| A0A2K4ZLR1 | Formate acetyltransferase | 2 | 76.1 |
| A0A1K0FDI3 | Phosphoketolase | 2 | 92.2 |
| A0A1K0ET72 | Trigger factor | 2 | 46.3 |
| A0A1K0ERM9 | Phosphoglycerate kinase | 2 | 43.1 |
| A0A0R2FCT6 | GTP-binding protein | 2 | 68.4 |
| A0A0R2F2Q4 | ATP synthase subunit beta | 2 | 50.3 |
| I8A836 | Enoyl reductase domain of FAS1 | 1 | 198.4 |
| A0A375BT51 | DNA-directed RNA polymerase subunit beta' | 1 | 155.8 |
| A0A2K4ZMM8 | Chaperone protein HtpG | 1 | 106.7 |
| A0A2K4ZJ99 | ATP-dependent Clp protease ATP-binding subunit ClpC | 1 | 90.8 |
| A0A2K4ZHA5 | DNA-directed RNA polymerase subunit beta' | 1 | 140.1 |

Table S4. Changes in epitopes in Gly m 4 and Gly m 5 among extracted proteins from raw, boiled and autoclaved soybeans

| Amino acid sequence | Abundance | | | Allergens |
|-----------------------------|-------------|----------------|--------------------|-----------------------------|
| | Raw soybean | Boiled soybean | Autoclaved soybean | |
| ALVTDADNVIPK | 367.7 | 10.5 | 19.7 | Gly m 4 |
| SVENVEGNNGPGTIK | 407.4 | 8.6 | 5 | |
| SVENVEGNNGPGTIKK | 514.3 | 12.9 | 23 | |
| VEKEECEGEIPRPRRPQHPR | 0 | 29.4 | 0 | α subunit of Gly m 5 |
| EECEEGEIPRPRRPQHPR | 1.4 | 22.1 | 0 | |
| EPQQPGEKEEDEDEQPRPIPFPRPQPR | 62.6 | 76.2 | 259.2 | |
| EEDEDEQPRPIPFPRPQPR | 56.2 | 88.4 | 6.1 | |
| EEQEWPRKEEK | 32.5 | 88.1 | 65.8 | |
| EEQEWPR | 88.9 | 59.5 | 80.4 | |
| EEQEWPRK | 29.8 | 41.8 | 17.5 | |
| GSEEEDEDEDEEQDER | 311.2 | 56.4 | 14.7 | |
| QFPFPRPPHQK | 78.7 | 30.3 | 259.1 | |
| QFPFPRPPHQKEER | 137.7 | 5.2 | 32 | |
| KQEEDEDEEQQR | 68.6 | 129.7 | 36.1 | |
| QEEDEDEEQQR | 135.4 | 108.4 | 0 | |

| | | | | |
|-----------------------|-------|-------|-------|----------------------------------|
| ESEESDSELR | 616 | 0 | 0 | |
| ESEESDSELR | 575.7 | 0 | 0 | |
| NKNPFLFGSNR | 477.1 | 8.2 | 56.4 | |
| NPFLFGSNRFETLTK | 566.4 | 0 | 0 | |
| NPFLFGSNR | 296.2 | 3.3 | 29.1 | |
| LQSGDALR | 165.6 | 58.2 | 25.9 | |
| VPSGTTYVVPDNNENLR | 572.9 | 0 | 0 | |
| VLFSREEGQQQGEQR | 309.9 | 0 | 0 | |
| KTISSDCKPFNLR | 783.9 | 0 | 0 | |
| TISSDCKPFNLR | 548.8 | 1.4 | 4.3 | |
| SRDPIYSNK | 491.5 | 12.7 | 2.8 | |
| DPIYSNK | 437.8 | 0 | 0 | |
| FFEITPEKNPQLR | 473.8 | 19.3 | 6 | |
| FFEITPEK | 283.2 | 37.9 | 16.1 | |
| EQQQEQQQEQPLEVRK | 183.6 | 52.7 | 0 | |
| EQQQEQQQEQPLEVR | 195.3 | 33.7 | 11.7 | |
| ESYFVDAQPK | 308.9 | 0 | 153.1 | |
| VEEEECGQIPRPRQHPER | 54.7 | 53 | 6.2 | α' subunit of Gly m 5 |
| QQHGEKEEDEGEQPRPFPRPR | 8 | 2.3 | 845.1 | |
| EDEGEQPRPFPRPR | 29.8 | 64.6 | 9.3 | |
| EHPRPHQPHQKEEK | 14.2 | 8.6 | 370.3 | |
| EEKHEWQHK | 108.3 | 81.6 | 187.7 | |
| EEKHEWQHKQEK | 54.2 | 102.5 | 0 | |
| ESEEEEDQDEDEEQDK | 207.6 | 9.9 | 0 | |
| VLFGRGEGQQQGEER | 87.9 | 28.1 | 0 | |
| KTISSDCKPFNLR | 783.9 | 0 | 0 | |
| TISSDCKPFNLR | 548.8 | 1.4 | 4.3 | |
| LFEITPEKNPQLR | 543.5 | 12.4 | 4.7 | |
| LFEITPEK | 334.1 | 34.9 | 22.8 | |
| QQQEQPLEVR | 272.7 | 26.9 | 14.4 | |
| QQQEQPLEVRK | 361.6 | 0 | 0 | |
| LAIPVKNPGR | 118.6 | 102.6 | 27 | β -subunit 1 of Gly m 5 |
| QQEGVIVELSK | 843.7 | 0 | 20.5 | |
| TISSDEPFNLR | 610.9 | 0 | 0 | |
| SRNPIYSNNFGK | 883.6 | 0 | 0 | |
| NPIYSNNFGK | 495.4 | 0 | 0 | |
| FFEITPEKNPQLR | 473.8 | 19.3 | 6 | |
| FFEITPEK | 283.2 | 37.9 | 16.1 | |
| QKQEEPLEVQR | 295.9 | 50.3 | 75.6 | |
| QEEPLEVQR | 342.7 | 70.6 | 18.3 | |
| AILTLVNDDRDSYNLHPGDAQ | 834.1 | 2.4 | 0 | β -subunit 2 of Gly m 5 |
| AILTLVNDDR | 467 | 17.1 | 7.4 | |
| LAIPVKNPGR | 118.6 | 102.6 | 27 | |
| VLLGEEEQ | 240.5 | 74.7 | 17.5 | |
| VLLGEEEQQQEGVIVELSK | 663.2 | 0 | 0 | |
| QQEGVIVELSK | 843.7 | 0 | 20.5 | |
| TISSDEPFNLR | 610.9 | 0 | 0 | |
| SRNPIYSNNFGK | 883.6 | 0 | 0 | |

| | | | | |
|---------------|---------|--------|--------|--|
| NPIYSNNFGK | 495.4 | 0 | 0 | |
| FFEITPEKNPQLR | 473.8 | 19.3 | 6 | |
| FFEITPEK | 283.2 | 37.9 | 16.1 | |
| QKQEEEEPLEVQR | 295.9 | 50.3 | 75.6 | |
| QEEEEPLEVQR | 342.7 | 70.6 | 18.3 | |
| Total | 23888.7 | 2076.7 | 2940.7 | |