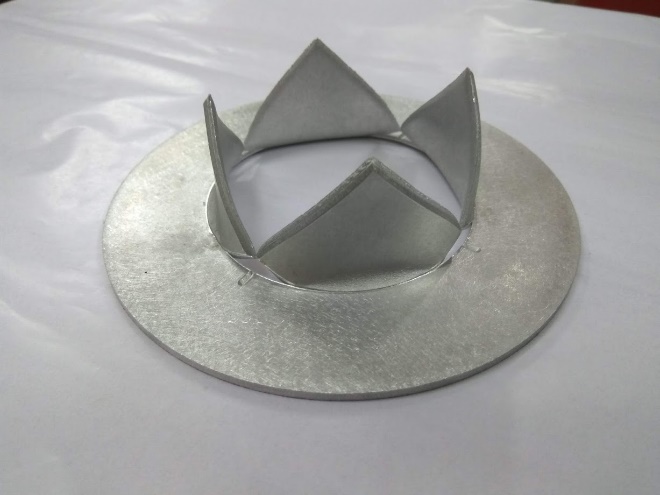
**Supplementary material # 1**



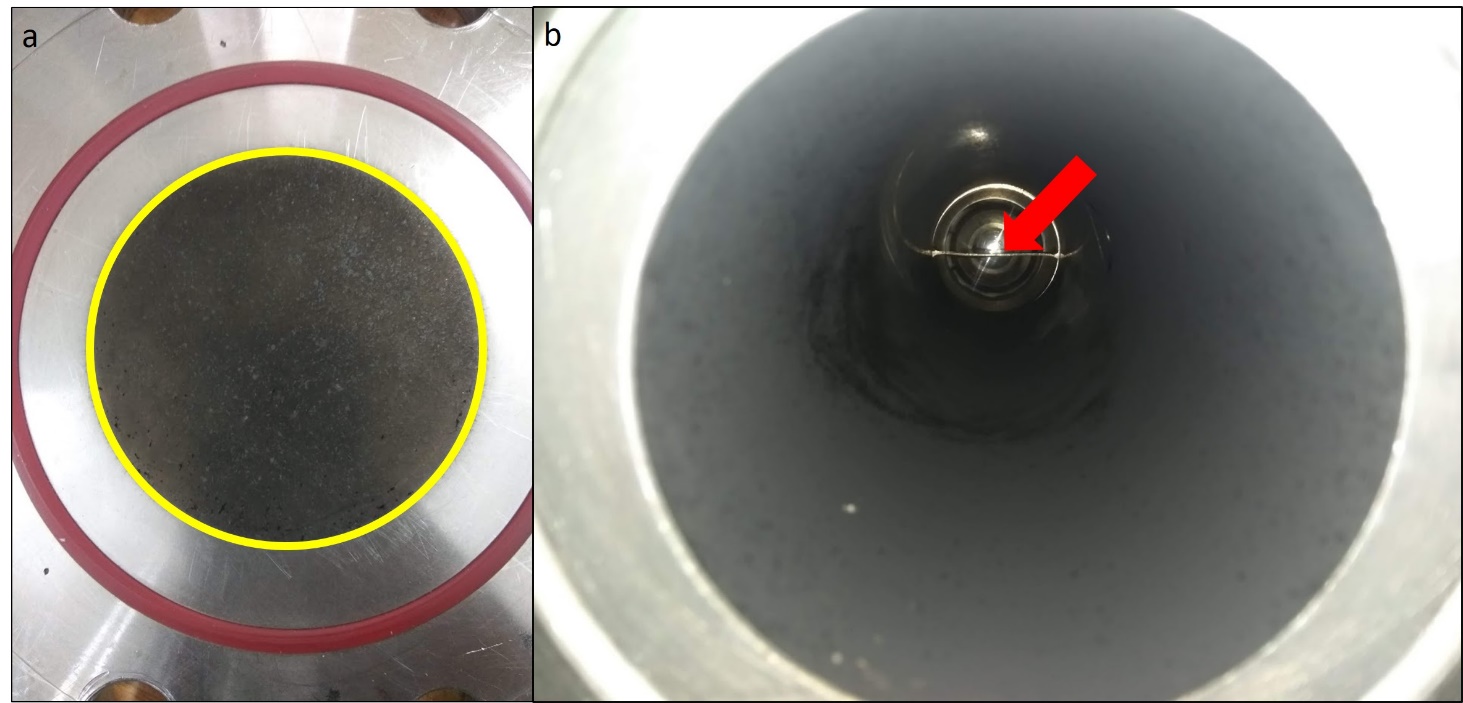
b

a

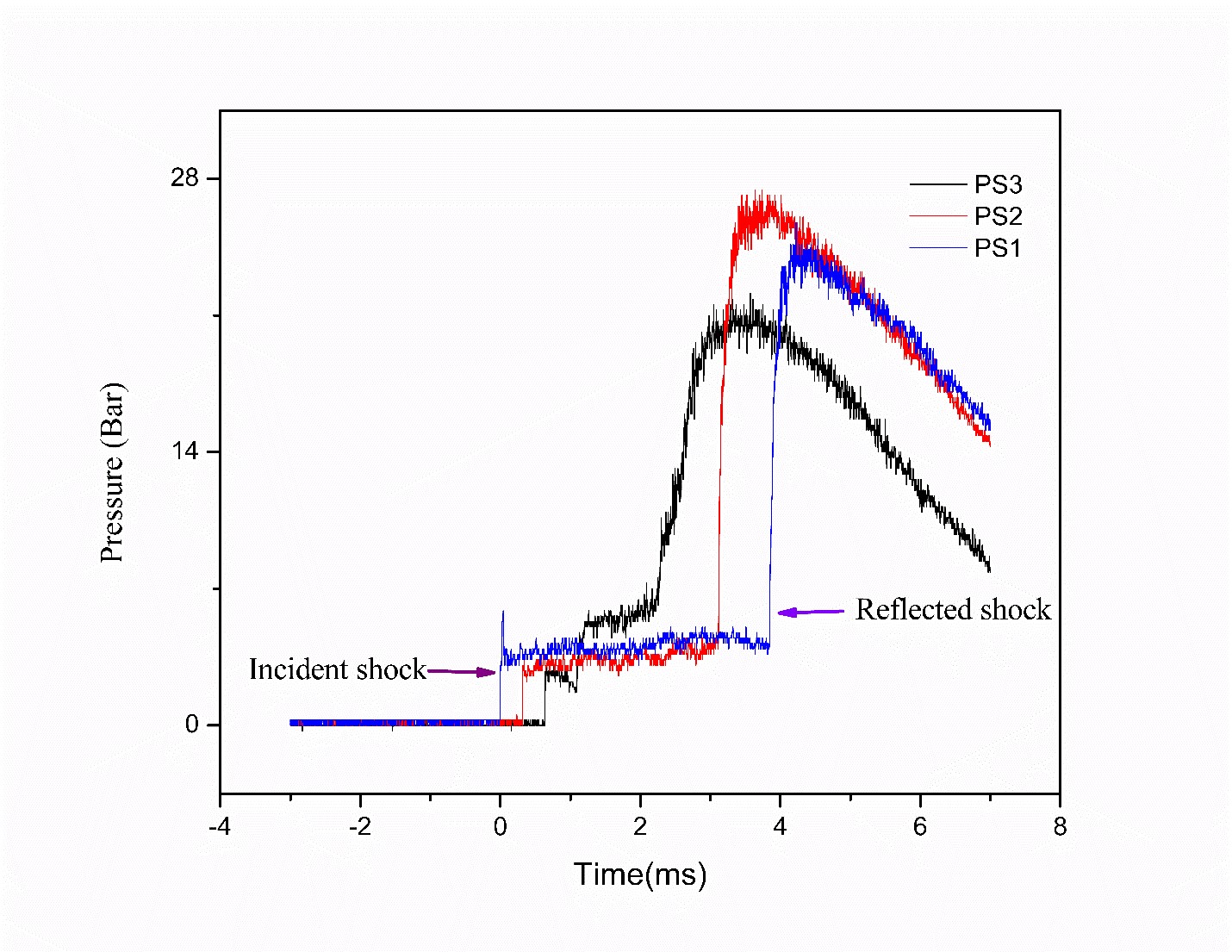
**Figure S1:** Aluminium diaphragm (**a**) before shock with V groove and (**b**) petals are opened after bursting



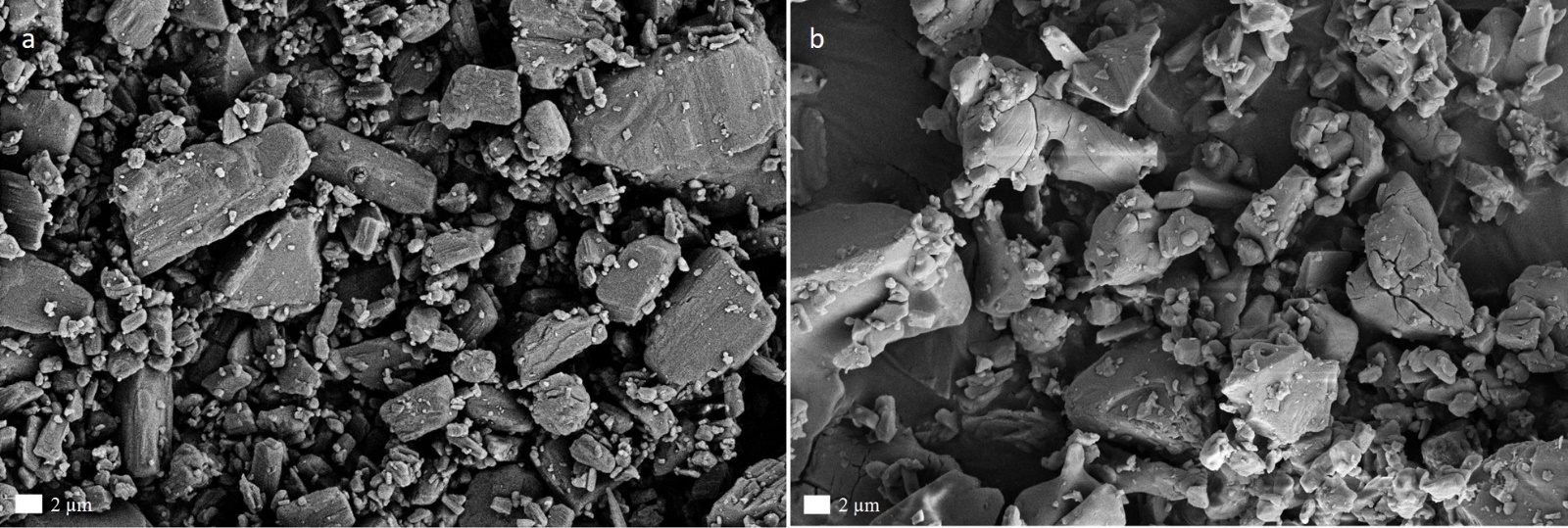
**Figure S2:** Amino acid powder uniformly distributed on the sample holder (thin plate) mounted next to the ball valve before shock treatment



**Figure S3:** After shock processing the solid residue sample distributed (**a**) on the end flange with sample on the surface marked within the yellow circle and (**b**) the surface of reaction chamber mounted behind the sample holder shown in Figure S2 (red arrow), the shock processed sample is removed from their wall surface and stored in inert condition.



**Figure S4:** Pressure signal recorded using digital storage oscilloscope for shock speed and pressure measurements



**Figure S5:** SEM micrographs of unprocessed amino acids (**a**) glycine (**b**) mixture of four amino acid

c

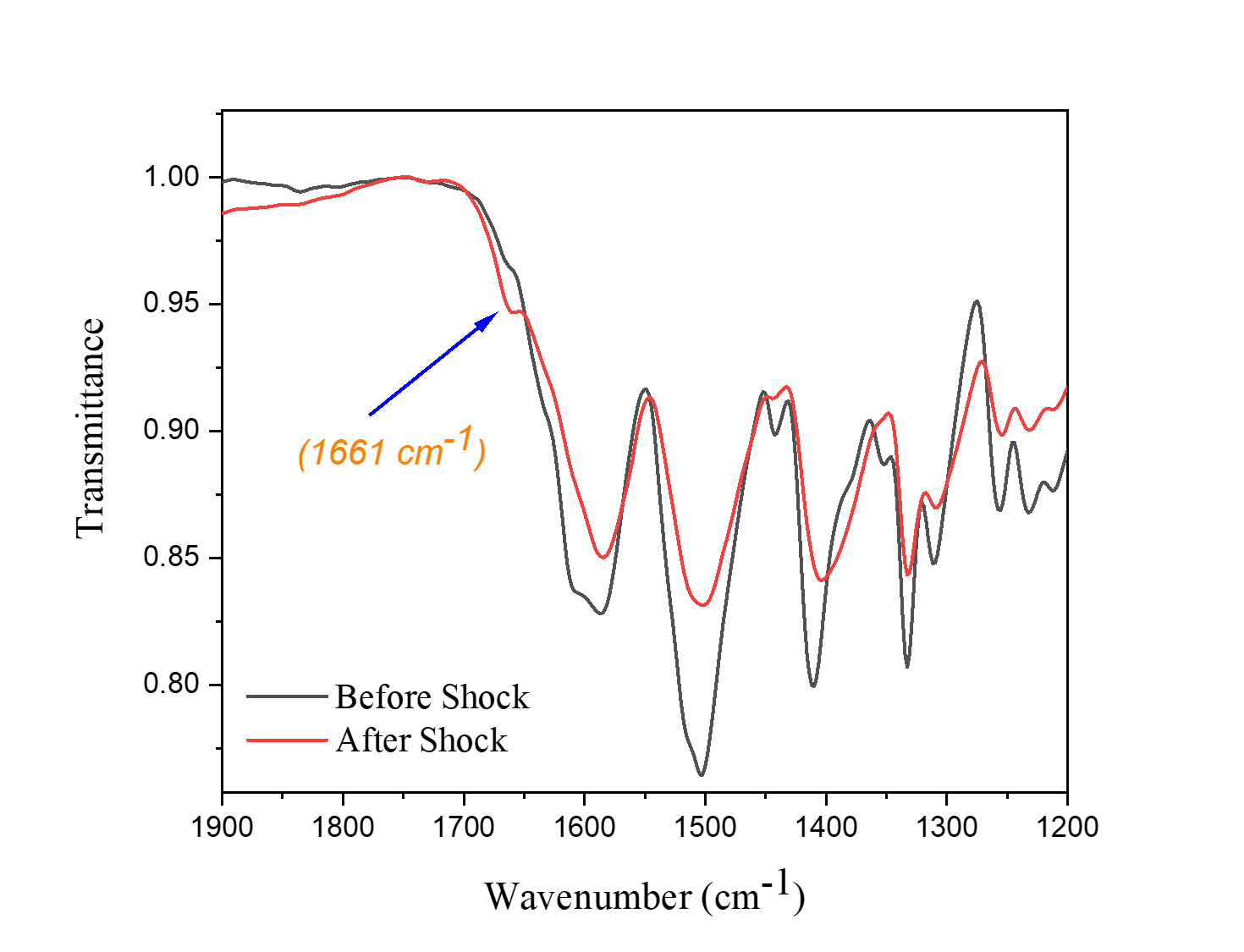
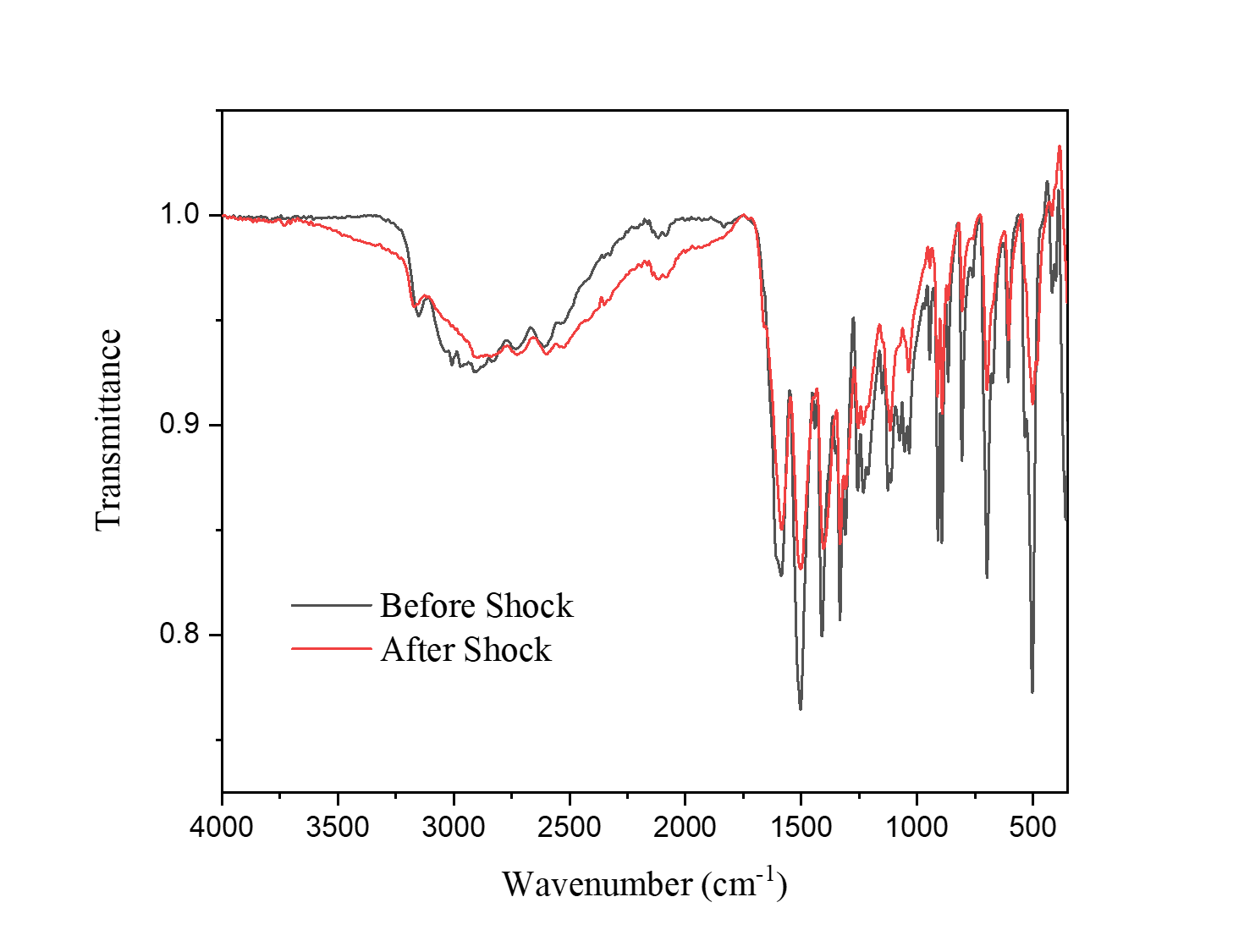
**IR spectra of shock processed residue**

1. C:\Users\LHR\AppData\Local\Microsoft\Windows\INetCache\Content.Word\Glycine2.tifC:\Users\LHR\AppData\Local\Microsoft\Windows\INetCache\Content.Word\glycine1.tif**#825-Glycine**

Full range mid IR spectra ssssssssssspectra spectraspectra

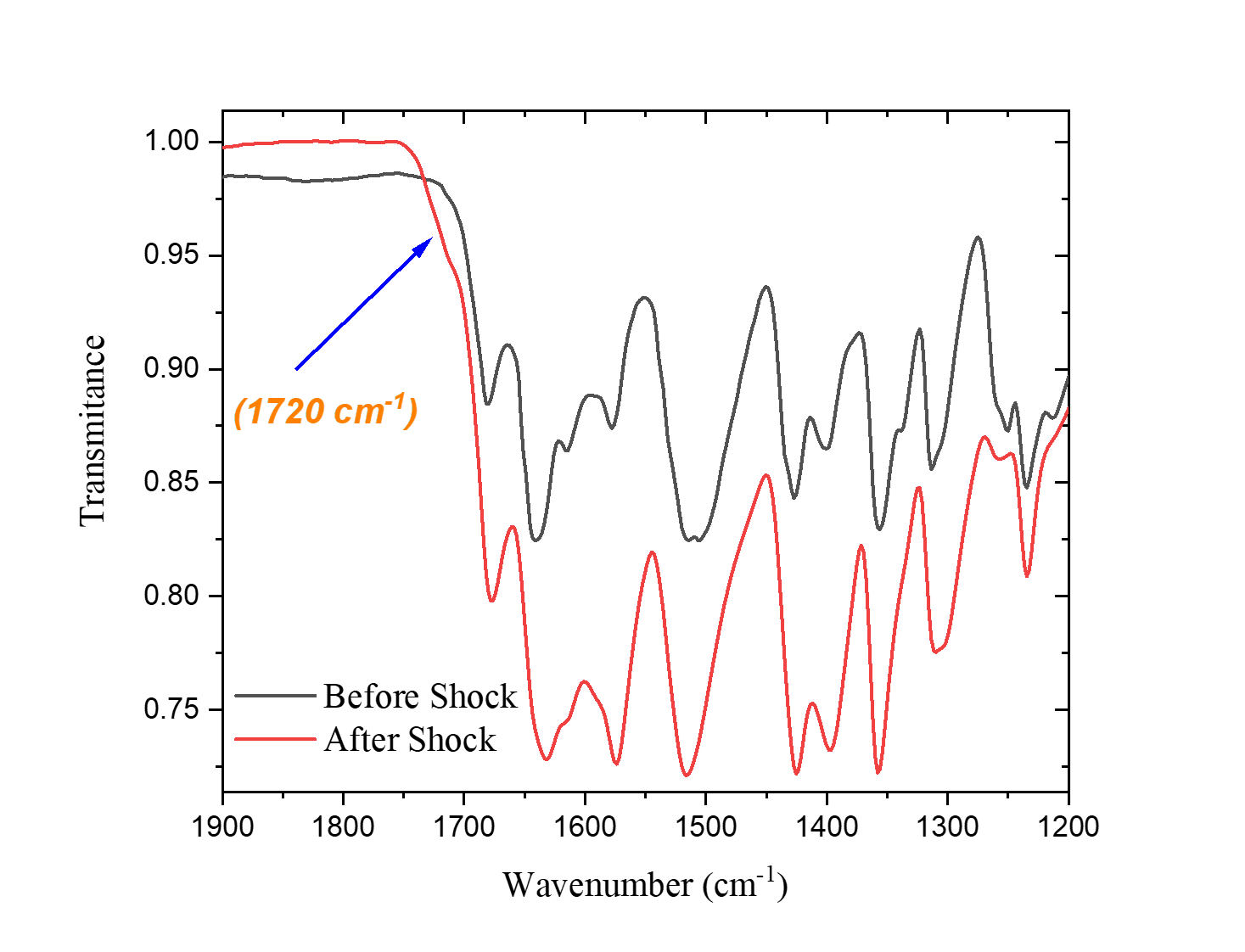
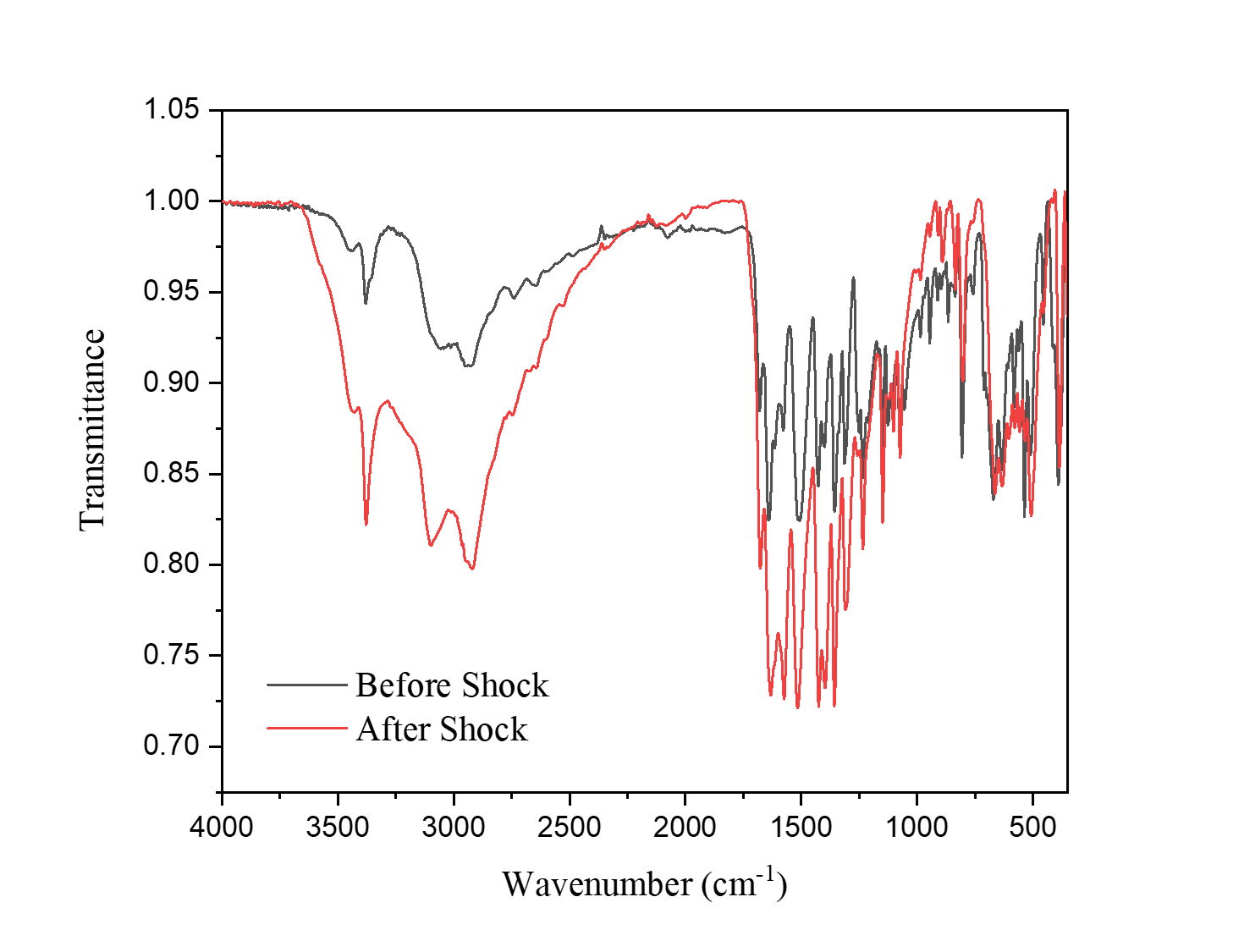
IR spectra with signature of amide-I band

1. **#823-Glycine Glutamic acid mixture**



Full range mid IR spectra

IR spectra with signature of amide-I band

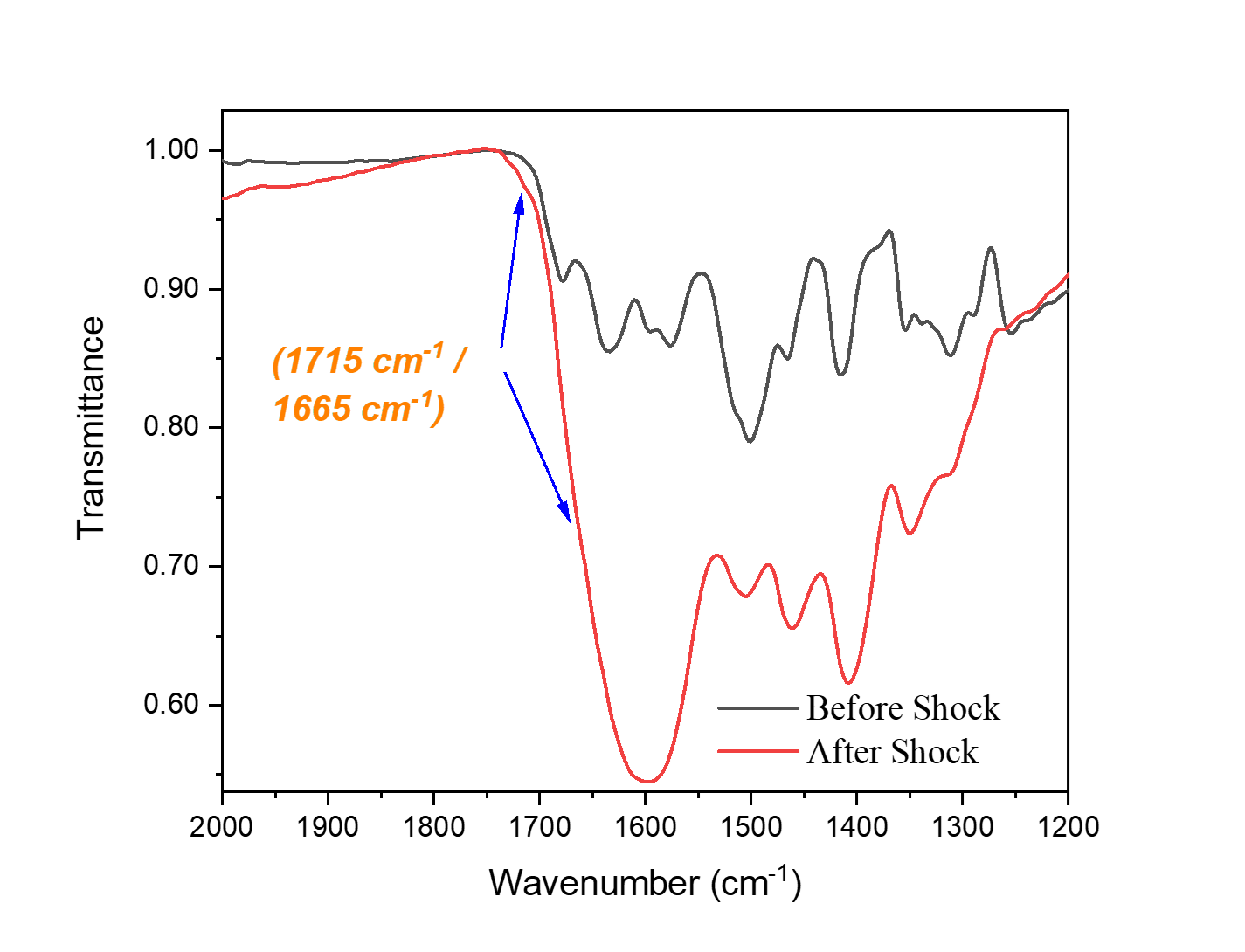
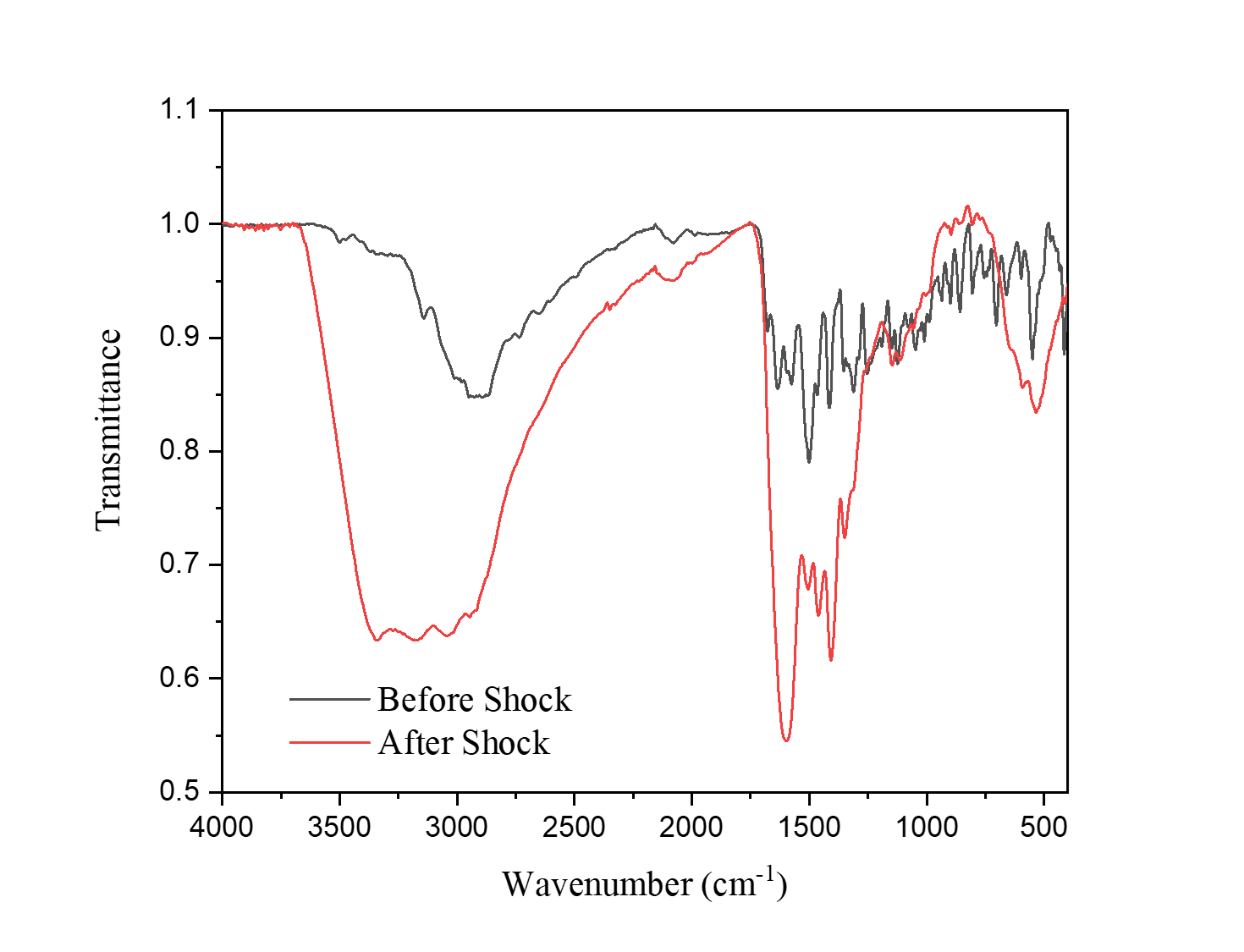


1. **#711-Asparagine Glutamic acid mixture**

IR spectra with signature of amide-I band

Full range mid IR spectra

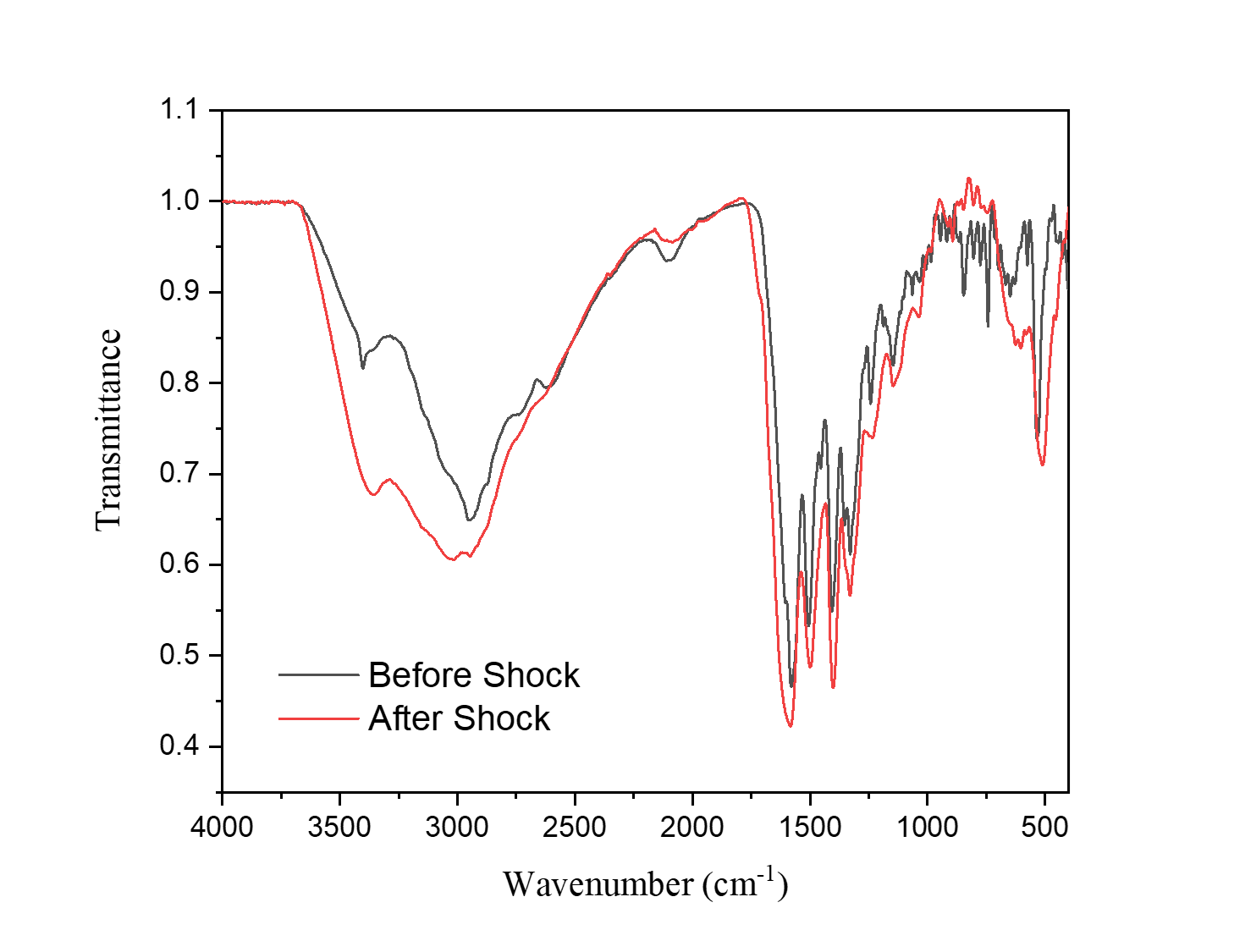
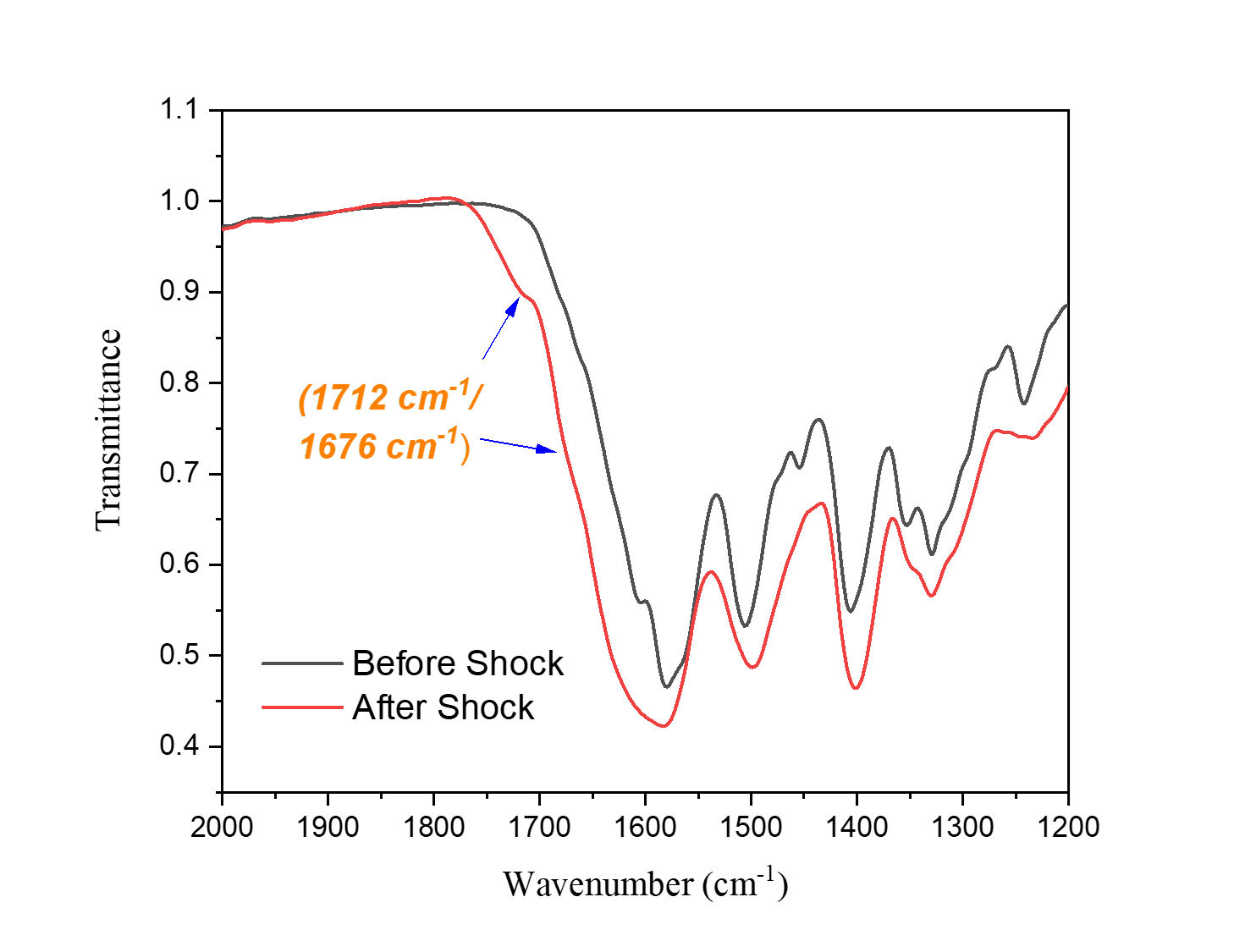
1. **# 819 - Mixture of four amino acids**



Full range mid IR spectra

IR spectra with signature of amide-I band

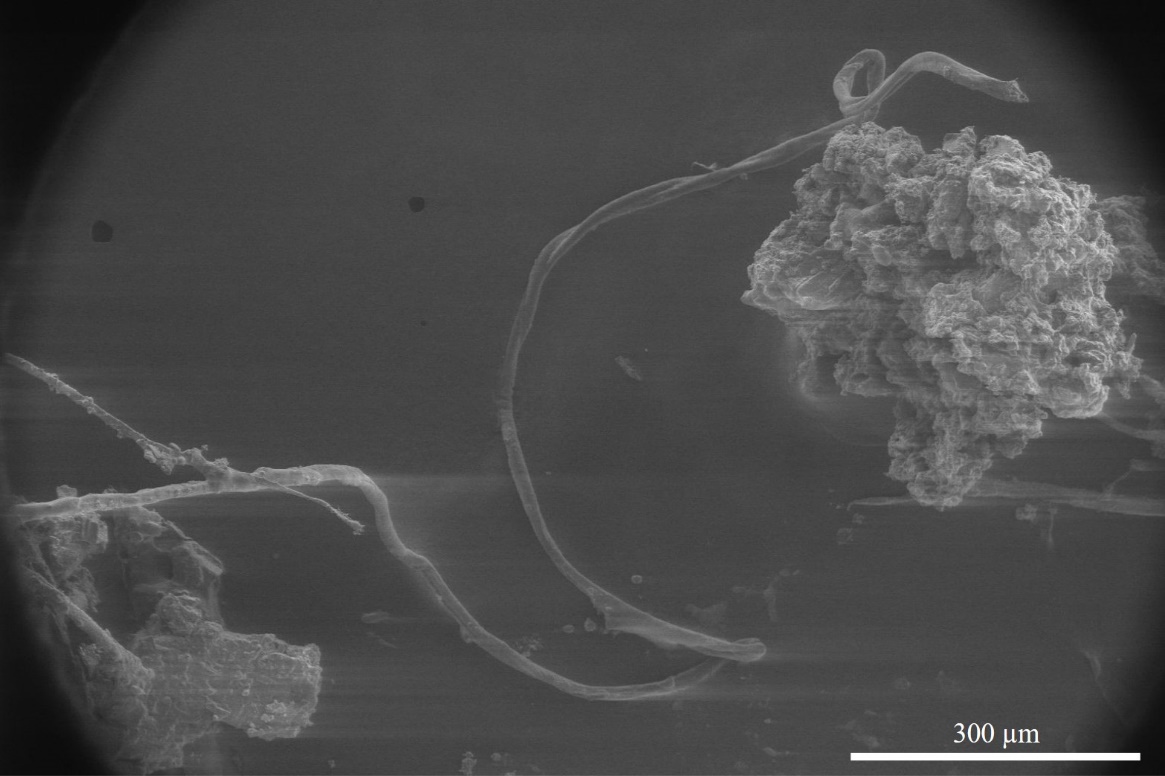
1. **#814 - Mixture of 18 amino acids**



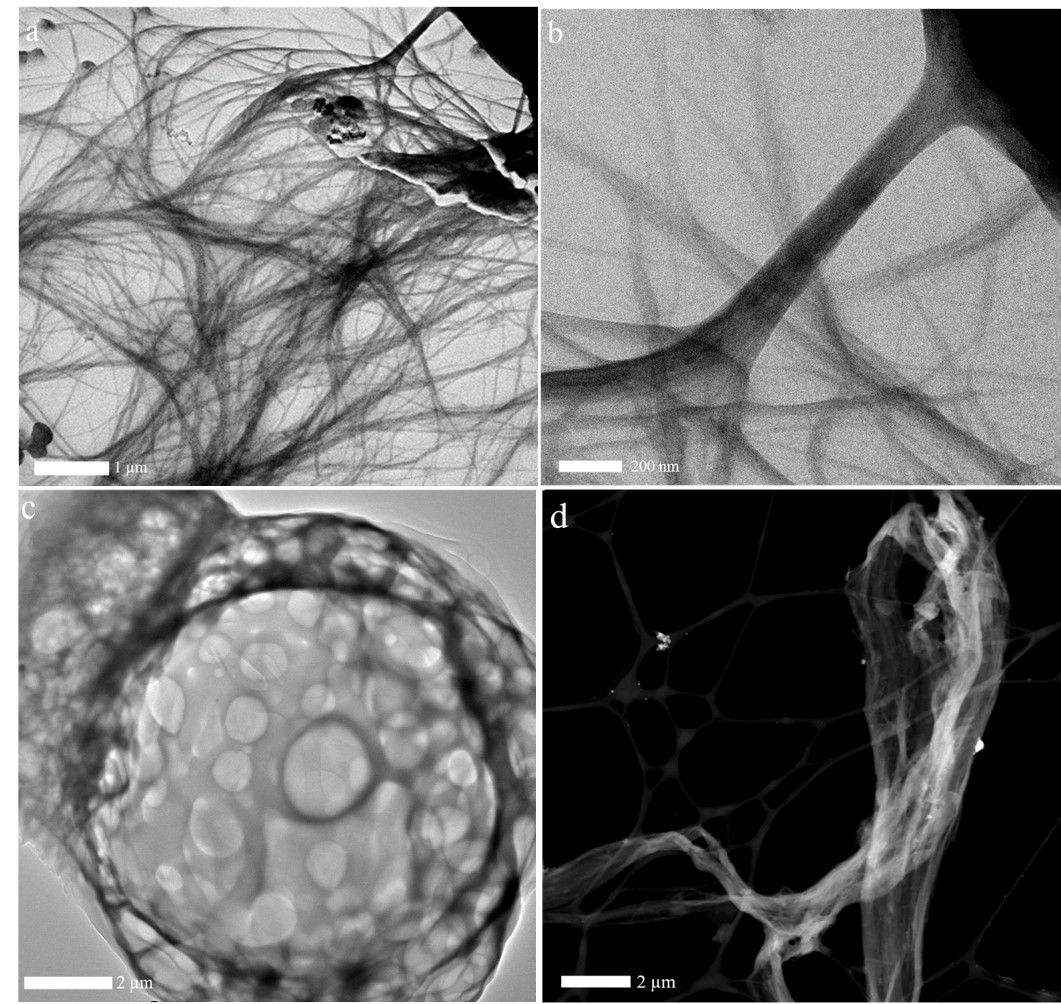
Full range mid IR spectra

IR spectra with signature of amide-I band

**Figure S6 (a-e):** IR spectra of shock processed amino acid residue along with unshocked sample (control). (**a**) glycine; two mixtures (**b**) glycine-glutamic acid & (**c**) asparagine-glutamic acid; (**d**) mixture of four amino acids; and (**e**) mixture of eighteen amino acids. Additional peaks in shock processed residue spectra (red curve) are marked with blue arrow. The amide-I band is recognized as peptide characteristic peak, governed by the stretching vibration of C=O and C-N groups and peaks between 1600-1720 cm-1 [41]. IR spectroscopy of samples from other experiments was also performed and found to be similar to the reported here.



**Figure S7:** The entire thread (length > 1 mm) of the branching filamentous thread seen in the SEM image shown in Figure 5c. This image was taken at the lower limit of the SEM imaging capabilities.



**Figure S8:** TEM micrographs of shocked amino acid mixtures (**a & b**) #814 (**c**) #828 (**d**) #711 (Table S1).

**Table S1:** Summarizes the experimental parameters and the estimated shock temperature

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **S. No.** | **Run No.** | **Quantity**  **(g)** | **Test gas pressure**  **(Bar)** | **Shock Mach number** | **Reflected shock temperature(K)** | **Reflected shock pressure (Bar)** | **Features seen in SEM** |
| **Glycine** | | | | | | | |
| **1** | 675 | 0.18 | 0.05 | 5.95 | 8088 | 28.4 | Folded threads |
| **2** | 677 | 0.18 | 0.154 | 4.67 | 5024 | 25.1 | NA |
| **3** | 825 | 0.4 | 0.075 | 5.18 | 6157 | 25.3 | Folded thread |
| **4** | 826 | 0.4 | 0.05 | 5.55 | 7047 | 21.8 | Globules |
| **5** | 827 | 0.4 | 0.194 | 4.08 | 3871 | 16.3 | Flower structure |
| **Two mixture of amino acids**  **(Glycine & Glutamic acid)** | | | | | | | |
| **6** | 823 | 0.4 | 0.075 | 5.25 | 6321 | 19.6 | Petals structure |
| **7** | 828 | 0.4 | 0.16 | 4.67 | 5024 | 16.8 | Petals and buds structure |
| **8** | 829 | 0.4 | 0.029 | 5.80 | 7679 | 18.8 | Threads and petals |
| **Two mixture of amino acids**  **(Asparagine & Glutamic acid)** | | | | | | | |
| **9** | 696 | 0.2 | 0.25 | 4.21 | 4118 | 25.4 | NA |
| **10** | 711 | 0.8 | 0.25 | 4.36 | 4413 | 25.1 | Threads |
| **11** | 726 | 0.5 | 0.25 | 4.27 | 4228 | 24.0 | NA |
| **12** | 731 | 0.5 | 0.25 | 2.53 | 1574 | 3.2 | Cubes |
| **13** | 830 | 0.4 | 0.075 | 5.20 | 6197 | 22.8 | Thread, sheet of woven petals |
| **14** | 831 | 0.4 | 0.16 | 4.67 | 5024 | 22.0 | Small folded threads |
| **15** | 832 | 0.4 | 0.029 | 5.80 | 7679 | 22.2 | Petals |
| **Four mixture of amino acids**  **(Lysine, Aspartic acid, Arginine, Glutamic acid)** | | | | | | | |
| **16** | 694 | 0.2 | 0.1 | 5.34 | 6633 | 32.9 | Thread , tube like |
| **17** | 695 | 0.2 | 0.25 | 3.92 | 3594 | 19.5 | Folded thick flat threads ,woven tube |
| **18** | 712 | 0.5 | 0.25 | 4.02 | 3775 | 19.5 | Small folded flat thread, root like feature |
| **19** | 819 | 0.5 | 0.20 | 4.32 | 4329 | 22.3 | Threads |
| **20** | 820 | 0.5 | 0.20 | 4.18 | 4020 | 17.6 | Cracked sheets and balls |
| **21** | 833 | 0.5 | 0.075 | 5.09 | 5961 | 24.4 | Folded threads |
| **22** | 834 | 0.5 | 0.025 | 5.86 | 7850 | 20.1 | Threads |
| **18 mixture of amino acids**  **(Glycine, Alanine, Valine, Leucine, Proline, Serine, Aspartic acid, Glutamic acid, Cysteine, Methionine, Asparagine, Glutamine, Arginine, Histidine, Phenylalanine, Lysine, Tyrosine, Tryptophan)** | | | | | | | |
| **23** | 676 | 0.186 | 0.055 | 5.63 | 7284 | 28.2 | Folded threads |
| **24** | 678 | 0.12 | 0.25 | - | - | - | Full threads |
| **25** | 692 | 0.18 | 0.25 | 4.07 | 3851 | 22.2 | NA |
| **26** | 702 | 1.08 | 0.25 | 3.97 | 3683 | 21.3 | NA |
| **27** | 704 | 0.9 | 0.25 | 3.93 | 3611 | 16.8 | Long thick thread |
| **28** | 705 | 1.016 | 0.5 | 3.35 | 2666 | 16.3 | NA |
| **29** | 814 | 0.5 | 0.25 | 4.22 | 4139 | 24.7 | Threads, Tube |
| **30** | 815 | 0.4 | 0.2 | 4.13 | 3971 | 15.5 | Small thread |
| **31** | 835 | 0.54 | 0.075 | 5.29 | 6405 | 22.2 | Long folded thick threads |
| **32** | 836 | 0.54 | 0.1 | 4.86 | 5429 | 22.8 | Small threads |

NA- Sample used for other analysis

**Table S2:** List of amino acids used in the experiments (Sourced from Sigma Aldrich)

|  |  |
| --- | --- |
| **Amino acid** | **Purity** |
| L-Alanine | >99.5% |
| L-Arginine hydrochloride | >99.5% |
| L-Asparagine | >98% |
| L-Aspartic acid | >99.5% |
| L-Cysteine, free base | >98% |
| L-Cysteine | >98.5% |
| L-Glutamic acid | >99.5% |
| L-Glutamine | >99.5% |
| Glycine | >99% |
| L-Histidine hydrochloride Monohydrate | >99% |
| 4-Hydroxy-L-proline | >99% |
| L-Leucine | >99.5% |
| L-Isoleucine | >99.5% |
| L-Lysine hydrochloride | >99.5% |
| L-Methionine | >99.5% |
| L-Phenylalanine | >99% |
| L-Proline | >99.5% |
| L-Serine | >99.5% |
| L-Threonine | >99.5% |
| L-Tryptophan | >99.5% |
| L-Tyrosine | >99.0% |
| L-Valine | >99.5% |

**SEM and TEM analysis**

SEM analysis was performed to investigate the morphology of shock processed residue and for control samples. Carbon tape was stuck on SEM sample stub, on which sample was spread. A gold coating was applied on the top of the sample to make it conductive for analysis. The SEM was conducted utilizing ZEISS ULTRA 55 at an operating voltage of 5 kV at different magnification.

TEM analysis was also performed to investigate the internal structure of shock processed residue at higher magnification. The tiny amount of sample was taken in 1.5 ml acetone solvent and then sonicated for 10-20 min to improve the suspension. A small drop was taken from the middle level of the solvent using a micro pipet and drop cast carefully on 200 mesh copper grid taking care of agglomeration and left at room temperature to dry entirely before subjecting to TEM. TEM studies was performed utilizing Titan Themis from FEI, at an operating voltage of 300 kV in HRTEM and STEM mode at various resolution.

**FTIR spectroscopy**

All reported FT-IR spectra were obtained with a Bruker Tensor 27 FT-IR spectrometer in ATR mode with diamond crystal used in ATR mode.