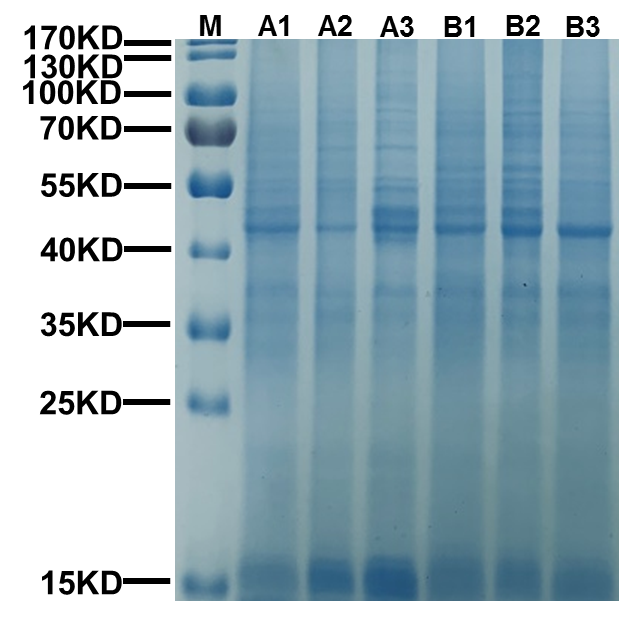
**Quality inspection of protein sample and the result of preliminary experimental**

[**Extraction**](https://cn.bing.com/dict/search?q=extraction&FORM=BDVSP6&cc=cn)[**method**](https://cn.bing.com/dict/search?q=method&FORM=BDVSP6&cc=cn): SDT split

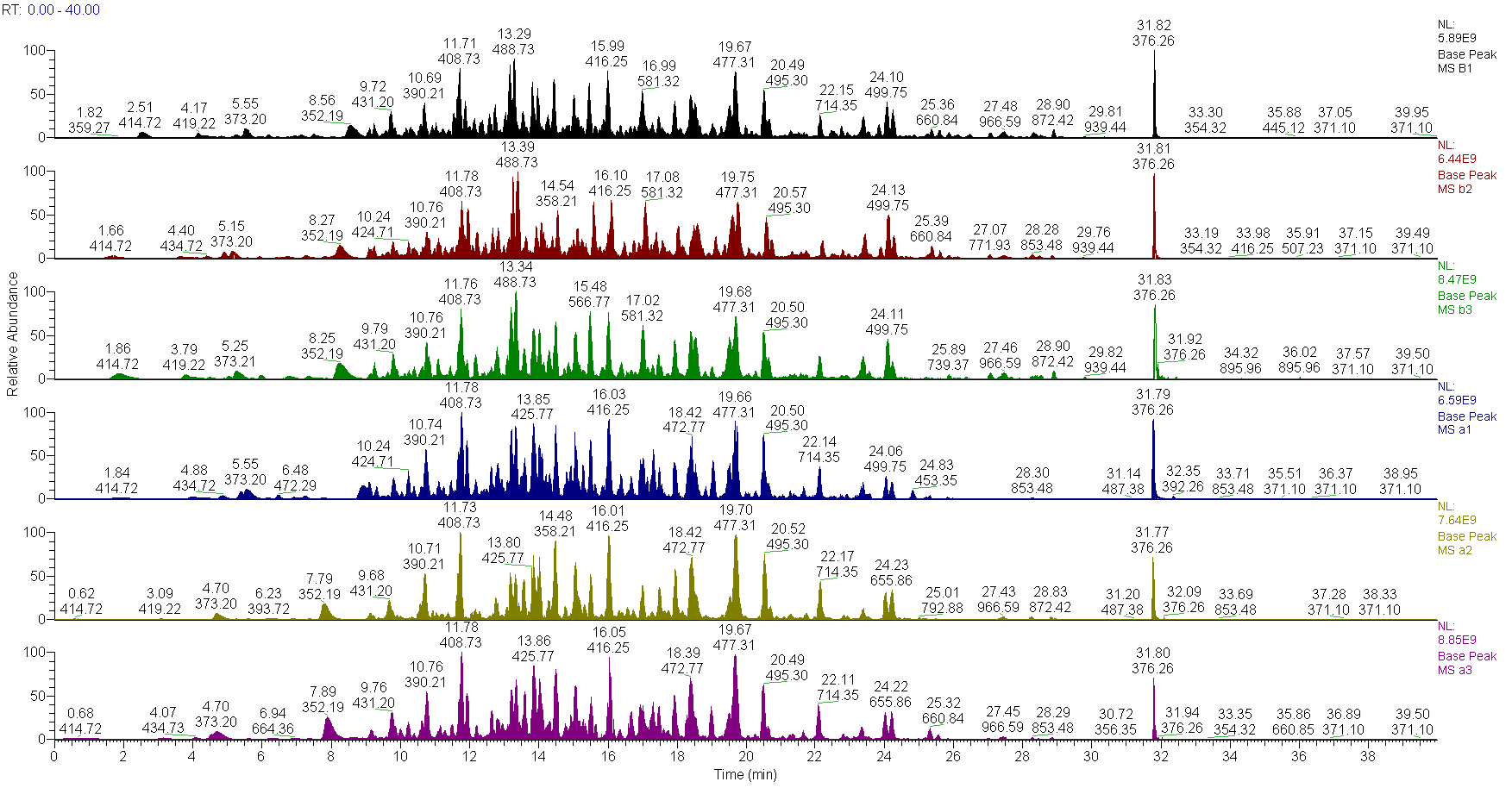
**Method**: SDS-PAGE, LC-MS/MS（equipment: QE PLUS; software: PD/Sequence HT）

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | | **A1(KBD1)** | **A2(KBD2)** | **A3(KBD3)** | **B1(normal1)** | **B2(normal2)** | **B3(normal3)** |
| [**quantitative**](https://cn.bing.com/dict/search?q=quantitative&FORM=BDVSP6&cc=cn)[**result**](https://cn.bing.com/dict/search?q=result&FORM=BDVSP6&cc=cn) | **concentration (μg/μl)** | **1.6** | **4.6** | **2.7** | **1.3** | **3.6** | **1.5** |
| [**volume**](https://cn.bing.com/dict/search?q=volume&FORM=BDVSP6&cc=cn) **(μl)** | **300** | **400** | **180** | **300** | **400** | **300** |
| [**Amount**](https://cn.bing.com/dict/search?q=Amount&FORM=BDVSP6&cc=cn) **(μg)** | **480** | **1840** | **486** | **390** | **1440** | **450** |
| **Mass spectrometry analysis result** | **Database** | **Uniprot\_HomoSapiens\_20367\_20200226** | | | | | |
| **Protein**  **group** | **1693** | **1868** | **1900** | **1395** | **1652** | **1751** |
| **Protein**  **group**  **(Unique**  **Peptide≥2)** | **1029** | **1143** | **1166** | **805** | **1008** | **1084** |

**SDS-PAGE** [**electrophoretogram**](https://cn.bing.com/dict/search?q=electrophoretogram&FORM=BDVSP6&cc=cn)

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**Basepeak maps of Mass spectrometry analysis**

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