**Table S7. Nano LC-MS/MS data acquisition parameters.**

|  |
| --- |
| **LC-Parameters** |
| Instrument  | Ultimate 3000 RSLC (Thermo Fisher Scientific)  |
| Trap column  | Acclaim PepMap, 2 cm, 100 µm, 100 Å pore size (Thermo Fisher Scientific) |
| Analytical column  | Accucore, 25 cm, 2.6 µm, 150 Å pore size (Thermo Fisher Scientific) |
| Buffer system  | Binary buffer system consisting of 0.1% acetic acid in *A. dest.* (buffer A) and 0.1% acetic acid in 100% ACN (buffer B) |
| Flow rate  | 300 nl/min  |
| Gradient  | 0 min 2% B 🡪2 min 5% B 🡪10 min 5% B 🡪130 min 25% B 🡪135 min 40% B 🡪137 min 90% B 🡪142 min 90% B 🡪145 min 2% B 🡪155 min 2% B |
| Gradient length | 155 min |
| Column oven temperature  | 40°C  |
| **MS-Parameters** |
| Instrument  | Q Exactive mass spectrometer (Thermo Fisher Scientific)  |
| Operation mode  | Data-dependent acquisition |
| **Full MS-Parameters** |
| MS scan resolution  | 70,000  |
| AGC target  | 3e6  |
| Maximum ion injection time for the MS scan  | 120 ms  |
| Scan range  | 350 to 1650 m/z |
| Spectra data type  | Centroid  |
| **MS2-Parameters** |
| Resolution  | 17,500  |
| MS/MS AGC target  | 2e5  |
| Maximum ion injection time for the MS/MS scans  | 120 ms  |
| Selection for MS/MS  | 10 most abundant isotope patterns with charge ≥2 from the survey scan  |
| Isolation window  | 3 m/z  |
| Fixed first mass  | 100 m/z  |
| Dissociation mode  | Higher energy collisional dissociation (HCD)  |
| Normalized collision energy  | 27.5%  |
| Dynamic exclusion  | 30 s  |
| Charge exclusion | 1, >7 |