|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein name  （Swiss Prot accession No.） | Matched peptidesa | Protein score b  (sequence coverage) | Matched in gel tryptic digests | | | | |
| Observed *m/z* (MH+) | Mr | | Peptide sequence | Residues |
| Expected | Calculated |
| Na+-translocating NADH-quinone reductase subunit A  (Q9KPS1) | 14/52 | 101  (32%) | 2186.1130 | 2185.1057 | 2185.1500 | KVALLGEEYVGMRPTMHVR | 28-46 |
| 2058.0280 | 2057.0207 | 2057.0550 | VALLGEEYVGMRPTMHVR | 29-46 |
| 3305.7420 | 3304.7347 | 3304.6939 | VLQSVVIEVAGDDQVTFDKFEANQLASLNR | 86-115 |
| 1935.0020 | 1933.9947 | 1934.0262 | DAIKTQLVESGLWTAFR | 116-132 |
| 1507.7610 | 1506.7537 | 1506.7831 | TQLVESGLWTAFR | 120-132 |
| 668.2560 | 667.2487 | 667.3363 | VYVCK | 189-193 |
| 1335.7820 | 1334.7747 | 1334.8034 | VVSLAGPVVNKPR | 261-273 |
| 2261.1000 | 2260.0927 | 2260.1079 | TVMGASLEQLVDSEIMPGEVR | 277-297 |
| 1042.5170 | 1041.5097 | 1041.5356 | ATGPHAYLGR | 309-318 |
| 2138.1240 | 2137.1167 | 2137.1545 | ATGPHAYLGRYHLQVSVLR | 309-327 |
| 1114.6140 | 1113.6067 | 1113.6295 | YHLQVSVLR | 319-327 |
| 1527.8000 | 1526.7927 | 1526.8200 | VMPLDMEPTLLLR | 383-395 |
| 1543.7810 | 1542.7737 | 1542.8150 | VMPLDMEPTLLLR; Oxidation (M) | 383-395 |
| 1041.5230 | 1040.5157 | 1040.5291 | YEYGQLLR | 429-436 |

**Result.** MALDI-TOF MS analysis of the *“in gel”* tryptic digests of NqrA subunit of Na+-NQR

aNumber of matched peptides/total observed peptides. bProtein score is -10\*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 65 are significant (*p*<0.05). The peptide sequences verified by MS/MS (MALDI-TOF/TOF, Figure S6) are underlined.