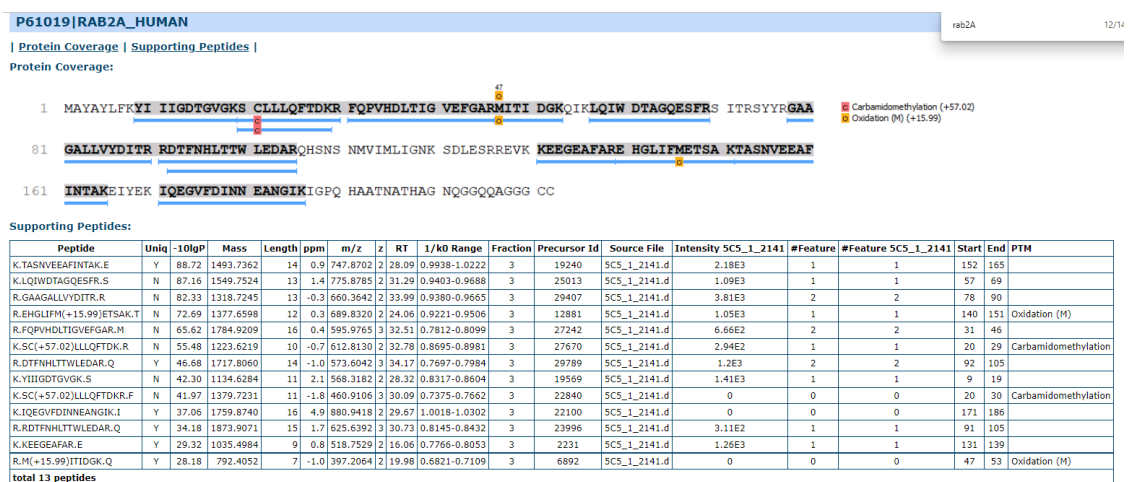
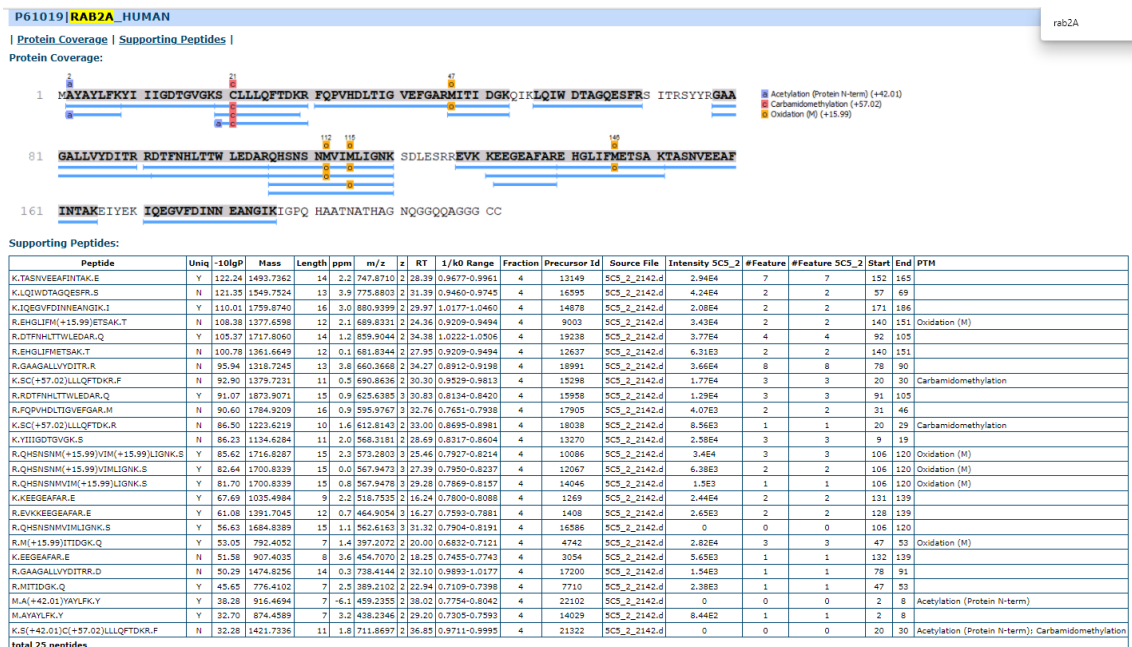


# PŘÍLOHY

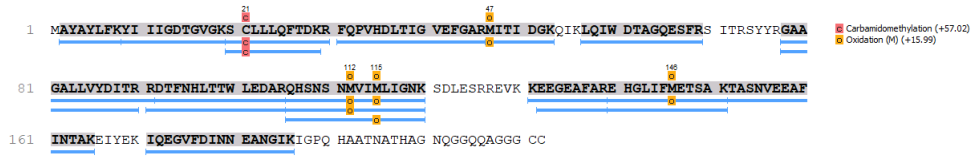
Následující přílohy jsou výsledky získané z analýzy hmotnostní spektrometrie:



P61019 | RAB2A\_HUMAN

Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

| Peptide                             | Uniq | -10lgP | Mass      | Length | ppm  | m/z      | z | RT    | 1/k0 Range    | Fraction | Precursor Id | Source File  | Intensity SCS_3 | #Feature | #Feature SCS_3 | Start | End | PTM                  |
|-------------------------------------|------|--------|-----------|--------|------|----------|---|-------|---------------|----------|--------------|--------------|-----------------|----------|----------------|-------|-----|----------------------|
| K.LQIWDTAGQESFR.S                   | N    | 107.72 | 1549.7524 | 13     | 0.9  | 775.8779 | 2 | 31.69 | 0.9540-0.9825 | 5        | 15464        | SCS_3_2143.d | 5.48E3          | 2        | 2              | 57    | 69  |                      |
| K.TASNVEEAFINTAK.E                  | Y    | 106.25 | 1493.7362 | 14     | 1.9  | 747.8707 | 2 | 28.53 | 0.9369-0.9654 | 5        | 12698        | SCS_3_2143.d | 1.15E4          | 2        | 2              | 152   | 165 |                      |
| R.FQPVHDLTIGVEFGAR.M                | N    | 94.67  | 1784.9209 | 16     | 3.2  | 595.9780 | 3 | 32.87 | 0.8329-0.8615 | 5        | 16581        | SCS_3_2143.d | 3.01E3          | 2        | 2              | 31    | 46  |                      |
| R.GAAGALLVYDITR.R                   | N    | 93.46  | 1318.7245 | 13     | 1.6  | 660.3652 | 2 | 34.47 | 0.8912-0.9198 | 5        | 17704        | SCS_3_2143.d | 1.96E4          | 2        | 2              | 78    | 90  |                      |
| R.EHGLIFM(+15.99)ETSAK.T            | N    | 85.00  | 1377.6598 | 12     | 2.0  | 689.8329 | 2 | 24.50 | 0.9186-0.9472 | 5        | 8935         | SCS_3_2143.d | 7.51E3          | 2        | 2              | 140   | 151 | Oxidation (M)        |
| K.SC(+57.02)LLQLQFTDKR.F            | N    | 83.65  | 1379.7231 | 11     | -3.0 | 690.8612 | 2 | 30.56 | 0.9529-0.9813 | 5        | 14404        | SCS_3_2143.d | 3.72E3          | 2        | 2              | 20    | 30  | Carbamidomethylation |
| R.EHGLIFMETS.K.T                    | N    | 80.25  | 1361.6649 | 12     | -1.5 | 681.8332 | 2 | 28.14 | 0.9198-0.9483 | 5        | 12323        | SCS_3_2143.d | 8.02E2          | 1        | 1              | 140   | 151 |                      |
| K.SC(+57.02)LLQLQFTDKR.R            | N    | 77.31  | 1223.6219 | 10     | 0.0  | 612.8133 | 2 | 33.20 | 0.8729-0.9015 | 5        | 16808        | SCS_3_2143.d | 1.91E3          | 1        | 1              | 20    | 29  | Carbamidomethylation |
| K.IQEGVFDINN EANGIK.I               | Y    | 76.39  | 1759.8740 | 16     | 1.4  | 880.9384 | 2 | 30.15 | 0.1043-1.0426 | 5        | 14019        | SCS_3_2143.d | 3.06E3          | 1        | 1              | 171   | 186 |                      |
| R.QHSNSNM(+15.99)VIM(+15.99)LIGNK.S | Y    | 72.96  | 1716.8287 | 15     | 1.4  | 573.2797 | 3 | 25.62 | 0.7363-0.7651 | 5        | 9997         | SCS_3_2143.d | 4.29E3          | 2        | 2              | 106   | 120 | Oxidation (M)        |
| R.RDTFNHLTTW LEDAR.Q                | Y    | 67.82  | 1873.9071 | 15     | 1.3  | 625.6387 | 3 | 31.11 | 0.8145-0.8432 | 5        | 14939        | SCS_3_2143.d | 1.39E3          | 1        | 1              | 91    | 105 |                      |
| R.DTFNHLTTW LEDAR.Q                 | Y    | 67.81  | 1717.8060 | 14     | -0.3 | 859.9030 | 2 | 34.66 | 0.1088-1.0472 | 5        | 17904        | SCS_3_2143.d | 5.84E3          | 2        | 2              | 92    | 105 |                      |
| K.VIIGDGTGVGK.S                     | N    | 61.96  | 1134.6284 | 11     | 3.2  | 568.3187 | 2 | 28.78 | 0.8283-0.8569 | 5        | 12873        | SCS_3_2143.d | 7.92E3          | 1        | 1              | 9     | 19  |                      |
| K.KEEGEAFAR.E                       | Y    | 60.58  | 1035.4984 | 9      | 1.5  | 518.7531 | 2 | 15.90 | 0.7777-0.8065 | 5        | 1371         | SCS_3_2143.d | 5.98E3          | 1        | 1              | 131   | 139 |                      |
| R.QHSNSNM(+15.99)VIM(+15.99)LIGNK.S | Y    | 51.33  | 1700.8339 | 15     | -0.5 | 567.9470 | 3 | 27.58 | 0.7386-0.7674 | 5        | 11923        | SCS_3_2143.d | 0               | 0        | 0              | 106   | 120 | Oxidation (M)        |
| R.QHSNSNMVIM(+15.99)LIGNK.S         | Y    | 49.58  | 1700.8339 | 15     | 7.1  | 567.9513 | 3 | 29.41 | 0.7835-0.8122 | 5        | 13511        | SCS_3_2143.d | 0               | 0        | 0              | 106   | 120 | Oxidation (M)        |
| M.MAYAYLFKYI                        | Y    | 46.59  | 874.4589  | 7      | 5.4  | 438.2355 | 2 | 29.32 | 0.7282-0.7570 | 5        | 13438        | SCS_3_2143.d | 1.8E3           | 1        | 1              | 2     | 8   |                      |
| R.M(+15.99)IITDQK.Q                 | Y    | 40.54  | 792.4052  | 7      | 2.6  | 397.2077 | 2 | 19.93 | 0.6832-0.7121 | 5        | 4762         | SCS_3_2143.d | 2.28E3          | 1        | 1              | 47    | 53  | Oxidation (M)        |
| R.GAAGALLVYDITR.D                   | N    | 35.18  | 1474.8256 | 14     | 5.2  | 738.4179 | 2 | 32.33 | 0.9881-1.0165 | 5        | 16107        | SCS_3_2143.d | 2.08E2          | 1        | 1              | 78    | 91  |                      |
| K.KEEGEAFAR.E                       | N    | 30.99  | 907.4035  | 8      | 4.5  | 454.7074 | 2 | 18.08 | 0.7386-0.7674 | 5        | 3105         | SCS_3_2143.d | 7.23E2          | 1        | 1              | 132   | 139 |                      |

total 20 peptides

P61019 | RAB2A\_HUMAN

Protein Coverage | Supporting Peptides |

Protein Coverage:



Supporting Peptides:

| Peptide                             | Uniq | -10lgP | Mass      | Length | ppm  | m/z      | z | RT    | 1/k0 Range    | Fraction | Precursor Id | Source File  | Intensity SCS_4 | #Feature | #Feature SCS_4 | Start | End | PTM           |
|-------------------------------------|------|--------|-----------|--------|------|----------|---|-------|---------------|----------|--------------|--------------|-----------------|----------|----------------|-------|-----|---------------|
| K.LQIWDTAGQESFR.S                   | Y    | 87.41  | 1549.7524 | 13     | -0.7 | 775.8766 | 2 | 31.45 | 0.9483-0.9768 | 6        | 16669        | SCS_4_2144.d | 3.38E2          | 1        | 1              | 57    | 69  |               |
| K.TASNVEEAFINTAK.E                  | Y    | 85.98  | 1493.7362 | 14     | 0.6  | 747.8698 | 2 | 28.39 | 0.9380-0.9665 | 6        | 13352        | SCS_4_2144.d | 1.83E3          | 1        | 1              | 152   | 165 |               |
| R.GAAGALLVYDITR.R                   | Y    | 83.68  | 1318.7245 | 13     | -1.3 | 660.3633 | 2 | 34.19 | 0.9346-0.9631 | 6        | 19558        | SCS_4_2144.d | 2.79E3          | 2        | 2              | 78    | 90  |               |
| R.QHSNSNM(+15.99)VIM(+15.99)LIGNK.S | Y    | 56.23  | 1716.8287 | 15     | -8.6 | 573.2740 | 3 | 25.56 | 0.7363-0.7651 | 6        | 10652        | SCS_4_2144.d | 0               | 0        | 0              | 106   | 120 | Oxidation (M) |
| R.FQPVHDLTIGVEFGAR.M                | Y    | 46.22  | 1784.9209 | 16     | 3.2  | 595.9780 | 3 | 32.64 | 0.7800-0.8088 | 6        | 17899        | SCS_4_2144.d | 0               | 0        | 0              | 31    | 46  |               |
| R.EHGLIFM(+15.99)ETSAK.T            | Y    | 45.98  | 1377.6598 | 12     | 2.3  | 689.8332 | 2 | 24.32 | 0.9186-0.9472 | 6        | 9361         | SCS_4_2144.d | 7.47E2          | 1        | 1              | 140   | 151 | Oxidation (M) |
| K.VIIGDGTGVGK.S                     | Y    | 38.22  | 1134.6284 | 11     | 2.2  | 568.3181 | 2 | 28.59 | 0.8294-0.8581 | 6        | 13575        | SCS_4_2144.d | 0               | 0        | 0              | 9     | 19  |               |
| R.DTFNHLTTW LEDAR.Q                 | Y    | 37.69  | 1717.8060 | 14     | 5.3  | 573.6077 | 3 | 34.37 | 0.7685-0.7973 | 6        | 19732        | SCS_4_2144.d | 7.8E2           | 2        | 2              | 92    | 105 |               |
| K.KEEGEAFAR.E                       | Y    | 32.77  | 1035.4984 | 9      | 1.5  | 518.7531 | 2 | 15.80 | 0.7708-0.7996 | 6        | 1381         | SCS_4_2144.d | 8.71E2          | 1        | 1              | 131   | 139 |               |

total 9 peptides