

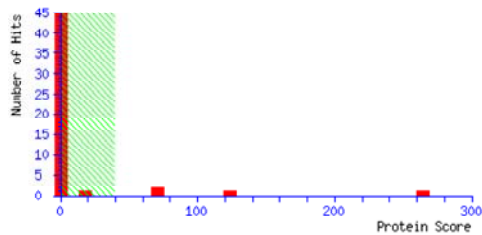


Mascot Search Results

User : JPROS
Email : pro@jbios.co.jp
Search title : D:\JPROS\L015\c(x5)_6micro.wiff (sample number 1)
MS data file : mas8DC.tmp
Database : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
Taxonomy : Homo sapiens (human) (327411 sequences)
Timestamp : 13 Feb 2019 at 09:59:13 GMT
Protein hits : [EAW48850.1](#) RNA U, small nuclear RNA export adaptor (phosphorylation regulated), partial [Homo sapiens]
[NP_006112.3](#) keratin, type II cytoskeletal 1 [Homo sapiens]
[AAA60544.1](#) keratin 10 [Homo sapiens]
[NP_000412.3](#) keratin, type I cytoskeletal 10 [Homo sapiens]
[EAX00626.1](#) prolactin regulatory element binding, isoform CRA_a [Homo sapiens]

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 39 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

| | | |
|---------------------------|---|---|
| Format As | Peptide Summary | Help |
| Significance threshold p< | 0.05 | Max. number of hits |
| Standard scoring | <input type="radio"/> MudPIT scoring <input checked="" type="radio"/> | Display non-significant matches <input checked="" type="checkbox"/> |
| Show pop-ups | <input checked="" type="radio"/> Suppress pop-ups <input type="radio"/> | Sort unassigned |
| Preferred taxonomy | All entries | Require bold red <input type="checkbox"/> |

Select All Select None Search Selected ☐ Error tolerant

1. [EAW48850.1](#) Mass: 46023 Score: 265 Matches: 19(7) Sequences: 13(7) emPAI: 0.74

RNA U, small nuclear RNA export adaptor (phosphorylation regulated), partial [Homo sapiens]

☐ Check to include this hit in error tolerant search

| Query | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Rank | Unique | Peptide |
|---|----------|-----------|-----------|---------|------|-------|---------|------|--------|--|
| <input checked="" type="checkbox"/> 256 | 468.7217 | 935.4288 | 935.4712 | -0.0424 | 0 | 50 | 0.0065 | 1 | U | K.VADEISFR.L |
| <input checked="" type="checkbox"/> 257 | 468.7299 | 935.4452 | 935.4712 | -0.0260 | 0 | (25) | 2 | 1 | U | K.VADEISFR.L |
| <input checked="" type="checkbox"/> 258 | 468.7352 | 935.4558 | 935.4712 | -0.0155 | 0 | (20) | 5.8 | 1 | U | K.VADEISFR.L |
| <input checked="" type="checkbox"/> 325 | 579.8145 | 1157.6145 | 1157.6808 | -0.0664 | 0 | 60 | 0.0007 | 1 | U | R.TPGGVFLNLLK.N |
| <input checked="" type="checkbox"/> 328 | 585.2680 | 1168.5214 | 1168.5764 | -0.0551 | 0 | 41 | 0.064 | 1 | U | K.DIFYIENQK.E |
| 349 | 413.1913 | 1236.5520 | 1236.5921 | -0.0401 | 0 | 13 | 28 | 5 | U | R.LGNRPENMYK.G + Oxidation (M) |
| 354 | 623.2606 | 1244.5066 | 1244.6248 | -0.1182 | 0 | (9) | 93 | 2 | U | K.NTPSISEEQIK.D |
| <input checked="" type="checkbox"/> 355 | 623.2745 | 1244.5345 | 1244.6248 | -0.0903 | 0 | (15) | 23 | 1 | U | K.NTPSISEEQIK.D |
| <input checked="" type="checkbox"/> 356 | 623.2841 | 1244.5536 | 1244.6248 | -0.0713 | 0 | (24) | 2.6 | 1 | U | K.NTPSISEEQIK.D |
| <input checked="" type="checkbox"/> 357 | 623.2959 | 1244.5772 | 1244.6248 | -0.0476 | 0 | 34 | 0.3 | 1 | U | K.NTPSISEEQIK.D |
| <input checked="" type="checkbox"/> 389 | 656.7624 | 1311.5102 | 1311.5830 | -0.0728 | 0 | 75 | 1.5e-05 | 1 | U | R.YEITAEDSQEK.V |
| <input checked="" type="checkbox"/> 393 | 438.9235 | 1313.7485 | 1313.7820 | -0.0334 | 1 | 17 | 12 | 1 | U | R.RTPGGVFLNLLK.N |
| <input checked="" type="checkbox"/> 395 | 665.2939 | 1328.5733 | 1328.6612 | -0.0878 | 0 | (7) | 1.3e+02 | 1 | U | R.QSETYNYLLAK.K |
| <input checked="" type="checkbox"/> 396 | 665.3000 | 1328.5855 | 1328.6612 | -0.0757 | 0 | 51 | 0.0046 | 1 | U | R.QSETYNYLLAK.K |
| <input checked="" type="checkbox"/> 415 | 713.7697 | 1425.5248 | 1425.6008 | -0.0760 | 0 | 80 | 3.1e-06 | 1 | U | K.SLNQEDDDTSR.E |
| <input checked="" type="checkbox"/> 427 | 509.2184 | 1524.6335 | 1524.7056 | -0.0721 | 1 | 46 | 0.015 | 1 | U | K.GRYEITAEDSQEK.V |
| <input checked="" type="checkbox"/> 449 | 555.8907 | 1664.6502 | 1664.7352 | -0.0850 | 1 | 39 | 0.049 | 1 | U | K.DLDKELDEYMHGK.K + Oxidation (M) |
| <input checked="" type="checkbox"/> 465 | 598.6098 | 1792.8076 | 1792.8315 | -0.0239 | 0 | 29 | 0.69 | 1 | U | R.AFQNTATACAPVSHYR.A + Carbamidomethyl (C) |
| <input checked="" type="checkbox"/> 469 | 611.5921 | 1831.7545 | 1831.8628 | -0.1083 | 1 | 19 | 5 | 1 | U | K.DIFYIENQKEYENK.K |

Proteins matching the same set of peptides:

[NP_115553.2](#) Mass: 44375 Score: 265 Matches: 19(7) Sequences: 13(7)
phosphorylated adapter RNA export protein [Homo sapiens]

2. [NP_006112.3](#) Mass: 65999 Score: 128 Matches: 8(3) Sequences: 8(3) emPAI: 0.18

keratin, type II cytoskeletal 1 [Homo sapiens]

☐ Check to include this hit in error tolerant search

| Query | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Rank | Unique | Peptide |
|---|----------|-----------|-----------|---------|------|-------|---------|------|--------|------------------|
| <input checked="" type="checkbox"/> 279 | 487.2528 | 972.4910 | 972.5240 | -0.0330 | 0 | 44 | 0.029 | 1 | U | K.IEISELNR.V |
| <input checked="" type="checkbox"/> 312 | 533.2155 | 1064.4164 | 1064.5138 | -0.0974 | 0 | 15 | 20 | 1 | U | K.AQYEDIAQK.S |
| <input checked="" type="checkbox"/> 329 | 590.2745 | 1178.5344 | 1178.5931 | -0.0587 | 0 | 58 | 0.00093 | 1 | U | K.YEELQITAGR.H |
| <input checked="" type="checkbox"/> 365 | 633.2916 | 1264.5687 | 1264.6299 | -0.0613 | 0 | 23 | 3.2 | 1 | U | R.TNAENEFVTIK.K |
| <input checked="" type="checkbox"/> 405 | 692.3088 | 1382.6031 | 1382.6830 | -0.0799 | 0 | 35 | 0.18 | 1 | U | K.SLNNQFASFIDK.V |
| 409 | 465.2254 | 1392.6543 | 1392.7249 | -0.0706 | 1 | 37 | 0.13 | 1 | U | R.TNAENEFVTIKK.D |

| | | | | | | | | | | | | |
|-------------------------------------|---------------------|----------|-----------|-----------|---------|---|----|--------|---|---|------------------|--|
| <input checked="" type="checkbox"/> | | | | | | | | | | | | |
| <input checked="" type="checkbox"/> | 421 | 738.3406 | 1474.6667 | 1474.7416 | -0.0749 | 0 | 30 | 0.66 | 1 | U | K.WELLQQVDTSTR.T | |
| <input checked="" type="checkbox"/> | 422 | 738.3558 | 1474.6970 | 1474.7780 | -0.0810 | 0 | 56 | 0.0017 | 1 | U | R.FLEQQNQVLQTK.W | |

Proteins matching the same set of peptides:

| | | | | |
|----------------------------|-------------|------------|---------------|-----------------|
| AAG41947.1 | Mass: 66027 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |
| AFA52002.1 | Mass: 66013 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |
| AFA52003.1 | Mass: 66029 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |
| AFA52004.1 | Mass: 65930 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |
| AFA52005.1 | Mass: 66086 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |
| AFA52006.1 | Mass: 66026 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |
| AFA52007.1 | Mass: 66071 | Score: 128 | Matches: 8(3) | Sequences: 8(3) |
| keratin 1 [Homo sapiens] | | | | |

3. [AAA60544.1](#) Mass: 57213 Score: 68 Matches: 1(1) Sequences: 1(1) emPAI: 0.07
keratin 10 [Homo sapiens]

☐ Check to include this hit in error tolerant search

| Query | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Rank | Unique | Peptide |
|---|----------|-----------|-----------|---------|------|-------|---------|------|--------|------------------|
| <input checked="" type="checkbox"/> 403 | 691.2774 | 1380.5403 | 1380.6408 | -0.1005 | 0 | 68 | 9.2e-05 | 1 | | R.ALEESNYELEGK.I |

4. [NP_000412.3](#) Mass: 58766 Score: 67 Matches: 2(1) Sequences: 2(1) emPAI: 0.06
keratin, type I cytoskeletal 10 [Homo sapiens]

☐ Check to include this hit in error tolerant search

| Query | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Rank | Unique | Peptide |
|---|----------|-----------|-----------|---------|------|-------|---------|------|--------|------------------|
| 403 | 691.2774 | 1380.5403 | 1380.6408 | -0.1005 | 0 | 68 | 9.2e-05 | 1 | | R.ALEESNYELEGK.I |
| <input checked="" type="checkbox"/> 423 | 498.5538 | 1492.6396 | 1492.7270 | -0.0874 | 1 | 22 | 3.7 | 1 | U | R.SQYQLAEQNRK.D |

Proteins matching the same set of peptides:

| | | | | |
|---|-------------|-----------|---------------|-----------------|
| P13645.6 | Mass: 58792 | Score: 67 | Matches: 2(1) | Sequences: 2(1) |
| RecName: Full=Keratin, type I cytoskeletal 10; AltName: Full=Cytokeratin-10; Short=CK-10; AltName: Full=Keratin-10; Short=K10 | | | | |
| CAA32649.1 | Mass: 59492 | Score: 67 | Matches: 2(1) | Sequences: 2(1) |
| unnamed protein product [Homo sapiens] | | | | |
| AAH34697.1 | Mass: 58792 | Score: 67 | Matches: 2(1) | Sequences: 2(1) |
| Keratin 10 [Homo sapiens] | | | | |
| AAA59468.1 | Mass: 46359 | Score: 67 | Matches: 2(1) | Sequences: 2(1) |
| keratin-10 [Homo sapiens] | | | | |
| EAW60681.1 | Mass: 63308 | Score: 67 | Matches: 2(1) | Sequences: 2(1) |
| keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens] | | | | |
| XP_005257400.1 | Mass: 63308 | Score: 67 | Matches: 2(1) | Sequences: 2(1) |
| keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens] | | | | |

5. [EAX00626.1](#) Mass: 39579 Score: 20 Matches: 1(0) Sequences: 1(0)
prolactin regulatory element binding, isoform CRA_a [Homo sapiens]

☐ Check to include this hit in error tolerant search

| Query | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Rank | Unique | Peptide |
|---|----------|-----------|-----------|---------|------|-------|--------|------|--------|----------------------|
| <input checked="" type="checkbox"/> 479 | 477.2383 | 1904.9242 | 1904.9315 | -0.0073 | 1 | 20 | 5.7 | 1 | U | R.YQACRFGQVPDQAGLR.L |

Proteins matching the same set of peptides:

| | | | | |
|---|-------------|-----------|---------------|-----------------|
| EAX00628.1 | Mass: 38325 | Score: 20 | Matches: 1(0) | Sequences: 1(0) |
| prolactin regulatory element binding, isoform CRA_c, partial [Homo sapiens] | | | | |
| AAG01692.1 | Mass: 45474 | Score: 20 | Matches: 1(0) | Sequences: 1(0) |
| prolactin regulatory element-binding protein [Homo sapiens] | | | | |
| NP_037520.1 | Mass: 45440 | Score: 20 | Matches: 1(0) | Sequences: 1(0) |
| prolactin regulatory element-binding protein isoform 1 [Homo sapiens] | | | | |
| BAF84867.1 | Mass: 45454 | Score: 20 | Matches: 1(0) | Sequences: 1(0) |
| unnamed protein product [Homo sapiens] | | | | |
| NP_001317413.1 | Mass: 37808 | Score: 20 | Matches: 1(0) | Sequences: 1(0) |
| prolactin regulatory element-binding protein isoform 2 [Homo sapiens] | | | | |
| NP_001317415.1 | Mass: 37863 | Score: 20 | Matches: 1(0) | Sequences: 1(0) |
| prolactin regulatory element-binding protein isoform 4 [Homo sapiens] | | | | |

Peptide matches not assigned to protein hits: (no details means no match)

| Query | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Rank | Unique | Peptide |
|---|----------|-----------|-----------|---------|------|-------|--------|------|--------|-----------------|
| <input checked="" type="checkbox"/> 185 | 428.7459 | 855.4773 | 855.5290 | -0.0517 | 1 | 33 | 0.27 | 1 | | IAEVLRR |
| <input checked="" type="checkbox"/> 186 | 428.7460 | 855.4774 | 855.5178 | -0.0404 | 0 | 21 | 4.2 | 1 | | LASIVTPR |
| <input checked="" type="checkbox"/> 160 | 421.7341 | 841.4537 | 841.5022 | -0.0485 | 0 | 19 | 6.2 | 1 | | GITLSVRP |
| <input checked="" type="checkbox"/> 466 | 897.8619 | 1793.7093 | 1793.7704 | -0.0611 | 1 | 19 | 4.7 | 1 | | SEDDDQSVRVSEWDK |
| <input checked="" type="checkbox"/> 159 | 421.7170 | 841.4195 | 841.5022 | -0.0826 | 0 | 18 | 9.3 | 1 | | GITLSVRP |
| <input checked="" type="checkbox"/> 310 | 530.7682 | 1059.5219 | 1059.6176 | -0.0956 | 1 | 16 | 18 | 1 | | LTLTEDKIK |
| <input checked="" type="checkbox"/> 300 | 523.2569 | 1044.4992 | 1044.5716 | -0.0724 | 0 | 16 | 17 | 1 | | LSSAHVYLR |
| <input checked="" type="checkbox"/> 349 | 413.1913 | 1236.5520 | 1236.7442 | -0.1922 | 1 | 16 | 14 | 1 | | IGLKDPVPAVK |
| <input checked="" type="checkbox"/> 128 | 412.7368 | 823.4591 | 823.5279 | -0.0688 | 0 | 15 | 12 | 1 | | AALPILAR |
| <input checked="" type="checkbox"/> 299 | 523.2529 | 1044.4912 | 1044.6179 | -0.1267 | 0 | 15 | 21 | 1 | | ILAINSSSLK |
| <input checked="" type="checkbox"/> 301 | 523.2575 | 1044.5004 | 1044.6583 | -0.1579 | 0 | 15 | 22 | 1 | | LLTFLPIK |

| | | | | | | | | | | |
|---|-----|----------|-----------|-----------|---------|---|----|---------|---|------------------------------------|
| ✓ | 155 | 419.3003 | 836.5860 | 836.4868 | 0.0992 | 0 | 15 | 11 | 1 | APQPVVAR |
| ✓ | 338 | 407.8527 | 1220.5364 | 1220.6989 | -0.1625 | 0 | 15 | 33 | 1 | LGLAGRPDDLGR |
| ✓ | 207 | 437.2204 | 872.4262 | 872.4967 | -0.0705 | 1 | 14 | 30 | 1 | EADLAKVK |
| ✓ | 303 | 523.2699 | 1044.5253 | 1044.5716 | -0.0463 | 0 | 14 | 26 | 1 | LSSAHVYLR |
| ✓ | 125 | 412.7271 | 823.4396 | 823.5280 | -0.0883 | 0 | 14 | 17 | 1 | VQLVRPL |
| ✓ | 94 | 730.5000 | 729.4927 | 729.4385 | 0.0542 | 0 | 14 | 10 | 1 | GSNIVLK |
| ✓ | 141 | 416.2128 | 830.4110 | 830.4498 | -0.0388 | 0 | 13 | 35 | 1 | ISLDDLR |
| ✓ | 96 | 400.1954 | 798.3763 | 798.4348 | -0.0585 | 1 | 13 | 20 | 1 | KSSVNHK |
| ✓ | 166 | 425.1834 | 848.3522 | 848.4644 | -0.1121 | 0 | 12 | 36 | 1 | EVTPIYK |
| ✓ | 390 | 656.7877 | 1311.5609 | 1311.7398 | -0.1789 | 0 | 12 | 33 | 1 | EVVELNNALALK |
| ✓ | 305 | 523.7506 | 1045.4866 | 1045.4975 | -0.0109 | 0 | 12 | 53 | 1 | CVQASTAPGGR |
| ✓ | 354 | 623.2606 | 1244.5066 | 1244.6725 | -0.1658 | 0 | 12 | 44 | 1 | QSITLISSPSGR |
| ✓ | 147 | 419.2830 | 836.5514 | 836.3884 | 0.1629 | 0 | 12 | 27 | 1 | DMLMGVR + Oxidation (M) |
| ✓ | 179 | 427.2287 | 852.4429 | 852.4818 | -0.0388 | 0 | 12 | 32 | 1 | LVTDHLR |
| ✓ | 360 | 419.2842 | 1254.8307 | 1254.6820 | 0.1488 | 0 | 12 | 23 | 1 | SLVLDGPAALDGK |
| ✓ | 204 | 435.7567 | 869.4988 | 869.4971 | 0.0017 | 0 | 11 | 37 | 1 | VVDVSVPR |
| ✓ | 225 | 444.2027 | 886.3908 | 886.5236 | -0.1328 | 1 | 11 | 71 | 1 | TQELIRK |
| ✓ | 253 | 465.2116 | 928.4087 | 928.4866 | -0.0779 | 0 | 11 | 54 | 1 | SLVEQTPVG |
| ✓ | 158 | 420.2137 | 838.4129 | 838.4436 | -0.0308 | 0 | 11 | 36 | 1 | GLTVTVYS |
| ✓ | 348 | 413.1888 | 1236.5445 | 1236.6251 | -0.0806 | 1 | 11 | 48 | 1 | LGGGETWFRSK |
| ✓ | 181 | 428.7300 | 855.4455 | 855.5065 | -0.0610 | 0 | 11 | 48 | 1 | LGSEILPK |
| ✓ | 182 | 428.7319 | 855.4493 | 855.5429 | -0.0937 | 0 | 10 | 49 | 1 | LVLSSLPK |
| ✓ | 241 | 453.2079 | 904.4013 | 904.5018 | -0.1005 | 0 | 10 | 69 | 1 | GLQLFEAK |
| ✓ | 183 | 428.7363 | 855.4580 | 855.5429 | -0.0850 | 0 | 10 | 50 | 1 | LVLSSLPK |
| ✓ | 340 | 408.2867 | 1221.8383 | 1221.7193 | 0.1190 | 1 | 10 | 18 | 1 | LNPKTINPGLR |
| ✓ | 332 | 599.3535 | 1196.6924 | 1196.5898 | 0.1026 | 0 | 10 | 55 | 1 | TNVEHLSGGQR |
| ✓ | 342 | 408.2924 | 1221.8553 | 1221.7193 | 0.1360 | 1 | 10 | 12 | 1 | LNPKTINPGLR |
| ✓ | 252 | 463.1069 | 924.1992 | 924.3946 | -0.1954 | 1 | 10 | 6.9 | 1 | RMEGWCK + Oxidation (M) |
| ✓ | 377 | 640.7704 | 1279.5262 | 1279.6013 | -0.0751 | 0 | 10 | 58 | 1 | LSSIANAMCGTR + Carbamidomethyl (C) |
| ✓ | 202 | 435.7506 | 869.4867 | 869.5195 | -0.0328 | 1 | 10 | 55 | 1 | VVRNNLR |
| ✓ | 118 | 409.1963 | 816.3780 | 816.4024 | -0.0245 | 1 | 10 | 68 | 1 | AGAPRCR |
| ✓ | 266 | 476.2015 | 950.3885 | 950.4855 | -0.0970 | 1 | 10 | 73 | 1 | RIMETASK + Oxidation (M) |
| ✓ | 187 | 428.7481 | 855.4817 | 855.4199 | 0.0618 | 0 | 10 | 61 | 1 | ISQEHRS |
| ✓ | 483 | 481.2464 | 1920.9564 | 1920.8200 | 0.1364 | 0 | 9 | 56 | 1 | SAYEFYHALDSENMTK + Oxidation (M) |
| ✓ | 239 | 451.2023 | 900.3900 | 900.4301 | -0.0401 | 0 | 9 | 90 | 1 | LDSQEPGR |
| ✓ | 216 | 441.3152 | 880.6159 | 880.4403 | 0.1756 | 0 | 9 | 45 | 1 | SQGSVTFR |
| ✓ | 222 | 442.2815 | 882.5484 | 882.4671 | 0.0812 | 1 | 9 | 85 | 1 | AEAATRHK |
| ✓ | 275 | 483.2582 | 964.5019 | 964.4396 | 0.0622 | 0 | 9 | 1.3e+02 | 1 | TTSNICNR + Carbamidomethyl (C) |
| ✓ | 215 | 441.2997 | 880.5848 | 880.3895 | 0.1954 | 0 | 9 | 64 | 1 | MTAANMAR + Ox |

| | | | | | | | | | |
|-----|----------|-----------|-----------|---------|---|---|---------|---|---|
| 235 | 449.2281 | 896.4417 | 896.3909 | 0.0508 | 0 | 4 | 2.3e+02 | 1 | EATGTSMGK + Oxidation (M) |
| 156 | 419.3011 | 836.5877 | 836.4868 | 0.1009 | 0 | 4 | 1.3e+02 | 1 | APQPVVAR |
| 518 | 925.1000 | 2772.2782 | 2772.1183 | 0.1599 | 1 | 4 | 1.6e+02 | 1 | GEDGM ^C AGPLAGPALTFDDCC ^C QRGR + 2 Carbamidomethyl (C) |
| 120 | 411.1511 | 820.2877 | 820.3749 | -0.0872 | 0 | 4 | 2e+02 | 1 | LMSAEDR |
| 135 | 414.2010 | 826.3874 | 826.4661 | -0.0786 | 1 | 4 | 1.8e+02 | 1 | SNLTKKH |
| 283 | 499.2728 | 996.5311 | 996.4481 | 0.0830 | 1 | 4 | 2.6e+02 | 1 | KSAC ^S AMAR + Carbamidomethyl (C); Oxidation (M) |
| 148 | 419.2935 | 836.5725 | 836.3923 | 0.1802 | 1 | 4 | 1.5e+02 | 1 | MGRSSQR + Oxidation (M) |
| 290 | 507.2132 | 1012.4119 | 1012.5706 | -0.1586 | 0 | 4 | 2.5e+02 | 1 | LPWAGQLTK |
| 344 | 408.2961 | 1221.8666 | 1221.7193 | 0.1472 | 1 | 4 | 42 | 1 | LNPKTINPGLR |
| 149 | 419.2944 | 836.5743 | 836.3923 | 0.1821 | 1 | 4 | 1.5e+02 | 1 | MGRSSQR + Oxidation (M) |
| 150 | 419.2962 | 836.5778 | 836.4868 | 0.0909 | 0 | 4 | 1.5e+02 | 1 | APQPVVAR |
| 224 | 443.2631 | 884.5117 | 884.4174 | 0.0943 | 1 | 4 | 2.5e+02 | 1 | CTPDKHK + Carbamidomethyl (C) |
| 337 | 405.3000 | 1212.8782 | 1212.7125 | 0.1657 | 1 | 3 | 52 | 1 | CAVGVVAILRR + Carbamidomethyl (C) |
| 436 | 534.3139 | 1599.9199 | 1599.7926 | 0.1273 | 0 | 3 | 1.9e+02 | 1 | LGSEEP ^L CPAATLSGR |
| 437 | 401.1433 | 1600.5440 | 1600.7086 | -0.1646 | 1 | 3 | 72 | 1 | TYSTS ^C VSPA ^C CRGR + 2 Carbamidomethyl (C) |
| 326 | 580.3376 | 1158.6607 | 1158.5643 | 0.0965 | 1 | 3 | 3.2e+02 | 1 | GGNFRGGAPGNNR |
| 153 | 419.2980 | 836.5814 | 836.4868 | 0.0946 | 0 | 3 | 1.5e+02 | 1 | APQPVVAR |
| 270 | 477.4000 | 952.7854 | 952.6069 | 0.1785 | 0 | 3 | 7.5 | 1 | TVLAAPLL |
| 211 | 441.2000 | 880.3854 | 880.4225 | -0.0371 | 0 | 3 | 2.7e+02 | 1 | Q ^C QVVGR + Carbamidomethyl (C) |
| 358 | 418.1787 | 1251.5142 | 1251.5892 | -0.0750 | 1 | 3 | 2.5e+02 | 1 | APKMC ^P WTYR |
| 112 | 408.2844 | 814.5543 | 814.4046 | 0.1497 | 1 | 3 | 2.4e+02 | 1 | GD ^P GRGTR |
| 254 | 465.2328 | 928.4511 | 928.5130 | -0.0620 | 0 | 3 | 3.4e+02 | 1 | NASIHFLK |
| 151 | 419.2963 | 836.5781 | 836.3923 | 0.1859 | 1 | 3 | 1.7e+02 | 1 | MGRSSQR + Oxidation (M) |
| 212 | 441.2466 | 880.4786 | 880.4766 | 0.0020 | 0 | 3 | 2.8e+02 | 1 | EP ^P QAQLR |
| 246 | 459.2610 | 916.5074 | 916.4866 | 0.0208 | 0 | 3 | 3.8e+02 | 1 | TNLLDLVK |
| 260 | 471.2804 | 940.5463 | 940.5269 | 0.0193 | 0 | 3 | 2.8e+02 | 1 | EYLLV ^L K |
| 152 | 419.2974 | 836.5803 | 836.4868 | 0.0935 | 0 | 3 | 1.7e+02 | 1 | APQPVVAR |
| 267 | 476.2229 | 950.4313 | 950.4603 | -0.0290 | 1 | 3 | 3.4e+02 | 1 | MSRSQ ^A K + Oxidation (M) |
| 261 | 472.2376 | 942.4606 | 942.4342 | 0.0264 | 1 | 3 | 3.2e+02 | 1 | RGHDV ^N M + Oxidation (M) |
| 401 | 449.2242 | 1344.6506 | 1344.6786 | -0.0280 | 0 | 3 | 3.6e+02 | 1 | TNPGLT ^P QFSR |
| 236 | 449.3371 | 896.6597 | 896.5556 | 0.1042 | 1 | 3 | 1.5e+02 | 1 | EVRLPK |
| 167 | 425.1837 | 848.3528 | 848.4240 | -0.0712 | 0 | 3 | 3.4e+02 | 1 | TVTS ^D QAK |
| 193 | 430.2587 | 858.5028 | 858.4559 | 0.0469 | 0 | 3 | 4.4e+02 | 1 | AEVISNAR |
| 230 | 445.1000 | 888.1854 | 888.3461 | -0.1607 | 0 | 3 | 18 | 1 | ADPGADGEAS |
| 313 | 535.2705 | 1068.5264 | 1068.6291 | -0.1027 | 0 | 3 | 3.1e+02 | 1 | AKPTAK ^P SAAK |
| 286 | 500.2802 | 998.5458 | 998.5913 | -0.0454 | 0 | 3 | 3.5e+02 | 1 | LNTIW ^K PK |
| 323 | 568.2674 | 1134.5203 | 1134.6258 | -0.1055 | 1 | 3 | 4.4e+02 | 1 | TVRTSYRR |
| 117 | 409.1801 | 816.3456 | 816.4705 | -0.1249 | 1 | 3 | 3.5e+02 | 1 | TPKATATK |
| 142 | 418.1787 | 834.3428 | 834.4824 | -0.1396 | 1 | 2 | 3.2e+02 | 1 | APRAAPP |
| 214 | 441.2889 | 880.5633 | 880.4701 | 0.0932 | 1 | 2 | 3.1e+02 | 1 | VPR ^C PPR + Carbamidomethyl (C) |
| 324 | 577.3128 | 1152.6111 | 1152.5887 | 0.0224 | 0 | 2 | 4.4e+02 | 1 | AVPTHSGSELR |
| 435 | 530.2000 | 1587.5782 | 1587.7675 | -0.1893 | 0 | 2 | 1.7e+02 | 1 | DPAIGAAMGQLTASNR + Oxidation (M) |
| 277 | 486.7517 | 971.4889 | 971.4859 | 0.0030 | 1 | 2 | 4.4e+02 | 1 | CP ^P QGTGK + Carbamidomethyl (C) |
| 464 | 449.2041 | 1792.7874 | 1792.8533 | -0.0659 | 1 | 2 | 3e+02 | 1 | LDQWLSDFWQRGDK |
| 508 | 581.2987 | 2321.1657 | 2321.2276 | -0.0618 | 1 | 2 | 2.6e+02 | 1 | LGMPPQLSPEAQSLLE ^M LFK + Oxidation (M) |
| 509 | 776.1000 | 2325.2782 | 2325.2198 | 0.0584 | 1 | 2 | 2.3e+02 | 1 | GGLGCVRAIQCLVPSYSPSPRR |
| 178 | 427.2258 | 852.4371 | 852.4090 | 0.0281 | 0 | 2 | 2.9e+02 | 1 | LAGGGDHQV |
| 168 | 425.2000 | 848.3854 | 848.3811 | 0.0044 | 0 | 2 | 3.9e+02 | 1 | Q ^C QD ^T IR + Carbamidomethyl (C) |
| 144 | 419.1461 | 836.2776 | 836.4392 | -0.1616 | 0 | 2 | 2.3e+02 | 1 | VHDPEIK |
| 472 | 925.1000 | 1848.1854 | 1848.0001 | 0.1853 | 1 | 2 | 40 | 1 | MTLGKLPHLQMPPLEK + Oxidation (M) |
| 192 | 429.2145 | 856.4145 | 856.4225 | -0.0080 | 0 | 2 | 4.7e+02 | 1 | AAPGMA ^S PR |
| 220 | 442.2642 | 882.5139 | 882.4923 | 0.0216 | 1 | 2 | 4.3e+02 | 1 | KSPGLEPR |
| 511 | 585.3108 | 2337.2141 | 2337.0722 | 0.1419 | 0 | 2 | 2.3e+02 | 1 | EEFECAFFTLQISSEISTK |
| 262 | 472.2479 | 942.4813 | 942.3973 | 0.0840 | 1 | 2 | 3.9e+02 | 1 | TCKVCM ^D K + Oxidation (M) |
| 226 | 445.0889 | 888.1632 | 888.3544 | -0.1912 | 0 | 2 | 8.2 | 1 | CFIC ^M EK + Oxidation (M) |
| 327 | 585.2634 | 1168.5123 | 1168.5876 | -0.0754 | 1 | 2 | 5.1e+02 | 1 | QYFKEAEVR |
| 307 | 524.8000 | 1047.5855 | 1047.4920 | 0.0935 | 1 | 2 | 4.4e+02 | 1 | HSRFIQ ^M N + Oxidation (M) |
| 146 | 419.2801 | 836.5456 | 836.4248 | 0.1208 | 0 | 2 | 2.6e+02 | 1 | MSVMVVR + Oxidation (M) |
| 263 | 472.2681 | 942.5216 | 942.4341 | 0.0874 | 0 | 2 | 4e+02 | 1 | MGQLDAHR + Oxidation (M) |
| 288 | 502.7966 | 1003.5786 | 1003.5385 | 0.0400 | 1 | 2 | 5e+02 | 1 | FGARAVPMR |
| 343 | 408.2935 | 1221.8588 | 1221.7193 | 0.1395 | 1 | 2 | 79 | 1 | LNPKTINPGLR |
| 391 | 657.5000 | 1312.9854 | 1312.7900 | 0.1954 | 1 | 2 | 11 | 1 | LKPLKSC ^L NIK + Carbamidomethyl (C) |
| 237 | 450.2496 | 898.4847 | 898.3814 | 0.1033 | 1 | 2 | 3.7e+02 | 1 | TESSRS ^T AS |
| 165 | 424.2646 | 846.5146 | 846.3607 | 0.1539 | 0 | 2 | 4.6e+02 | 1 | CESISGSE |
| 176 | 427.1000 | 852.1854 | 852.3726 | -0.1871 | 0 | 2 | 61 | 1 | EEDAPHR |
| 517 | 685.1462 | 2736.5557 | 2736.4810 | 0.0747 | 1 | 2 | 82 | 1 | EKPAYPPGTEAGSTRAVVIVPVLTR |
| 320 | 560.2776 | 1118.5407 | 1118.4233 | 0.1174 | 0 | 2 | 5.5e+02 | 1 | CHMEENQR + Carbamidomethyl (C); Oxidation (M) |
| 209 | 437.3490 | 872.6835 | 872.4902 | 0.1933 | 0 | 2 | 2e+02 | 1 | QLMALAAR |
| 496 | 528.2397 | 2108.9296 | 2109.0702 | -0.1406 | 1 | 2 | 2.7e+02 | 1 | TQAHTKNEVIDALNEAIDK |
| 169 | 425.2000 | 848.3854 | 848.3811 | 0.0044 | 0 | 2 | 4.5e+02 | 1 | Q ^C QD ^T IR + Carbamidomethyl (C) |
| 296 | 517.2614 | 1032.5082 | 1032.5022 | 0.0060 | 0 | 1 | 5.2e+02 | 1 | MGPSNSVGLR + Oxidation (M) |
| 177 | 427.1000 | 852.1854 | 852.3726 | -0.1871 | 0 | 1 | 64 | 1 | EEDAPHR |
| 227 | 445.0917 | 888.1689 | 888.3535 | -0.1846 | 0 | 1 | 14 | 1 | SYESGIS ^M + Oxidation (M) |
| 361 | 419.2912 | 1254.8517 | 1254.7044 | 0.1473 | 1 | 1 | 1.9e+02 | 1 | GQATAAATAPRIK |
| 425 | 502.6000 | 1504.7782 | 1504.7059 | 0.0723 | 0 | 1 | 4.7e+02 | 1 | GFTAASNWEGAAPR |
| 493 | 519.2765 | 2073.0767 | 2073.0742 | 0.0026 | 1 | 1 | 3.1e+02 | 1 | GIRTGAAATPEE ^F EIAELK |
| 264 | 474.2200 | 946.4255 | 946.5270 | -0.1015 | 1 | 1 | 5.5e+02 | 1 | Q ^C QVVSKK + Carbamidomethyl (C) |
| 289 | 503.2599 | 1004.5053 | 1004.4960 | 0.0093 | 1 | 1 | 5.2e+02 | 1 | CGKGAAELEK |
| 481 | 639.7000 | 1916.0782 | 1916.0289 | 0.0493 | 1 | 1 | 2.6e+02 | 1 | AVDMSGGTVTVLEKVPVSK |
| 438 | 402.1739 | 1604.6664 | 1604.7729 | -0.1065 | 1 | 1 | 3.5e+02 | 1 | DNAKNSLYLQ ^M HR + Oxidation (M) |
| 491 | 517.2790 | 2065.0867 | 2065.0150 | 0.0717 | 0 | 1 | 3.2e+02 | 1 | NFITAC ^I GVGSIVTEGEGNGK + Carbamidomethyl (C) |
| 157 | 420.1931 | 838.3717 | 838.5501 | -0.1784 | 1 | 1 | 3.4e+02 | 1 | RPGLLRK |
| 138 | 415.3000 | 828.5854 | 828.4817 | 0.1037 | 1 | 1 | 4.2e+02 | 1 | SKAKPN ^G K |
| 291 | 508.7641 | 1015.5137 | 1015.4440 | 0.0697 | 1 | 1 | 6.3e+02 | 1 | MSPCHGGRR + Oxidation (M) |
| 514 | 852.1000 | 2553.2782 | 2553.0862 | 0.1920 | 0 | 1 | 3.5e+02 | 1 | SGHENLALEM ^T DL ^C MF ^E YAK + Carbamidomethyl (C); 2 Ox |

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| <input checked="" type="checkbox"/> | 484 | 481.2507 | 1920.9735 |
| <input checked="" type="checkbox"/> | 486 | 485.0839 | 1936.3063 |
| <input checked="" type="checkbox"/> | 488 | 657.5000 | 1969.4782 |
| <input checked="" type="checkbox"/> | 492 | 519.1166 | 2072.4375 |
| <input checked="" type="checkbox"/> | 494 | 521.1126 | 2080.4212 |
| <input checked="" type="checkbox"/> | 497 | 536.1242 | 2140.4676 |
| <input checked="" type="checkbox"/> | 498 | 536.1516 | 2140.5773 |
| <input checked="" type="checkbox"/> | 499 | 538.1111 | 2148.4153 |
| <input checked="" type="checkbox"/> | 500 | 730.5000 | 2188.4782 |
| <input checked="" type="checkbox"/> | 501 | 549.2714 | 2193.0567 |
| <input checked="" type="checkbox"/> | 503 | 554.1358 | 2212.5139 |
| <input checked="" type="checkbox"/> | 504 | 554.1407 | 2212.5336 |
| <input checked="" type="checkbox"/> | 505 | 577.2862 | 2305.1157 |
| <input checked="" type="checkbox"/> | 506 | 579.2885 | 2313.1251 |
| <input checked="" type="checkbox"/> | 507 | 581.2930 | 2321.1428 |
| <input checked="" type="checkbox"/> | 510 | 776.1831 | 2325.5274 |
| <input checked="" type="checkbox"/> | 513 | 817.2000 | 2448.5782 |
| <input checked="" type="checkbox"/> | 515 | 639.4431 | 2553.7431 |
| <input checked="" type="checkbox"/> | 516 | 658.3974 | 2629.5605 |

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : Trypsin
 Variable modifications : [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.2 Da
 Fragment Mass Tolerance: ± 0.2 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Number of queries : 518

Mascot: <http://www.matrixscience.com/>