

Erratum to: Characterization of Nitrotyrosine-Modified Proteins in Cerebrospinal Fluid

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The original version of this article unfortunately missed the annotation for the oxidized methionines and nitrated tyrosines in Table 1 and on Figure 4, the images of the samples have appeared in thick black frames. The corrected Table 1 and Figure 4 are as follows

The online version of the original article can be found at <http://dx.doi.org/10.1007/s12014-010-9041-4>

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Table 1 Tryptic products of *in vitro* n-BSA

| Peptide sequence | Charge | Peptide ID probability | Mascot Ion score | Mascot Identity score | X! Tandem -log(e) score | Observed m/z | Actual peptide mass (AMU) | Calculated +1H Peptide Mass (AMU) | Actual minus calculated peptide mass (AMU) |
|-------------------|--------|------------------------|------------------|-----------------------|-------------------------|--------------|---------------------------|-----------------------------------|--|
| TVM* ENFVAFVDK | 2 | 95.00% | 71.6 | 38 | 5.02 | 708.3477 | 1,414.68 | 1,415.69 | -0.0004417 |
| IETM*REKVLTSAR | 3 | 64.20% | 0 | 0 | 1.31 | 546.623 | 1,636.85 | 1,636.87 | 0.9842 |
| DAFLGSFLYEY*SR | 2 | 95.00% | 41.8 | 38.3 | 5.48 | 806.8712 | 1,611.73 | 1,612.73 | 0.006302 |
| LGEY*GFQNALIVR | 2 | 95.00% | 86.9 | 38.6 | 8.09 | 762.8956 | 1,523.78 | 1,524.78 | 0.002306 |
| RHPEY*AVSVLLR | 3 | 95.00% | 47.5 | 38.8 | 4.57 | 495.6044 | 1,483.79 | 1,484.80 | 0.0003256 |
| Y*LYEIAR | 2 | 65.50% | 29.8 | 36.6 | 0 | 486.7436 | 971.4716 | 972.4791 | 0.0004075 |
| YLY*EIAR | 2 | 68.90% | 30.5 | 36.6 | 0 | 486.7436 | 971.4716 | 972.4791 | 0.0004075 |
| Y*LY*EIAR | 2 | 85.30% | 35.6 | 36.5 | 0 | 509.2361 | 1,016.46 | 1,017.46 | 0.0003306 |
| AEFVEVTK | 2 | 95.00% | 54.1 | 35.9 | 0 | 461.7474 | 921.4792 | 922.4886 | -0.001529 |
| AEFVEVTK | 1 | 85.60% | 43.3 | 35.9 | 0 | 922.4875 | 921.4797 | 922.4886 | -0.001053 |
| AEFVEVTKLVTDLTK | 2 | 95.00% | 0 | 0 | 3.44 | 847.9707 | 1,693.93 | 1,692.94 | 1.991 |
| AFDEK | 2 | 74.70% | 29.8 | 34.4 | 0 | 305.1478 | 608.28 | 609.2885 | -0.0006331 |
| ATEEQLK | 1 | 76.10% | 27.9 | 36.3 | 0 | 818.4245 | 817.4167 | 818.4261 | -0.001546 |
| ATEEQLK | 2 | 95.00% | 51.1 | 36.3 | 0 | 409.7164 | 817.4172 | 818.4261 | -0.001022 |
| CCTKPESER | 2 | 95.00% | 64.7 | 36.6 | 1.48 | 526.7297 | 1,051.44 | 1,052.45 | 0.001065 |
| CCTKPESER | 3 | 95.00% | 30.8 | 36.6 | 2 | 351.489 | 1,051.44 | 1,052.45 | 0.0008892 |
| DAFLGSFLYEYSR | 2 | 95.00% | 79 | 38.3 | 8.03 | 784.3771 | 1,566.74 | 1,567.74 | 0.003179 |
| DAFLGSFLYEYSRR | 3 | 95.00% | 26.8 | 45.6 | 1.74 | 575.2875 | 1,722.84 | 1,723.84 | 0.002598 |
| DAIPENLPLTADFAEDK | 2 | 95.00% | 50.8 | 46.3 | 5 | 978.4852 | 1,954.95 | 1,955.96 | 0.002055 |
| DLGEEHFK | 2 | 95.00% | 51.1 | 36.6 | 0 | 487.7336 | 973.4516 | 974.4585 | 0.0009688 |
| DTHKSEIAHR | 3 | 95.00% | 43.9 | 43.9 | 1.7 | 398.5388 | 1,192.59 | 1,193.60 | -0.001902 |
| FKDLGEEHFK | 2 | 95.00% | 59.3 | 37.6 | 3.72 | 625.3146 | 1,248.61 | 1,249.62 | -0.0004376 |
| FKDLGEEHFK | 3 | 95.00% | 59.6 | 37.6 | 3.96 | 417.2124 | 1,248.61 | 1,249.62 | -0.0002136 |
| FKDLGEEHFK | 4 | 95.00% | 27.5 | 37.5 | 1.29 | 313.1605 | 1,248.61 | 1,249.62 | -0.00319 |
| FPKAEFVEVTK | 2 | 68.50% | 0 | 0 | 1.85 | 648.3491 | 1,294.68 | 1,294.70 | 0.9857 |
| FPKAEFVEVTK | 3 | 95.00% | 27.3 | 38.1 | 1.12 | 432.2374 | 1,293.69 | 1,294.70 | -0.008115 |
| FQNALLVR | 2 | 93.50% | 44.8 | 44 | 0 | 480.7861 | 959.5566 | 960.5631 | 0.001377 |
| HLVDEPQNLK | 2 | 95.00% | 52.2 | 38.1 | 5.66 | 653.3591 | 1,304.70 | 1,305.72 | -0.006416 |
| HLVDEPQNLK | 3 | 95.00% | 39.1 | 38.1 | 1.27 | 435.9096 | 1,304.71 | 1,305.72 | -0.003592 |
| HPEYAVSVLLR | 2 | 95.00% | 40.1 | 38.1 | 2.08 | 642.3597 | 1,282.70 | 1,283.71 | 0.0004832 |
| HPEYAVSVLLR | 3 | 95.00% | 47.3 | 38.1 | 3.68 | 428.5756 | 1,282.70 | 1,283.71 | 0.0001072 |
| IETMR | 1 | 58.40% | 18.1 | 34.9 | 0 | 649.3345 | 648.3267 | 649.3344 | 0.0001521 |
| IETMR | 2 | 77.10% | 31 | 34.9 | 0 | 325.1712 | 648.3268 | 649.3344 | 0.0002761 |
| KQATALVELLK | 2 | 95.00% | 77 | 38.8 | 0 | 571.8612 | 1,141.71 | 1,142.72 | -0.0004154 |
| KQATALVELLK | 3 | 95.00% | 58.5 | 38.8 | 0 | 381.5762 | 1,141.71 | 1,142.72 | -0.001991 |
| KVPQVSTPTLVEVSR | 2 | 95.00% | 94.1 | 39.8 | 7.64 | 820.4717 | 1,638.93 | 1,639.94 | -0.002713 |
| KVPQVSTPTLVEVSR | 3 | 95.00% | 76.8 | 39.8 | 5.64 | 547.319 | 1,638.93 | 1,639.94 | 0.003111 |
| LCVLHEK | 2 | 95.00% | 47 | 35.7 | 0 | 421.232 | 840.4484 | 841.4607 | -0.004421 |
| LGEYGFQNALIVR | 2 | 95.00% | 85.2 | 38.8 | 5.66 | 740.4017 | 1,478.79 | 1,479.80 | -0.0004167 |
| LSQKFPK | 2 | 95.00% | 43.7 | 36.5 | 0 | 424.2566 | 846.4976 | 847.5043 | 0.001177 |
| LSQKFPKAEFVEVTK | 3 | 95.00% | 0 | 0 | 2.59 | 584.9897 | 1,751.95 | 1,750.97 | 1.979 |
| LSQRFPK | 2 | 93.40% | 43.9 | 43.2 | 0 | 438.2521 | 874.4886 | 875.5104 | -0.01393 |
| LVNELTEFAK | 1 | 95.00% | 33.6 | 37.4 | 4.31 | 1,163.63 | 1,162.62 | 1,163.63 | -0.001753 |
| LVNELTEFAK | 2 | 95.00% | 74.4 | 37.4 | 2.82 | 582.3201 | 1,162.62 | 1,163.63 | 0.001171 |
| HAGCEK | 3 | 95.00% | 34.7 | 40.1 | 2.54 | 832.05 | 2,493.13 | 2,494.16 | -0.02511 |
| LVTDLTK | 1 | 79.70% | 34.6 | 36.3 | 0 | 789.4715 | 788.4637 | 789.4724 | -0.0008407 |
| LVTDLTK | 2 | 95.00% | 53.2 | 36.3 | 0 | 395.2392 | 788.4628 | 789.4724 | -0.001717 |
| LVVSTQTALA | 2 | 95.00% | 68.3 | 37.2 | 3.44 | 501.795 | 1,001.57 | 1,002.58 | -0.001308 |
| QTALVELLK | 2 | 95.00% | 77.3 | 37.6 | 0 | 507.8132 | 1,013.61 | 1,014.62 | -0.001414 |

Table 1 (continued)

| Peptide sequence | Charge | Peptide ID probability | Mascot Ion score | Mascot Identity score | X! Tandem -log(e) score | Observed m/z | Actual peptide mass (AMU) | Calculated +1H Peptide Mass (AMU) | Actual minus calculated peptide mass (AMU) |
|------------------|--------|------------------------|------------------|-----------------------|-------------------------|--------------|---------------------------|-----------------------------------|--|
| RHPEYAVSVLLR | 2 | 95.00% | 0 | 0 | 4.51 | 720.9116 | 1,439.81 | 1,439.81 | 1.003 |
| RHPEYAVSVLLR | 3 | 95.00% | 83.1 | 38.9 | 4.43 | 480.6088 | 1,438.80 | 1,439.81 | -0.001398 |
| SLHTLFGDELCK | 2 | 95.00% | 27.9 | 44.4 | 1.74 | 681.8406 | 1,361.67 | 1,362.67 | 0.000476 |
| TCVADESHAGCEK | 2 | 95.00% | 66.3 | 37.7 | 6.1 | 675.2777 | 1,348.54 | 1,349.55 | 0.000973 |
| TCVADESHAGCEK | 3 | 95.00% | 44 | 37.8 | 2.57 | 450.5207 | 1,348.54 | 1,349.55 | -0.000103 |
| TPVSEKVTK | 2 | 95.00% | 72.7 | 43.8 | 4.43 | 494.7871 | 987.5586 | 988.568 | -0.001521 |
| TVMENFVAFVDK | 2 | 95.00% | 70.1 | 38.1 | 3.43 | 700.3507 | 1,398.69 | 1,399.69 | 0.0004733 |
| VASLR | 2 | 78.80% | 33.1 | 36.5 | 0 | 273.1742 | 544.3328 | 545.3411 | -0.0004225 |
| VPQVSTPTLVEVSR | 2 | 95.00% | 102 | 39.2 | 7.68 | 756.4266 | 1,510.84 | 1,511.84 | 0.002089 |
| YLYEIAR | 2 | 95.00% | 45 | 36.3 | 0 | 464.2495 | 926.4834 | 927.494 | -0.002716 |

M*- Oxidized Methionine

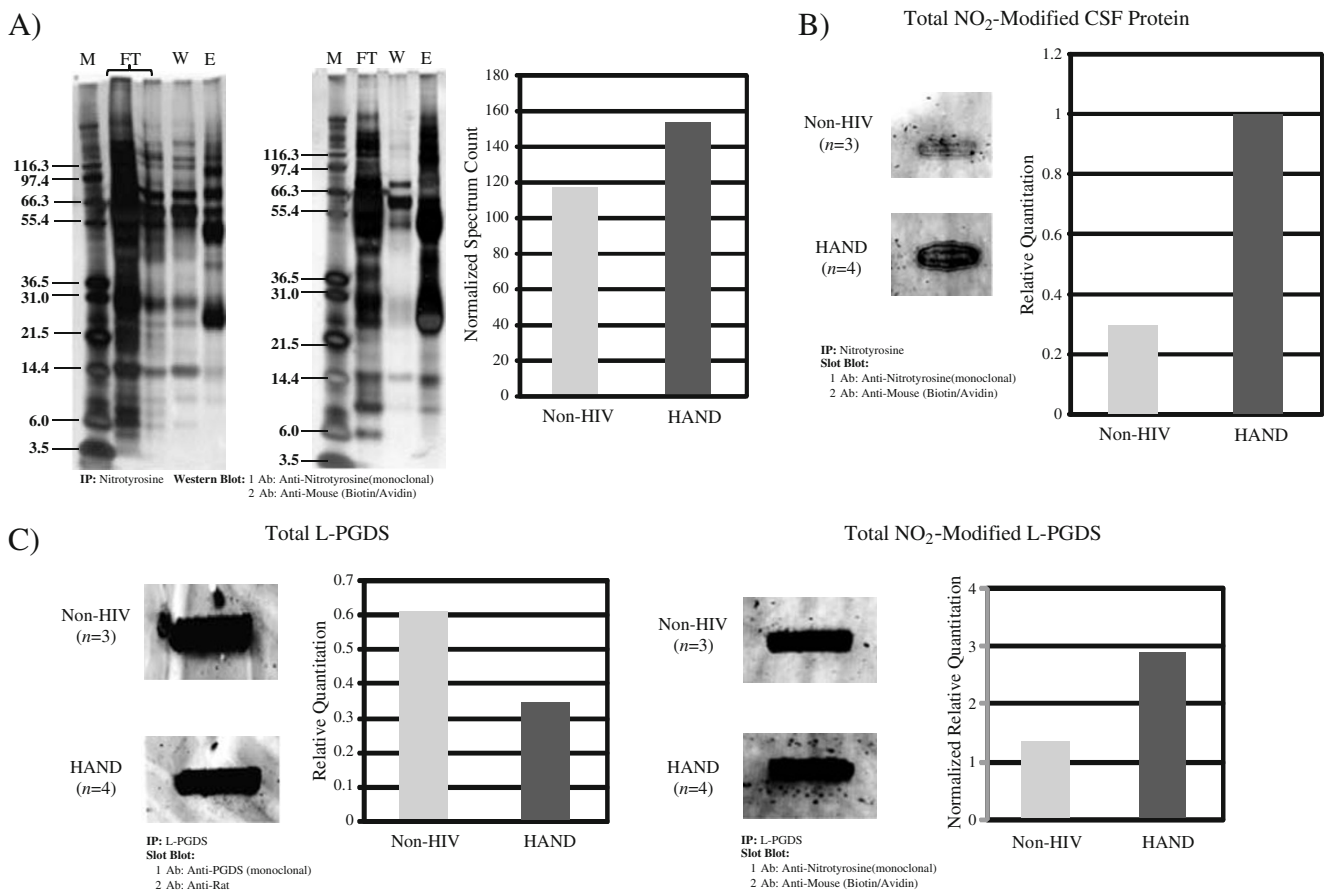
Y*- NO₂-modified Tyrosine

Fig. 4 1-D electrophoresis **(a)** of nitrotyrosine enrichment fractions from pooled non-HIV (control) and HAND CSF. Lane 1, MW marker; lane 2, flowthrough (non-nitrated proteins); lane 3, pre-elution PBS wash; and lane 4, 5% formic acid elution (enriched nitrated proteins). The total number of spectra acquired (normalized spectrum count)

from Non-HIV (control) and HAND CSF nitrotyrosine-modified subproteome **(a)**. Quantitative immunoblot analysis of nitrotyrosine content in albumin/IgG-depleted non-HIV (control) and HAND (diseased) CSF **(b)** and L-PGDS **(c)** determined by slot blot analysis