Here we present original data related to the research paper entitled "Proteome analysis in dystrophic mdx mouse muscle reveals a drastic alteration of Key Metabolic and Contractile Proteins after chronic exercise and the potential modulation by anti-oxidant compounds" (Gamberi et al., 2018) [1]. The dystrophin-deficient mdx mouse is the most common animal model for Duchenne muscular dystrophy. The mdx mouse phenotype of the disorder is milder than in human sufferers and it can be worsened by chronic treadmill exercise. Apocynin and taurine are two antioxidant compounds proved to be beneficial on some pathology related parameters (Schröder and Schoser, 2009) [2]. This article reports the detailed proteomic data on protein abundance alterations, in tibialis anterior muscle of mdx mice, induced by chronic exercise protocol. A selected group of mdx mice was also treated with apocynin and taurine during this protocol. Detailed MS data, comparison between mdx vs wild type, exercised mdx vs wild type.
type, and complete analysis of spot variation are provided. Furthermore, in wild type mice subjected to the same exercise protocol, the abundance of key proteins, resulted modified in exercised mdx, were analyzed by western blot.

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Specifications Table

| Subject area                  | Biology                                                                 |
|-------------------------------|-------------------------------------------------------------------------|
| More specific subject area    | Mdx mice model for Duchenne muscular dystrophy.                         |
| Type of data                  | Table, text file, graph                                                 |
| How data was acquired         | 2DE gels were analyzed with Progenesis SameSpots software v4.0 (Nonlinear Dynamics, UK). MS and MSMS data were obtained with Ultraflex III MALDI- TOF/TOF mass spectrometer (Bruker Daltonics) Analyzed |
| Data format                   | Effect of chronic exercise on muscle protein abundance in mdx mice model for Duchene muscular dystrophy. Modulation by two natural compounds apocynin and taurine |
| Experimental factors         | Animal model. Male mdx mice divided in:                                  |
|                               | - sedentary mdx (mdx) mice                                              |
|                               | - exercised mdx (mdx exe) mice                                         |
|                               | - mdx exercised mice treated with taurine (mdx exe tau)                |
|                               | - mdx exercised mice treated with apocynin (mdx exe apo)               |
|                               | - C57/BL wild-type mice exercised (wt exe) and control (wt).            |
|                               | Age-matched male wild-type mice (C57BL/10) has been used as referring phenotype. The training protocol consisted of a 30 min running on a horizontal treadmill (Columbus Instruments, USA) at 12 m/min, twice a week for at least 4 weeks. The doses of taurine and apocynin were 1 g/kg (orally) and 38 mg/kg (1.5 mmol/l in drinking water) respectively. Proteomics: 2DE and MS were used in order to identify differences in protein abundance between groups. |
| Data source location          | Male mdx mice (C57BL/10ScSn-Dmdmdx/J from Jackson Laboratories) and C57/BL wild-type (wt) mice (from Jackson Laboratories) |
| Data accessibility            | Data is provided by this article                                      |

Value of the data

- These data report for the first time the effect of chronic exercise protocol on protein abundance in mdx mice.
- These data can provide information about muscle damage induced by an inappropriate exercise in dystrophic patients.
- These data show the ability of taurine and apocynin to counteract some of exercise-induced protein alterations.
Table 1  
Differentially abundant protein spots that significantly differed between groups, identified by MALDI-TOF/TOF mass spectrometry analysis. The complete list of the proteins, identified by MALDI-TOF is reported in [1].

| Spot No. | Protein name | AC | Gene Name | Cellular component | Theoretical Mr (kDa)/pI | Observed Mr (kDa)/pI | Mascot score | Matched Pept. | Seq. coverage (%) |
|----------|--------------|----|-----------|--------------------|-------------------------|----------------------|--------------|---------------|-----------------|
| 1        | LIM domain-binding protein 3 | Q9JKS4 | Ldb3 | Z-disc | 77.6/7.9 | 30.1/9.7 | 86 | 9/45 | 17% |
| 3        | LIM domain-binding protein 3 | Q9JKS4 | Ldb3 | Z-disc | 77.6/7.9 | 30.2/9.3 | 76 | 8/34 | 16% |
| 6        | Myozenin-1 | Q9JK37 | Myoz1 | Cytoskeleton | 31.4/8.6 | 31.7/7.9 | 121 | 15/77 | 67% |
| 11       | Troponin T, fast skeletal muscle | Q9QZ47 | Tnnt3 | Troponin complex | 32.2/5.3 | 31.5/7.8 | 82 | 10/43 | 33% |
| 12       | Troponin T, fast skeletal muscle | Q9QZ47 | Tnnt3 | Troponin complex | 32.2/5.3 | 31.9/9.2 | 74 | 8/27 | 26% |
| 13       | Myosin regulatory light chain 2, skeletal muscle isoform | P97457 | Mylpf | Myosin complex | 19/4.8 | 16/1.4/8 | 88 | 10/42 | 63% |
| 16       | Myosin regulatory light chain 2, skeletal muscle isoform | P97457 | Mylpf | Myosin complex | 19/4.8 | 17/1.4/9 | 72 | 6/36 | 37% |
| 23       | Actin, alpha skeletal muscle and Actin, alpha cardiac muscle | P68134 and P68033 | Acta1 and Actc1 | Cytoskeleton | 42.3/5.2 | 42.4/5.2 | 72 | 14/32 | 44% |
| 34       | Triosephosphate isomerase | P17751 | Tpi1 | cytoplasm | 32.7/5.5 | 25/6.7 | 91 | 8/26 | 34% |

Metabolism (Glucose metabolism)

| Spot No. | Protein name | AC | Gene Name | Cellular component | Theoretical Mr (kDa)/pI | Observed Mr (kDa)/pI | Mascot score | Matched Pept. | Seq. coverage (%) |
|----------|--------------|----|-----------|--------------------|-------------------------|----------------------|--------------|---------------|-----------------|
| 30       | Fructose-bisphosphate aldolase A | P05064 | Aldoa | cytoplasm | 39.7/8.3 | 30.4/7.1 | 60 | 6/25 | 16% |
| 34       | Triosephosphate isomerase | P17751 | Tpi1 | cytoplasm | 32.7/5.5 | 25/6.7 | 91 | 8/26 | 34% |
| Spot No. | Protein name | AC | Gene Name | Cellular component | Go term | Theoretical Mr (kDa)/pI | Observed Mr (kDa)/pI | Mascot search results | Peptide Sequence |
|---------|--------------|----|-----------|-------------------|---------|------------------------|---------------------|----------------------|------------------|
| 37      | Beta-enolase  | P21550 | Eno3      | cytoplasm         | (Respiratory chain complex) | 47.3/6.7 | 46.6/6.3 | 95 | 8/22 | 23% | [150-163] R.HVFGESDELICOKV [256-270] R.IYCGSVTGTACKE [15-29] R.GNTVEVLHIAK.G [239-254] K.VVJGMVAAEFYR.N |
| 48      | NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial | Q9D6J6 | Ndufv2 | mitochondrion | 27.6/7 | 23.9/5.4 | 71 | 8/32 | 38% | [238-247] K.GPGFGVQAGL [110-124] R.YVEVATFMYTVN.R [41-61] R.DTPNPPTedPDTPenYK.R [334-348] K.EAYPDVFYLYSHR.L |
| 51      | ATP synthase subunit alpha, mitochondrial | Q03265 | Atp5a1 | mitochondrion | 59.8/9.22 | 22.5/6.6 | 72 | 7/22 | 17% | |
| 55      | Creatine kinase M-type | P07310 | Ckm | cytoplasm | Energy transfer | 43.2/6.6 | 24.3/6.3 | 61 | 7/20 | 21% | [116-131] K.GGDLDVPVLSVSR.V [156-171] K.LSVEALNSLTFEK.G [116-131] K.GGDLDVPVLSVSR.V [156-171] K.LSVEALNSLTFEK.G [210-215] R.DWDAR.G [223-237] K.SLWVNEEDLR.V [259-267] K.IEEIKF.K [269-381] K.GSGSDIMP.K [341-359] R.LGSSEVEQVQLVVGK.L [9-22] K.IHFVGGPSGK.G [31-45] K.GYTHLSTGQDLR.A [9-22] K.IHFVGGPGSGK.G [131-139] K.ERGTSGR.V [139-148] R.VDDNEEICK.R |
| 57      | Creatine kinase M-type | P07310 | Ckm | Cytoplasm | 43.2/6.6 | 29.6/6.6 | 66 | 10/39 | 27% | [116-131] K.GGDLDVPVLSVSR.V [156-171] K.LSVEALNSLTFEK.G [116-131] K.GGDLDVPVLSVSR.V [156-171] K.LSVEALNSLTFEK.G [210-215] R.DWDAR.G [223-237] K.SLWVNEEDLR.V [259-267] K.IEEIKF.K [269-381] K.GSGSDIMP.K [341-359] R.LGSSEVEQVQLVVGK.L [9-22] K.IHFVGGPSGK.G [31-45] K.GYTHLSTGQDLR.A [9-22] K.IHFVGGPGSGK.G [131-139] K.ERGTSGR.V [139-148] R.VDDNEEICK.R |
| 58      | Creatine kinase M-type | P07310 | Ckm | Cytoplasm | 43.2/6.6 | 29.7/6.6 | 61 | 7/35 | 21% | |
| 60      | Creatine kinase M-type | P07310 | Ckm | Cytoplasm | 43.2/6.6 | 17.4/7.9 | 68 | 9/34 | 29% | |
| 70      | Adenylate kinase isoenzyme 1 | Q9R0Y5 | Ak1 | Cytoplasm | Transport | 21.6/5.7 | 21.5/5.3 | 58 | 5/20 | 36% | [109-123] K.LTITDSSSPNITG.K [87-107] K.WNTDINTGTETYVEDQAR.G [250-270] KVNNSSLSGLYTQTLKPGA.K |
| 71      | Adenylate kinase isoenzyme 1 | Q9R0Y5 | Ak1 | Cytoplasm | 21.6/5.7 | 22/5.5 | 104 | 11/40 | 55% | |

a Spot numbers match those reported in the representative 2DE images shown in Fig. 1 and Table 1 in ref. [1].
b Accession number in Swiss-Prot/UniprotKB.
c Based on the calculation using Progenesis SameSpots 4.0 software.
d Mascot MS score (Matrix Science, London, UK; http://www.matrixscience.com). MS matching score greater than 56 was required for a significant MS hit (p-value < 0.05).
e Number of matched peptides correspond to peptide masses matching the top hit from Ms-Fit PMF, searched peptide are also reported.
f Sequence coverage = (number of the identified residues/total number of amino acid residues in the protein sequence) x100%.
g Peptide sequence obtained by Maldi TOF/TOF analysis using an Ultraflex III MALDI-TOF/TOF mass spectrometer (Bruker Daltonics).
Table 2
Sequence coverage (in bold) of identified proteins that show an experimental Mr different from expected.

| Spot No | AC  | Gene Name | Sequence coverage | \(^a_{Theoretical Mr (kDa)}\) | \(^b_{Observed Mr (kDa)}\) |
|---------|-----|-----------|------------------|-----------------|----------------|
| Spot No | AC | Gene Name | Sequence coverage | Theoretical Mr (kDa)/ pI | Observed Mr (kDa)/ pI |
|---------|----|-----------|-------------------|-------------------------|----------------------|
| 3       | Q9JKS4 | Ldb3      | 1 MSYSVTLCGP PWGFRLQGQ KDFNMLPTIS RITPGSKAAQ SLSQSDLVV | 77.6/7.9 | 30.2/9.3 |
| 51      | AIDCVNIDTM THLEAQNKK SASYNLSTL QKSSRIPPIST TTAPPIQPL | 101 PVPHQKDPDA LDTNSLTAP SPSPEARASP GALEGDTFS SFSQATCS | 59.8/9.22 | 22.5/6.6 |
| 51      | Q03265 | Atp5a1    | 1 MLSVRVAAV ARALPBRAGL VSKNALCSSF VGARNLHASN TRLOKCTGAE | 59.8/9.22 | 22.5/6.6 |
| 55      | P07310 | Ckm       | 1 MPFQTNHTFK KLNYKPCQEY PDLSKHNHM AKVLTPDLYL KLRDKETPSG | 43.2/6.6 | 24.3/6.3 |
| Spot No | AC     | Gene Name | Sequence coverage | Theory Mr (kDa)/ pI | Observed Mr (kDa)/ pI |
|---------|--------|-----------|------------------|--------------------|---------------------|
| 60      | P07310 | Ckm       | 1 MPFGNTHNKF KLINYKQEEY PDLSKHNNHM AKVLTPDLYN KLKDKEPSG | 43.2/6.6           | 17.4/7.9            |
| 90      | Q9R1S8 | Capn7     | 1 MDASALERDA VQFARLAVQR DHEGRYSEAV FYYKEAAQAL IYAEMAGSSL | 93.3/8.1           | 17.6/10.3          |
1 MYKSVSETRH PLQSEEQEVG IDPLFSYSNK TRGDLSONGR GSNSLTDTEG
51 TFNSYMKEWE ELFVNNYLVA TVRQKGINGQ LRRSRFRSIC WKILFLCVLPQ
101 DKSQWISKIK ELRAWYSSIK EIHITNPRIA AGQQDMINNN PLSQDEGLSW
151 NKFFQDKELR SMIEQDVKRT FP EMQFFQEQE NVRKILTVDL FCYARENEQL
201 LYYQCMHEL APFITLHCQ LQAFHLHASE AQPSEEMKTL LNPEYLEHDA
251 YAMSQMLMET AE PWSTFEH DGQKCKETLM APIPQAPQOQ LDGPTVAVTK
301 VNOIQDHLKL KDHIEYMHL NRLEAPQYI GLRWWVRLFEG REFPLQDLLV
351 VWDALFAEDSL NLSLVYDVFAMLLYIRDAL ISSNYTCLG LLMHYIPLG
401 HSLILKALF LRDNPKNRPR ATYQFHPNLD YYKARGDLML NIKSTNARGA
451 PLNIHKSNS LINFGRKLIS PASAPGSMGG PVPGNNSSSS FSAAIPTRTS
501 TEAPRHHLQQ QQQQQQHQQQ QQQQQQQQQ QQHQQQQQQR LMKSESMPVQ
551 LNKQQSSSTT SSSPSESLP GGREFTGSPPP S PATKDSFF SNIARSRSHS
601 KTMGRKREEE ELRAWQFLQ GQLNLDLAMC KYACKVMDMH LVNIXQVDVLQ
651 ENLEKEDQIQL VSLAGLQKIQ DILKGLRFN QSQLEAGENE QITIADDHYC
701 SSGQDMQSVQ PQRAQASSE MPGCTGTTTP DDFILVSKED EGHRARGAFS
751 GGQAPLTTLR STGKSRAAPA CSPFLLFDPL MPGASASSASS SNPSSSSPDDD
801 SSSCSSFIV SPLDV

Spot numbers match those reported in the representative 2DE images shown in Fig. 1 and Table 1 in ref. [1]

Accession number in Swiss-Prot/UniprotKB.

Sequence coverage refers to the identified peptides of the protein sequence (bold letters).

Theoretical molecular mass (Mr) and isoelectric point (pI) according to protein sequence.

Molecular mass (Mr) and isoelectric point (pI) based on the calculation using software Progenesis SameSpots
Fig. 1. Histograms represent the abundance of each spot (normalized volume, arbitrary units) in all groups studies, namely mdx, mdx exe, mdx exe apo, mdx exe tau (indicated as mdx+apo and mdx+tau respectively) and wt, evaluated with Progenesis SameSpot software. All spots show a False Discovery Rate (FDR) ≤ 0.05. The significant differences between groups were calculated with GraphPad Prism v6.0 software, using Tukey correction for multiple comparison. Significant differences between groups are indicated by a line.
Fig. 1. (continued)
Fig. 1. (continued)
Fig. 1. (continued)
Fig. 1. (continued)
Other metabolic process

Transport

Fig. 1. (continued)
Fig. 1. (continued)
1. Data

1.1. MS data

97 differentially abundant spots were identified through the study published in [1]. Among these, some spots showing low Mascot (PMF) score value or discrepancy between theoretical and calculated MW or pl, were further analyzed performing peptide sequencing by tandem mass spectrometry. MS/MS analysis was carried out by using an Ultraflex III MALDI-TOF/TOF mass spectrometer (Bruker Daltonics) as described in Materials and Methods, and Table 1 reports detailed MALDI-TOF/TOF data. 12 spots show an experimental Mr different from expected. The sequence coverage of these spots is reported in Table 2. The muscle protein LIM domain-binding protein 3 (LDB3) was found in three different spots showing a Mr lower than expected. This protein belongs to Z-disc proteins whose alteration was correlated with myofibrillar myopathies [2]. Creatin kinase (Ckm) was found in six spots showing a Mr lower than expected.

1.2. Apocynin and taurine modulate the effect of exercise on mdx mice muscle protein abundance

Fig. 1 reports 97 histograms representing the spot abundance, in each group analysed (mdx, mdx exe, mdx exe tau, mdx exe apo) evaluated by gel image analysis with ProgenesisSame Spot. Proteins are divided in categories according to their GO biological process. Protein spot abundance in wt mice was also evaluated as referring phenotype. Fig. 2 summarizes the modulatory effects of taurine and apocynin.

1.3. Comparison with wt strain

Table 3 reports differentially abundant protein spots and relative fold changes, between mdx exe vs wt and mdx vs wt tibialis anterior muscles. In Fig. 3a diagram represents the relationships between these three groups. The protocol used for mdx training consisted of a 30 min running on a horizontal treadmill (Columbus Instruments, USA) at 12 m/min, twice a week for at least 4 weeks. This protocol causes significant weakness in the limb strength as measured by a grip strength meter [3]. The in vivo weakness produced by such a protocol is observed exclusively in mdx mice with no similar effects in wild type mice [4,5]. In fact, protocols used to induce training effects in wild types mice usually consist of continuous running at 20 m/min for at least 15 min using a treadmill slope of 10°, five days a week, for eight weeks [6]. To exclude training effects in wt animals we checked the amount of selected proteins in wt animals subjected to the same exercise protocol of mdx mice. In particular, we...
Table 3
Differentially abundant protein spots between mdx exe vs wt and mdx vs wt tibialis anterior muscles.

| Spot No | Protein name                                      | fold change mdx vs wt | fold change mdx exe vs wt |
|---------|---------------------------------------------------|-----------------------|----------------------------|
| 3       | LIM domain-binding protein 3                      | ns                    | 1.5                        |
| 4       | LIM domain-binding protein 3                      | ns                    | 1.7                        |
| 5       | LIM domain-binding protein 3                      | ns                    | 1.8                        |
| 6       | Myozenin-1                                       | ns                    | 1.4                        |
| 7       | Troponin I, fast skeletal muscle                  | -2.2                  | ns                         |
| 8       | Troponin I, fast skeletal muscle                  | -1.6                  | ns                         |
| 9       | Troponin I, fast skeletal muscle                  | -1.8                  | ns                         |
| 14      | Myosin regulatory light chain 2, skeletal muscle isoform | ns                    | -2.1                       |
| 15      | Myosin regulatory light chain 2, skeletal muscle isoform | ns                    | -3.7                       |
| 16      | Myosin regulatory light chain 2, skeletal muscle isoform | -2.1                  | -4.1                       |
| 17      | Tropomyosin beta chain                            | -2.3                  | -2.8                       |
| 18      | Tropomyosin alpha-1 chain                         | -1.8                  | -2.8                       |
| 20      | Myosin light chain 1/3, skeletal muscle isoform   | ns                    | -2.9                       |
| 23      | Actin, alpha skeletal muscle and Actin, alpha cardiac muscle1 | -1.4                  | ns                         |
| 24      | Actin, alpha cardiac muscle 1                     | -1.4                  | -1.6                       |
| 26      | Myotilin                                         | ns                    | 1.7                        |
| 27      | Myotilin                                         | ns                    | 1.8                        |
| 30      | Fructose-bisphosphate aldolase A                  | ns                    | 1.6                        |
| 32      | Triosephosphate isomerase                         | -1.53                 | ns                         |
| 33      | Triosephosphate isomerase                         | -1.4                  | ns                         |
| 36      | Triosephosphate isomerase                         | -1.52                 | ns                         |
| 39      | Beta-enolase                                      | -1.4                  | ns                         |
| 41      | UTP–glucose-1-phosphate uridylyltransferase       | ns                    | 1.3                        |
| 42      | Fumarate hydratase, mitochondrial                 | ns                    | 1.4                        |
| 43      | Fumarate hydratase, mitochondrial                 | ns                    | 1.3                        |
| 44      | Malate dehydrogenase, mitochondrial               | -1.8                  | ns                         |
| 46      | Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial | ns                    | 1.5                        |
| 49      | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 | 1.8                  | ns                         |
| 50      | Cytochrome b-c1 complex subunit 1, mitochondrial | -1.6                  | -1.6                       |
| 54      | Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial | ns                    | 1.5                        |
| 55      | Creatine kinase M-type                            | -2                    | ns                         |
| 56      | Creatine kinase M-type                            | ns                    | 1.7                        |
| 57      | Creatine kinase M-type                            | -2.5                  | ns                         |
| 59      | Creatine kinase M-type                            | 1.8                   | ns                         |
| 68      | Creatine kinase M-type                            | -1.5                  | ns                         |
| 69      | Nucleoside diphosphate kinase B                   | ns                    | 3.7                        |
| 70      | Adenylyl kinase isoenzyme 1                      | ns                    | -2.6                       |
| 72      | Alcohol dehydrogenase [NADP( +)]                 | ns                    | 1.4                        |
analysed by western blot the amount of several proteins of glycolysis (all increased in mdx exe mice), oxophos proteins, and PGC-1-alpha and Sirt1 proteins. As shown in Fig. 4 none difference is observed in the expression level of these proteins.

### 2. Experimental design, materials and methods

The methodologies that allowed the data here presented are described in [1] and in cited references. Here, only the protocol for MS/MS data is described.

Trypsin digests of some spots with low Mascot (PMF) score value or with discrepancy between theoretical and calculated MW or pI were further analyzed performing peptide sequencing by tandem mass spectrometry. MS/MS analysis was performed by using an Ultraflex III MALDI-TOF/TOF mass spectrometer (Bruker Daltonics). Two to four PMF peaks showing a high intensity were CID fragmented using Argon as collision gas, and MALDI-TOF/TOF tandem MS was performed in LIFT mode by software controlled data acquisition. Fragmented ions were analyzed using the Flex Analysis software v.3.0. The MS/MS database searching was carried out in the UniProtKB database using the on-line available MASCOT MS/MS ion search software. The following parameters were applied for database

| Spot No | Protein name                                | fold change mdx vs wt | fold change mdx exe vs wt |
|---------|---------------------------------------------|-----------------------|-------------------------|
| 74      | Carbonic anhydrase 3                         | ns                    | 1.4                     |
| 75      | Carbonic anhydrase 3                         | ns                    | 1.3                     |
| 78      | Malate dehydrogenase, cytoplasmic            | 1.4                   | ns                      |
| 81      | Serotransferrin                              | 1.5                   | 1.8                     |
| 82      | Serotransferrin                              | ns                    | 1.7                     |
| 91      | 26S protease regulatory subunit 8            | ns                    | 1.6                     |
| 92      | Protein disulfide-isomerase A3               | ns                    | 1.5                     |
| 93      | Peroxiredoxin-6                             | -1.6                  | ns                      |
| 94      | Electron transfer flavoprotein subunit alpha, mitochondrial | ns | 1.4 |
| 96      | TBC1 domain family member 5                 | ns                    | 1.3                     |
| 97      | Alpha-crystallin B chain                    | ns                    | 1.8                     |

*a* Fold change was calculated dividing the average of %V of mdx or mdx exe by the average of %V of wt (%V = volume = integration of the optical density over the spot area; %V = V single spot/V total spots included in the reference gel).

Fig. 3. Diagram representing the distribution of differences in spot abundance between groups: 27 protein spots differ exclusively between mdx exe and wt, 15 protein spots differ exclusively between mdx and wt and 7 spots are different from wt in both mdx and mdx exe.
searching: taxonomy: *Mus musculus*, trypsin specificity, one missed cleavage allowed, peptide precursor mass tolerance: ± 100 ppm, fragment mass tolerance: ± 0.6 Da, peptide precursor charge state: +1, carbamidomethylation of cysteine as a fixed modification, oxidation of methionine as a possible modification. For protein identification, Mascot ion score, peptide coverage by "b" and "y" ions, and expected value were considered. We considered as significant, peptides with individual ion scores \(-10 \times \log(P)\), where P is the probability that the observed match is a random event, that indicated identity (p < 0.05).

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**Transparency document. Supporting information**

Supplementary data associated with this article can be found in the online version at [http://dx.doi.org/10.1016/j.dib.2018.03.037](http://dx.doi.org/10.1016/j.dib.2018.03.037).
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