Data Article

Dataset on the mass spectrometry-based proteomic profiling of the kidney from wild type and the dystrophic mdx-4cv mouse model of X-linked muscular dystrophy

Paul Dowling a,b, Margit Zweyer c, Maren Raucamp c, Michael Henry d, Paula Meleady d, Dieter Swandulla c, Kay Ohlendieck a,b,*

a Department of Biology, Maynooth University, National University of Ireland, Maynooth, W23F2H6, Co. Kildare, Ireland
b Kathleen Lonsdale Institute for Human Health Research, Maynooth University, Maynooth, W23F2H6, Co. Kildare, Ireland
c Institute of Physiology II, University of Bonn, D53115, Bonn, Germany
d National Institute for Cellular Biotechnology, Dublin City University, Dublin 9, Ireland

Article history:
Received 4 December 2019
Received in revised form 17 December 2019
Accepted 18 December 2019
Available online 2 January 2020

Keywords:
Kidney proteome
Mass spectrometry
Muscular dystrophy
Proteomics

Abstract
The proteomic data presented in this article provide supporting information to the related research article "Proteomic and cell biological profiling of the renal phenotype of the mdx-4cv mouse model of Duchenne muscular dystrophy" (Dowling et al., 2019) [1]. This article supplies additional datasets on protein species with increased versus decreased concentration in the kidney from the dystrophic mdx-4cv mouse, as well as tables with mass spectrometrically identified kidney marker proteins that exhibit characteristic tissue distributions, subcellular localizations and physiological functions. Information is provided on the underlying multi-consensus protein listings from the proteomic screening of both wild type and mdx-4cv mouse kidneys. The data article
provides comprehensive information on the systematic and mass spectrometric identification of the mouse kidney proteome. 
© 2019 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

1. Data

This data paper presents the findings from the mass spectrometric profiling of mouse kidney extracts, and relates to the comparative survey of the renal proteome from wild type versus the dystrophic mdx-4cv mouse model of Duchenne muscular dystrophy [1]. With the help of an Orbitrap Fusion Tribrid mass spectrometer, 5878 protein species were identified in renal tissue extracts. The multi-consensus file of mouse kidney that contains data from the analysis of 28 separate mass spectrometric sample runs, as well as the raw data underlying the cataloguing of the kidney, has been deposited to the Open Science Framework under the project title ‘Proteomic profiling of mouse kidney’; Link: https://osf.io/bz3kv/(Date created: 2018-10-04; Date made public: 2019-12-02). The analyses were carried out with 2 technical repeats of 7 biological repeats of 12-month old wild type kidney extracts, as well as 2 technical repeats of 7 biological repeats of 12-month old mdx-4cv kidney extracts. In relation to the report by Dowling et al. [1], additional datasets on proteins with an increased versus decreased concentration in the kidney from the dystrophic mdx-4cv mouse are presented in Tables 1 and 2. Table 1 lists the mass spectrometric identification of kidney proteins with a less than 1. 

Specifications Table

| Subject                      | Biochemistry                                      |
|-----------------------------|---------------------------------------------------|
| Specific subject area       | Biomedicine                                       |
| Type of data                | Tables                                            |
| How data were acquired      | LC-MS/MS analysis, using an Orbitrap Fusion Tribrid Mass Spectrometer (Thermo Scientific) |
| Data format                 | Raw data and analysed data                        |
| Parameters for data collection | Renal protein was extracted from whole kidneys from wild type and dystrophic mdx-4cv mice |
| Description of data collection | Comparative mass spectrometry-based proteomic profiling of kidney extracts |
| Data source location        | Maynooth, Co. Kildare, Ireland                    |
| Data accessibility          | The data on kidney marker proteins are available with this article. The multi-consensus file and raw data files of all identified kidney proteins is available through a public repository. Repository name: Open Science Framework Data identification number: bz3kv Direct URL to data: https://osf.io/bz3kv/ |
| Related research article    | Paul Dowling, Margit Zweyer, Maren Raucamp, Michael Henry, Paula Meleady, Dieter Swandulla and Kay Ohlendieck Proteomic and cell biological profiling of the renal phenotype of the mdx-4cv mouse model of Duchenne muscular dystrophy European Journal of Cell Biology (2019) (available online November 18, 2019, 151059) https://doi.org/10.1016/j.ejcb.2019.151059 |

Value of the Data

- Mass spectrometric data presented in this article provide a detailed listing of the protein isoforms of the assessable mouse kidney proteome.
- Proteomic data provide a summary of changed renal proteins in the dystrophic mdx-4cv mouse model of X-linked muscular dystrophy.
- The proteomic data give an overview of the identification of tissue-specific kidney marker proteins.
- The mass spectrometric data are valuable to serve as a comprehensive repository of the mouse proteome for comparative biochemical studies.

1. Data
Table 1
Proteomic identification of kidney proteins with an increased abundance below 1.5-fold in the mdx-4cv model of Duchenne muscular dystrophy.

| Accession | Protein                   | Gene                     | Unique peptides | Confidence score | Anova (p) | Max fold change |
|-----------|---------------------------|--------------------------|-----------------|------------------|-----------|----------------|
| O35657    | Sialidase-1                | Neu1                     | 2               | 4.6649           | 0.00419   | 1.49           |
| O54990    | Prominin-1                 | Prom1                    | 2               | 13.8091          | 0.01535   | 1.49           |
| Q91WU2    | Solute carrier family 22 member 7 | Scl22a7               | 2               | 5.6395           | 0.04080   | 1.49           |
| D3Z7P3    | Glutaminase kidney isom, mitochondrial | Gls                 | 3               | 12.9045          | 0.00653   | 1.48           |
| P48758    | Carbonyl reductase [NADPH] | Cbr1                    | 4               | 17.5670          | 0.00074   | 1.48           |
| Q61391    | Nephrilysin                | Mme                     | 4               | 12.3698          | 0.00261   | 1.48           |
| G5E829    | Plasma membrane calcium-transporting ATPase 1 | Atp2b1               | 2               | 7.9881           | 0.00011   | 1.47           |
| P24472    | Glutathione S-transferase A4 | Gsta4               | 2               | 5.6183           | 0.00201   | 1.47           |
| O88343    | Electrogentic sodium bicarbonate cotransporter 1 | Slc4a4               | 7               | 22.6034          | 1.04E-08  | 1.47           |
| Q9R257    | Heme-binding protein 1     | Hebp1                   | 2               | 8.7884           | 0.00369   | 1.46           |
| P61922    | 4-aminobutyrate aminotransferase, mitochondrial | Abat                | 6               | 21.8090          | 4.63E-05  | 1.46           |
| O70370    | Cathepsin S                | CtsS                    | 2               | 9.0446           | 0.00011   | 1.45           |
| P70172    | Ileal sodium/bile acid cotransporter | Scl10a2             | 2               | 5.4973           | 0.00038   | 1.45           |
| P24452    | Macrophage-capping protein | Capg                   | 2               | 5.5246           | 0.02331   | 1.45           |
| P97449    | Aminopeptidase N           | Anpep                   | 5               | 27.1718          | 0.00188   | 1.45           |
| Q8BMS1    | Trifunctional enzyme subunit alpha, mitochondrial | HadhA               | 2               | 6.4455           | 0.00174   | 1.44           |
| Q9QXE0    | 2-hydroxyacyl-CoA lyase 1  | Hacl1                   | 2               | 9.9044           | 0.00925   | 1.44           |
| Q9D687    | Sodium-dependent neutral amino acid transporter B0/AT1 | Slc6a19             | 3               | 10.4909          | 1.27E-06  | 1.43           |
| Q9D964    | Glycine amidinotransferase, mitochondrial | Gatm               | 2               | 7.0537           | 0.00819   | 1.42           |
| Q9Z306    | Solute carrier family 22 member 4 | Scl22a4             | 2               | 6.6313           | 0.00929   | 1.42           |
| Q49893    | Sodium-coupled monocarboxylate transporter 2 | Scl5a12             | 2               | 6.7141           | 1.69E-05  | 1.41           |
| Q9CQ65    | S-methyl-5-thioadenosine phospholylase | Mtap             | 2               | 5.9308           | 0.00323   | 1.41           |
| P23780    | Beta-galactosidase         | Glib1                   | 2               | 6.2503           | 0.00437   | 1.4           |
| P24668    | Cation-dependent mannose-6-phosphate receptor | M6pr              | 2               | 6.5894           | 0.04069   | 1.4           |
| P09470    | Angiotensin-converting enzyme | Ace            | 12              | 42.5194          | 0.00642   | 1.4           |
| Q8VCZ9    | Hydroxyproline dehydrogenase | Prodh2           | 2               | 10.6440          | 0.00172   | 1.39           |
| P45376    | Aldose reductase           | Akr1b1                 | 5               | 13.6831          | 0.00165   | 1.39           |
| O88986    | 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial | Gcat             | 3               | 10.1459          | 4.10E-05  | 1.38           |
| Q9WV92    | Band 4.1-like protein 3    | Ebp41I3                 | 4               | 14.7070          | 0.00046   | 1.38           |
| Q9DBT9    | Dimethylglycine dehydrogenase, mitochondrial | Dmgdh             | 5               | 18.8616          | 0.00028   | 1.38           |
| O88428    | Binfunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 | Papss2           | 11              | 37.6264          | 0.00095   | 1.38           |
| O09164    | Extracellular superoxide dismutase [Cu–Zn] | Sod3            | 2               | 11.3667          | 1.53E-05  | 1.37           |
| O70493    | Sorting nexin-12          | Snx12                   | 4               | 10.9785          | 6.57E-06  | 1.36           |
| Q9Z1G3    | V-type proton ATPase subunit C 1 | Atp6v1c1         | 4               | 14.1960          | 0.00010   | 1.36           |
| Q9R092    | 17-beta-hydroxysteroid dehydrogenase type 6 | Hsd17b6        | 2               | 7.8166           | 0.00030   | 1.35           |
| Q9EQ20    | Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial | Aldh6a1        | 2               | 7.8288           | 0.02301   | 1.35           |
| Q8K157    | Aldose 1-epimerase         | Galm                    | 3               | 10.5439          | 0.00726   | 1.35           |
| P16406    | Glutamyl aminopeptidase    | Enpep                   | 10              | 35.0875          | 1.14E-06  | 1.35           |
| Q5QWR8    | Alpha-N-acetylgalactosaminidase | Naga             | 3               | 8.7144           | 0.00102   | 1.34           |
| Q9DCJ9    | N-acetylneuraminic lyase   | Npl                    | 4               | 13.4008          | 0.00150   | 1.34           |
| Q8R3P0    | Aspartoacylase             | Aspa                    | 2               | 4.8961           | 5.94E-05  | 1.33           |
| P24527    | Leukotriene A-4 hydrolase  | Lta4h                   | 2               | 7.3695           | 0.00689   | 1.33           |

(continued on next page)
| Accession | Protein                                      | Gene         | Unique peptides | Confidence score | Anova (p) | Max fold change |
|-----------|----------------------------------------------|--------------|----------------|------------------|-----------|-----------------|
| P16675    | Lysosomal protective protein                 | Ctsa         | 2              | 7.8468           | 0.01961   | 1.33            |
| Q00519    | Xanthine dehydrogenase/oxidase               | Xdh          | 3              | 11.0764          | 0.00741   | 1.33            |
| P10649    | Glutathione S-transferase Mu 1               | Gstm1        | 4              | 16.5436          | 6.74E-05  | 1.33            |
| Q91X52    | L-xylose reductase                           | Dcxr         | 5              | 22.2456          | 5.55E-07  | 1.33            |
| P50431    | Serine hydroxymethyltransferase, cytosolic   | Shmt1        | 6              | 19.5642          | 0.00172   | 1.33            |
| Q9CN7     | Phenazine biosynthesis-like domain-containing protein 2 | Pbld2     | 3              | 13.0305          | 5.80E-07  | 1.32            |
| P15262    | Glutathione S-transferase Mu 2               | Gstm2        | 3              | 10.7236          | 0.00011   | 1.32            |
| Q99BL7    | Sarcosine dehydrogenase, mitochondrial       | Sardh        | 4              | 14.0763          | 6.64E-05  | 1.32            |
| Q99MZ6    | Unconventional myosin-VIIb                   | Myo7b        | 4              | 11.6505          | 0.00061   | 1.32            |
| Q91Y97    | Fructose-bisphosphate aldolase B             | Aldob        | 5              | 22.2473          | 0.02101   | 1.32            |
| P26443    | Glutamate dehydrogenase 1, mitochondrial     | Glud1        | 6              | 19.3021          | 2.20E-07  | 1.32            |
| P48774    | Glutathione S-transferase Mu 5               | Gstm5        | 3              | 8.8950           | 3.80E-05  | 1.31            |
| O88844    | Isocitrate dehydrogenase [NADP]              | Idh1         | 3              | 8.7557           | 0.00071   | 1.31            |
| Q62433    | Protein NDRG1                                | Ndr1         | 5              | 23.1403          | 1.78E-05  | 1.31            |
| Q91VA0    | Acyl-coenzyme A synthetase ACSM1, mitochondrial | Acsm1    | 5              | 19.1532          | 0.00374   | 1.31            |
| P10493    | Nidogen-1                                    | Nid1         | 2              | 8.7788           | 0.00333   | 1.3             |
| O70404    | Vesicle-associated membrane protein 8        | Vamp8        | 3              | 6.0734           | 0.00493   | 1.3             |
| Q61739    | Integrin alpha-6                            | Itga6        | 3              | 11.8001          | 0.00020   | 1.3             |
| P01027    | Complement C3                                | C3           | 3              | 9.6830           | 0.00063   | 1.3             |
| A2ARV4    | Low-density lipoprotein receptor-related protein 2 | Lrp2      | 5              | 22.3161          | 0.00409   | 1.3             |
| P12382    | ATP-dependent 6-phosphofructokinase, liver type | Pfkl       | 3              | 12.7193          | 0.00370   | 1.29            |
| P11881    | Inositol 1,4,5-trisphosphate receptor type 1 | Itpr1        | 5              | 17.8101          | 3.12E-05  | 1.29            |
| P28271    | Cytoplasmic aconitate hydratase              | Aco1         | 2              | 4.3600           | 0.00364   | 1.28            |
| Q8VCT4    | Carboxylesterase 1D                          | Ces1d        | 2              | 6.6902           | 0.01551   | 1.28            |
| Q91Y0     | Argininosuccinate lyase                      | Asl          | 2              | 8.7531           | 0.00032   | 1.27            |
| Q64471    | Glutathione S-transferase theta-1            | Gstt1        | 2              | 5.5587           | 0.00013   | 1.26            |
| Q6P1B1    | Xaa-Pro aminopeptidase 1                     | Xpnppep1     | 3              | 7.8825           | 0.03278   | 1.26            |
| P10852    | 4F2 cell-surface antigen heavy chain         | Slc3a4       | 4              | 10.4098          | 0.00265   | 1.26            |
| Q9VKV4    | EH domain-containing protein 1               | Ehf1         | 2              | 5.8015           | 0.00026   | 1.25            |
| Q71LX4    | Talin-2                                      | Tln2         | 2              | 6.9617           | 0.01162   | 1.25            |
| Q8VC30    | Triokinase/FMN cyclase                       | Tkc          | 3              | 10.8554          | 0.00073   | 1.25            |
| P06281    | Renin-1                                      | Ren1         | 4              | 10.7058          | 0.00451   | 1.25            |
| P63158    | High mobility group protein B1               | Hmbg1        | 2              | 6.2009           | 3.14E-05  | 1.24            |
| Q9D0F9    | Phosphoglucomutase-1                         | Pgm1         | 2              | 5.4388           | 0.00027   | 1.24            |
| O88909    | Solute carrier family 22 member 8            | Slc22a8      | 3              | 9.1520           | 5.17E-06  | 1.24            |
| Q3U47     | Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 | Pyroxd2     | 3              | 10.0392          | 0.00151   | 1.24            |
| Q9NYQ2    | Hydroxyacid oxidase                          | Hao2         | 3              | 11.4539          | 0.02747   | 1.24            |
| O70475    | UDP-glucose 6-dehydrogenase                  | Ugdh         | 5              | 19.0586          | 0.00356   | 1.24            |
| Q88UV3    | Gephyrin                                    | Gphn         | 2              | 6.3220           | 0.00830   | 1.22            |
| Q99K51    | Plastin-3                                    | Pl3          | 2              | 6.6408           | 0.01267   | 1.21            |
| Q99BM2    | Peroxisomal bifunctional enzyme              | Ehhadh       | 2              | 8.7039           | 0.01977   | 1.21            |
| Q9Z1N5    | Spliceosome RNA helicase Ddx39b               | Ddx39b       | 2              | 6.8126           | 0.02905   | 1.21            |
| Q8R0N6    | Hydroxyacid-oxoacid transhydrogenase, mitochondrial | Adhfe1    | 3              | 10.8822          | 5.79E-06  | 1.21            |
| P16546    | Spectrin alpha chain, non-erythrocytic 1      | Sptan1       | 3              | 11.5102          | 0.00302   | 1.21            |
| Q99JY0    | Trifunctional enzyme subunit beta, mitochondrial | Hadhb       | 4              | 13.9444          | 0.00113   | 1.2             |
Proteomic identification of kidney proteins with a decreased abundance below 1.5-fold in the mdx-4cv model of Duchenne muscular dystrophy.

| Accession | Protein                                                                 | Gene                                      | Unique peptides | Confidence score | Anova (p)     | Max fold change |
|-----------|--------------------------------------------------------------------------|-------------------------------------------|-----------------|-----------------|---------------|----------------|
| P48024    | Eukaryotic translation initiation factor 1                               | Eif1                                      | 2               | 8.4814          | 0.00013       | 1.49           |
| Q9HR7     | Insulin-degrading enzyme                                                 | Ide                                       | 2               | 5.2327          | 0.04111       | 1.46           |
| P11862    | Growth arrest-specific protein 2                                         | Gas2                                      | 3               | 9.2866          | 4.11E-05      | 1.46           |
| Q9DBG6    | Dolichyl-diphospho-oligosaccharide-protein glycosyltransferase subunit 2 | Rpn2                                      | 2               | 8.4270          | 0.00186       | 1.45           |
| Q61838    | Pregnancy zone protein                                                   | Pzp                                       | 9               | 29.2658         | 0.00065       | 1.42           |
| Q61847    | Meprin A subunit beta                                                    | Mep1b                                     | 2               | 7.1821          | 0.00095       | 1.4            |
| P12658    | Calbindin                                                               | Calb1                                     | 2               | 5.1746          | 0.01903       | 1.4            |
| Q9CPY7    | Cytosol aminopeptidase                                                   | Lap3                                      | 3               | 10.4237         | 0.02227       | 1.4            |
| Q9DCY0    | Glycine N-acetyltransferase-like protein Reg1                             | Reg1                                      | 2               | 4.7402          | 0.00128       | 1.39           |
| Q9CR67    | Transmembrane protein 33                                                 | Tmem3                                     | 2               | 6.1302          | 0.00735       | 1.38           |
| Q61207    | Prosaposin                                                              | Psap                                      | 2               | 5.1656          | 0.00022       | 1.37           |
| Q8JZ2O    | UDP-glucuronosyltransferase 3A2                                          | Ugt3a2                                    | 2               | 6.4221          | 0.02672       | 1.37           |
| Q9DBX3    | Sushi domain-containing protein 2                                         | Susd2                                     | 4               | 14.5368         | 0.00470       | 1.37           |
| Q9Z1J3    | Cysteine desulfurase, mitochondrial                                     | Nfs1                                      | 2               | 11.6958         | 1.28E-05      | 1.36           |
| Q3U9G9    | Lammin-B receptor                                                        | Lbr                                       | 2               | 7.4723          | 0.00013       | 1.36           |
| Q9CQH7    | Transcription factor BT3 homolog 4                                       | Btf3l4                                    | 2               | 8.2813          | 3.81E-05      | 1.34           |
| Q9CYH2    | Redox-regulatory protein FAM213A                                         | Fam213a                                   | 2               | 6.9334          | 0.00034       | 1.34           |
| Q05920    | Pyruvate carboxylase, mitochondrial                                      | Pct                                       | 2               | 5.6710          | 0.00120       | 1.32           |
| Q05793    | Basement membrane-specific heparan sulfate proteoglycan core protein     | Hspg2                                     | 2               | 5.5448          | 0.00348       | 1.32           |
| P12970    | 60S ribosomal protein L7a                                                | Rp7a                                      | 2               | 6.4383          | 0.01017       | 1.32           |
| P51885    | Lumican                                                                 | Lum                                       | 2               | 7.6116          | 0.02121       | 1.32           |
| Q00915    | Retinol-binding protein 1                                                | Rbp1                                      | 2               | 6.9546          | 0.00513       | 1.31           |
| Q8BFW7    | Lipoma-preferred partner homolog                                         | Lpp                                       | 2               | 5.7683          | 0.01836       | 1.31           |
| Q8QZT1    | Acetyl-CoA acetyltransferase, mitochondrial                              | Acat1                                     | 2               | 8.9227          | 0.00886       | 1.3            |
| O08638    | Myosin-1                                                                | Myh11                                     | 13              | 44.8107         | 5.02E-05      | 1.3            |
| P21107    | Tropomyosin alpha-3 chain                                                | Tpm3                                     | 2               | 7.0891          | 2.93E-05      | 1.29           |
| Q99B2     | Stomatin-like protein 2, mitochondrial                                   | Stom2                                     | 2               | 7.7193          | 4.81E-05      | 1.29           |
| Q32MW3    | Acyl-coenzyme A thioesterase 10, mitochondrial                            | Aco10                                     | 3               | 11.9828         | 0.00043       | 1.28           |
| P58774    | Tropomyosin beta chain                                                   | Tpm2                                     | 2               | 7.4480          | 0.00049       | 1.27           |
| P37804    | Transgeline                                                             | Tagln                                     | 2               | 5.2768          | 0.01312       | 1.27           |
| P21271    | Unconventional myosin-Vb                                                 | Myo5b                                     | 2               | 6.2358          | 0.02245       | 1.27           |
| P09103    | Protein disulfide-isomerase                                              | P4hb                                      | 2               | 5.3654          | 0.03115       | 1.27           |
| Q9CR98    | Protein FAM136A                                                          | Fam136a                                   | 2               | 5.8057          | 0.00522       | 1.26           |
| P28653    | Biglycan                                                                | Bgn                                       | 2               | 7.9254          | 0.00548       | 1.26           |
| Q88HN3    | Neutral alpha-glucosidase AB                                             | Ganab                                     | 3               | 8.1991          | 0.00178       | 1.26           |
| Q02257    | Junction plakoglobin                                                     | Jup                                       | 2               | 7.6926          | 0.01217       | 1.25           |
| Q9D7X8    | Gamma-glutamylcyclco-transferase                                        | Gct                                       | 2               | 7.4681          | 0.01870       | 1.25           |
| Q8BJ64    | Choline dehydrogenase, mitochondrial                                    | Chdh                                      | 4               | 9.5358          | 0.00213       | 1.25           |
| Q8CSC8    | von Willebrand factor A domain-containing protein                        | Vwa8                                     | 8               | 30.5625         | 0.01240       | 1.24           |
| Q8X9O0    | Filamin-B                                                               | Flnb                                      | 18              | 64.3416         | 0.00358       | 1.24           |
| P51174    | Long-chain specific acyl-CoA dehydrogenase, mitochondrial               | Acadl                                     | 2               | 5.1602          | 0.00186       | 1.23           |
| Q78K4     | MICOS complex subunit Mic27                                             | Apool                                     | 2               | 5.9301          | 3.43E-06      | 1.22           |
| Q06770    | Corticosteroid-binding globulin                                         | Serpina6                                  | 2               | 7.0902          | 0.00323       | 1.22           |
| Q7TPR4    | Alpha-actinin-1                                                         | Actn1                                     | 2               | 5.6749          | 0.00332       | 1.22           |
| Q91X72    | Hemopexin                                                               | Hpx                                       | 2               | 4.4037          | 0.03030       | 1.22           |
| Q8QZY2    | Glycerate kinase                                                        | Glyctk                                    | 3               | 12.7538         | 0.00018       | 1.22           |
| Q61543    | Golgi apparatus protein 1                                                | Ggl1                                      | 3               | 12.1393         | 0.00718       | 1.21           |
| Q3V3R4    | Integrin alpha-1                                                        | Itga1                                     | 4               | 11.2984         | 0.00068       | 1.21           |
| Q8VD00    | Myosin-9                                                                | Myh9                                      | 15              | 57.2338         | 0.00070       | 1.21           |
| Q8BL66    | Early endosome antigen 1                                                | Eea1                                      | 3               | 13.5801         | 5.59E-05      | 1.21           |
| Q64727    | Vinculin                                                                | Vcl                                       | 6               | 20.2663         | 0.00409       | 1.2            |
5-fold increase in the mdx-4cv mouse. Kidney proteins with a less than 1.5-fold increased concentration in the mdx-4cv mouse are presented in Table 2. The most abundant high-molecular-mass kidney proteins are presented in Table 3. Information on typical tissue-specific kidney marker proteins [2–6] is provided in Table 4. In Table 5 are listed mass spectrometrically identified kidney marker proteins with characteristic physiological functions in ion homeostasis, including specific isoforms of the sodium/calcium exchanger, sodium/glucose cotransporter, the plasma membrane calcium-transporting ATPase, the sodium/potassium-transporting ATPase, the endoplasmic reticulum calcium ATPase, calcium-binding proteins, voltage-dependent calcium channels and chloride channels [2]. In relation to

Table 3
List of mass spectrometrically identified high-molecular-mass mouse kidney proteins that are covered by a large number of unique peptide sequences.

| Accession | Protein name | Gene     | Peptides | Unique peptides | Coverage (%) | Molecular mass (kDa) |
|-----------|--------------|----------|----------|-----------------|--------------|---------------------|
| A2ARV4    | Low-density lipoprotein receptor-related protein 2 | Lrp2 | 187      | 187             | 56           | 518.9               |
| P16546    | Spectrin alpha chain, non-erythrocytic 1 | Sptan1 | 158      | 158             | 72           | 284.4               |
| Q02261    | Spectrin beta chain, non-erythrocytic 1 | Sptbn1 | 143      | 137             | 70           | 274.1               |
| Q0V8D5    | Myosin-9     | Myh9    | 125      | 103             | 64           | 226.2               |
| Q09HU4    | Cytoplasmic dynein 1 heavy chain 1 | Dync1h1 | 184      | 184             | 50           | 531.7               |
| Q0QX51    | Plectin      | Plec    | 119      | 119             | 30           | 533.9               |
| Q08X90    | Filamin-B    | Flnb    | 116      | 108             | 65           | 277.7               |
| Q0B7M8    | Filamin-A    | Flna    | 108      | 99              | 60           | 281                 |
| P26039    | Talin-1      | Tln1    | 107      | 94              | 65           | 269.7               |
| Q05793    | Basement membrane-specific heparan sulfate proteoglycan core protein | Hspg2 | 103      | 103             | 46           | 398                 |
| Q0QX20    | Microtubule-actin cross-linking factor 1 | Macf1 | 99       | 97              | 19           | 831.4               |
| Q06FD5    | Clathrin heavy chain 1 | Clic | 90       | 90              | 74           | 191.4               |
| Q0FLB4    | Cubilin      | Cubilin | 83       | 83              | 34           | 398.8               |
| Q01001    | Laminin subunit alpha-5 | Lama5 | 84       | 84              | 38           | 403.8               |
| Q08638    | Myosin-11    | Myh11   | 89       | 68              | 50           | 226.9               |
| Q061879   | Myosin-10    | Myh10   | 90       | 68              | 50           | 228.9               |
| Q0CC88    | von Willebrand factor A domain-containing protein 8 | Vwa8 | 88       | 88              | 61           | 213.3               |
| Q1T1X4    | Talin-2      | Tln2    | 81       | 68              | 51           | 253.5               |

5-fold increase in the mdx-4cv mouse. Kidney proteins with a less than 1.5-fold increased concentration in the mdx-4cv mouse are presented in Table 2. The most abundant high-molecular-mass kidney proteins are presented in Table 3. Information on typical tissue-specific kidney marker proteins [2–6] is provided in Table 4. In Table 5 are listed mass spectrometrically identified kidney marker proteins with characteristic physiological functions in ion homeostasis, including specific isoforms of the sodium/calcium exchanger, sodium/glucose cotransporter, the plasma membrane calcium-transporting ATPase, the sodium/potassium-transporting ATPase, the endoplasmic reticulum calcium ATPase, calcium-binding proteins, voltage-dependent calcium channels and chloride channels [2]. In relation to

Table 4
List of mass spectrometrically identified mouse kidney marker proteins with a characteristic cellular localization.

| Accession | Protein name | Gene     | Coverage (%) | Unique peptides | Cellular localization                  |
|-----------|--------------|----------|--------------|-----------------|----------------------------------------|
| Q91X05    | Podocin      | Nphs2    | 18           | 4               | Glomeruli podocytes                     |
| Q9Q2S7    | Nephrin      | Nphs1    | 7            | 5               | Glomeruli                              |
| P61148    | Fibroblast growth factor FGF1 | Fgf1 | 33           | 5               | Glomeruli                              |
| Q0XQXN5   | Inositol oxygenase | Mox | 74           | 12              | Proximal tubule cytoplasm              |
| O70577    | Solute carrier family 22 member 2 | Slc22a2 | 10           | 4               | Proximal tubule basolateral membrane   |
| O888909   | Solute carrier family 22 member 8 | Slc22a8 | 20           | 10              | Proximal tubule basolateral membrane   |
| Q06825    | Sodium-dependent phosphate transport protein 2A | Slc34a1 | 28           | 12              | Proximal tubule luminal membrane       |
| Q0CFZ5    | Solute carrier family 22 member 12 | Slc22a12 | 19           | 12              | Proximal tubule luminal membrane       |
| O88576    | Sodium-dependent neutral amino acid transporter B(O)AT3 | Slc6a18 | 14           | 7               | Proximal tubule luminal membrane       |
| Q1A4L0    | Solute carrier family 22 member 13 | Slc22a13 | 12           | 6               | Proximal tubule luminal membrane       |
| Q91X17    | Uromodulin   | Umod     | 33           | 18              | Distal tubule cytoplasm                |
| O88335    | ATP-sensitive inward rectifier potassium channel 1 | Kcnj1 | 10           | 3               | Distal tubule luminal membrane         |
| P55014    | Solute carrier family 12 member 1 | Slc12a1 | 40           | 32              | Distal tubule luminal membrane         |
| P59158    | Solute carrier family 12 member 3 | Slc12a3 | 29           | 20              | Distal tubule luminal membrane         |
| P56402    | Aquaporin-2  | Aqp2     | 13           | 3               | Collecting duct luminal membrane       |
Table 5
List of mass spectrometrically identified mouse kidney marker proteins with characteristic physiological functions in ion homeostasis.

| Accession | Protein name                                      | Gene   | Coverage (%) | Peptides | Unique Peptides | Molecular mass [kDa] |
|-----------|--------------------------------------------------|--------|--------------|----------|-----------------|---------------------|
| P70414    | Sodium/calcium exchanger 1                       | Slc8a1 | 6            | 5        | 5               | 108                 |
| Q8K596    | Sodium/calcium exchanger 2                       | Slc8a2 | 4            | 2        | 1               | 100.6               |
| Q8C3K6    | Sodium/glucose cotransporter 1                   | Slc5a1 | 22           | 13       | 13              | 73.4                |
| Q92317    | Sodium/glucose cotransporter 2                   | Slc5a2 | 16           | 10       | 9               | 73                  |
| Q8VDT1    | Sodium/glucose cotransporter 4                   | Slc5a9 | 18           | 8        | 7               | 75                  |
| Q5SVWY8   | Sodium/glucose cotransporter 5                   | Slc5a10| 20           | 8        | 8               | 64.7                |
| G5E829    | Plasma membrane calcium-transporting ATPase 1    | Atp2b1 | 30           | 27       | 17              | 134.7               |
| Q6Q477    | Plasma membrane calcium-transporting ATPase 4    | Atp2b4 | 25           | 22       | 12              | 133                 |
| Q8VDN2    | Sodium/potassium-transporting ATPase subunit alpha-1 | Atp1a1 | 50           | 47       | 31              | 112.9               |
| Q6PIE5    | Sodium/potassium-transporting ATPase subunit alpha-2 | Atp1a2 | 21           | 17       | 1               | 112.1               |
| Q6PIC6    | Sodium/potassium-transporting ATPase subunit alpha-3 | Atp1a3 | 24           | 17       | 2               | 111.6               |
| P14094    | Sodium/potassium-transporting ATPase subunit beta-1 | Atp1b1 | 52           | 15       | 15              | 35.2                |
| P97370    | Sodium/potassium-transporting ATPase subunit beta-3 | Atp1b3 | 19           | 4        | 4               | 31.8                |
| O55143    | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | Atp2a2 | 46           | 43       | 36              | 104.4               |
| Q64518    | Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 | Atp2a3 | 16           | 14       | 7               | 103.8               |
| Q80XR2    | Calcium-transporting ATPase type 2C member 1     | Atp2c1 | 10           | 6        | 6               | 91.8                |
| Q96138    | Calcium-binding protein 39                       | Cab39  | 40           | 14       | 10              | 34.1                |
| Q64374    | Regucalcin                                       | Rgn    | 23           | 8        | 8               | 29.9                |
| P0DP27    | Calmodulin-2                                     | Calm2  | 72           | 10       | 10              | 14.9                |
| Q9DB16    | Calcium-binding protein 39-like                  | Cab39l | 28           | 10       | 6               | 33.7                |
| P12658    | Calbindin                                       | Calb1  | 67           | 20       | 20              | 30                  |
| P97816    | Protein S100-G                                   | S100g  | 71           | 8        | 8               | 9                   |
| P14211    | Calreticulin                                     | Calr   | 68           | 19       | 19              | 48                  |
| O08532    | Voltage-dependent calcium channel subunit alpha-2/delta-1 | Caca2d1 | 17           | 14       | 14              | 110.3               |
| Q02789    | Voltage-dependent L-type calcium channel subunit alpha-1S | Caca1s | 1           | 1        | 1               | 188.0               |
| Q921L3    | Calcium load-activated calcium channel           | Tmco1  | 12           | 2        | 2               | 21.2                |
| Q60932    | Voltage-dependent anion-selective channel protein 1 | Vdac1  | 73           | 18       | 17              | 32.3                |
| Q60930    | Voltage-dependent anion-selective channel protein 2 | Vdac2  | 57           | 11       | 11              | 31.7                |
| Q60931    | Voltage-dependent anion-selective channel protein 3 | Vdac3  | 52           | 10       | 9               | 30.7                |
| Q9EPK8    | Transient receptor potential cation channel subfamily V member 4 | Trpv4 | 15           | 9        | 9               | 98                  |
| O88335    | ATP-sensitive inward rectifier potassium channel 1 | Kcnj1  | 10           | 3        | 3               | 42.7                |
| O88932    | ATP-sensitive inward rectifier potassium channel 15 | Kcnj15 | 6           | 3        | 3               | 42.6                |
| Q9Z307    | Inward rectifier potassium channel 16            | Kcnj16 | 9            | 4        | 4               | 48                  |
| Q9WUB7    | Chloride channel protein CIC-Ka                  | Clcnka | 11           | 6        | 6               | 68.7                |
| Q9WUB6    | Chloride channel protein CIC-Kb                  | Clcnkb | 13           | 6        | 6               | 68.7                |
| Q99L12    | Chloride channel CLIC-like protein 1             | Clcl1  | 12           | 4        | 4               | 53.9                |
| Q9Z1Q5    | Chloride intracellular channel protein 1         | Clic1  | 74           | 14       | 14              | 27                  |
| Q9QYB1    | Chloride intracellular channel protein 4         | Clic4  | 71           | 15       | 15              | 28.7                |
| Q8BXX9    | Chloride intracellular channel protein 5         | Clic5  | 57           | 11       | 9               | 28.3                |
the comparative survey of fatty acid binding proteins in the kidney from wild type versus the dystrophic mdx-4cv mouse model of dystrophinopathy [1]. Table 6 lists the fatty acid binding proteins that were identified by mass spectrometry. This includes fatty acid-binding protein isoforms FABP1, FABP3, FABP4, FABP5 and FABP7 [7]. Kidney dystrophin and its associated proteins were identified in renal extracts, including dystrophin (Dp140), dystroglycan, alpha-1-syntrophin, beta-2-syntrophin, epsilon-sarcoglycan, alpha-dystrobrevin and beta-dystrobrevin [8], as listed in Table 7.

2. Experimental design, materials, and methods

2.1. Biological samples and materials

The systematic cataloguing of the assessable kidney proteome was carried out with 12-month old wild type C57/BL6 mice and age-matched dystrophic mdx-4cv mice [9]. Animals were obtained from the Bioresource Unit of the University of Bonn [10] and kept under standard conditions and all procedures adhered to German legislation on the use of animals in experimental research.

For kidney protein extraction, protein digestion and the mass spectrometric analysis of the renal proteome, general materials and analytical grade reagents were purchased from Bio-Rad Laboratories (Hemel-Hempstead, Hertfordshire, UK), GE Healthcare (Little Chalfont, Buckinghamshire, UK) and Sigma Chemical Company (Dorset, UK). For the filter-aided sample preparation procedure, filter units Vivacon 500 (product number: VN0H22) were purchased from Sartorius (Göttingen, Germany). Protein digestion was carried out with sequencing grade modified trypsin from Promega (Madison, WI, USA). Pierce C18 spin columns and Acclaim PepMap 100 columns were from Thermo Fisher Scientific (Dublin, Ireland).

2.2. Kidney protein extraction and mass spectrometric analysis

Crude protein extracts were prepared as described in detail in the accompanying research paper [1]. The filter-aided sample preparation method was used as described by Wiśniewski et al. [11]. For the mass spectrometric establishment of the assessable mouse kidney proteome, peptide characterization was carried out by reverse-phased capillary high pressure liquid chromatography using an UltiMate...
3000 nano system from Thermo Scientific [12]. The liquid chromatographic separation of peptides was coupled directly in-line with a Orbitrap Fusion Tribrid Mass Spectrometer from Thermo Scientific. Data analysis was carried out as previously described in detail [13].

Acknowledgments

Research was supported by Medical Research Charities Group grant HRB/MRCG-2016-20 from the Health Research Board and Muscular Dystrophy Ireland, as well as funding from the Kathleen Lonsdale Institute for Human Health Research at Maynooth University. The Orbitrap Fusion Tribrid mass spectrometer was funded under a Science Foundation Ireland Infrastructure Award to Dublin City University (SFI 16/RI/3701).

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] P. Dowling, M. Zweyer, M. Raucamp, M. Henry, P. Meleady, D. Swandulla, K. Ohlendieck, Proteomic and cell biological profiling of the renal phenotype of the mdx−4cv mouse model of Duchenne muscular dystrophy, Eur. J. Cell Biol. (2019) 151059, https://doi.org/10.1016/j.ejcb.2019.151059, 2019 Nov 18.
[2] M. Habuka, L. Fagerberg, B.M. Hallström, C. Kampf, K. Edlund, Å. Sivertsson, T. Yamamoto, F. Pontén, M. Uhlén, J. Odeberg, The kidney transcriptome and proteome defined by transcriptomics and antibody-based profiling, PLoS One 9 (2014), e16125.
[3] J.Z. Clark, L. Chen, C.L. Chou, H.J. Jung, J.W. Lee, M.A. Knepper, Representation and relative abundance of cell-type selective markers in whole-kidney RNA-Seq data, Kidney Int. 95 (2019) 787–796.
[4] R.A. Fenton, Proteomic approaches in kidney disease biomarker discovery, Am. J. Physiol. Renal. Physiol. 315 (2018) F1817–F1821.
[5] J.M. Arthur, N. Karakala, R.D. Edmondson, Proteomic analysis for identification of biomarkers that predict severe acute kidney injury, Nephron 140 (2018) 129–133.
[6] M. Canadas-Garre, K. Anderson, J. McGoldrick, A.P. Maxwell, A.J. McKnight, Proteomic and metabolomic approaches in the search for biomarkers in chronic kidney disease, J Proteomics 193 (2019) 93–122.
[7] G.S. Hotamisligil, D.A. Bernlohr, Metabolic functions of FABPs-mechanisms and therapeutic implications, Nat. Rev. Endocrinol. 11 (2015) 592–605.
[8] S. Murphy, K. Ohlendieck, The biochemical and mass spectrometric profiling of the dystrophin complexome from skeletal muscle, Comput. Struct. Biotechnol. J. 14 (2015) 20–27.
[9] T.A. Partridge, The mdx mouse model as a surrogate for Duchenne muscular dystrophy, FEBS J. 280 (2013) 4177–4186.
[10] S. Murphy, M. Zweyer, M. Henry, P. Meleady, R.R. Mundegar, D. Swandulla, K. Ohlendieck, Proteomic profiling of liver tissue from the mdx−4cv mouse model of Duchenne muscular dystrophy, Clin. Proteomics 15 (2018) 34.
[11] J.R. Wiśniewski, A. Zougman, M. Mann, Combination of FASP and StageTip-based fractionation allows in-depth analysis of the hippocampal membrane proteome, J. Proteome Res. 8 (2009) 5674–5678.
[12] S. Murphy, M. Zweyer, M. Henry, P. Meleady, R.R. Mundegar, D. Swandulla, K. Ohlendieck, Proteomic analysis of the sarcolemma-enriched fraction from dystrophic mdx−4cv skeletal muscle, J Proteomics 191 (2019) 212–227.
[13] S. Murphy, M. Zweyer, M. Raucamp, M. Henry, P. Meleady, D. Swandulla, K. Ohlendieck, Proteomic profiling of the mouse diaphragm and refined mass spectrometric analysis of the dystrophic phenotype, J. Muscle Res. Cell Motil. 40 (2019) 9–28.