Prof. Dr. rer. nat. Katrin Marcus

geboren: 21.11.1972
Geburtsort: Remscheid, Deutschland

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DAS HOCHSCHULSTUDIUM

1999-2002	**Promotion** an der Fakultät für Chemie & Biochemie „Analyse des Phosphoproteoms humaner Thrombin-stimulierter Thrombozyten“, Proteinstrukturlabor, Prof. Dr. H.E. Meyer, Medizinischhes Proteom-Center, Ruhr-Universität Bochum, Note: sehr gut
1998 – 1999	**Diplomarbeit** in Biochemie an der Fakultät für Chemie & Biochemie „Massenspektrometrische Identifizierung thrombozytärer Proteine nach Isolierung durch 2D-Gelelektrophorese und Immunpräzipitation von Phosphotyrosinproteinen“ bei Herrn Prof. Dr. H.E. Meyer, Proteinstrukturlabor, Ruhr-Universität Bochum, Note: sehr gut
1994-1999	**Studium der Biochemie** an der Ruhr-Universität Bochum Abschluss: Diplom-Biochemikerin, Note: gut
1992-1994	**Berufsausbildung** bei der Rheinischen Akademie e.V., Köln als Zertifizierte Biologisch-Technische Assistentin

BERUFLICHER WERDEGANG

seit 10/2017	**Direktorin** von „km/h Katrin Marcus Hochschulcoaching“
seit 06/2017	Zertifizierte **Business-Coach**, „Akademie der Ruhr-Universität Bochum“
seit 03/2014	**Direktorin** des Medizinisches Proteom-Centers, Ruhr-Universität Bochum
seit Juni 2008	**Projektleiterin** verschiedener DFG, BMBF und EU geförderter Projekte (Einzelprojekte und Netzwerkprojekte)
Nov 2007	Ernennung zur **W2-Professorin für Funktionelle Proteomik**, Medizinische Fakultät, Ruhr-Universität Bochum
Juni 2007	**Ruf auf eine Professur/”Tenured academic staff”**, Universität Antwerpen, Chemistry Department, Faculty of Science
Mai 2007	**Ruf auf eine W2-Professur**, Universität Regenburg, Medizinische Fakultät
2003 – 2007	**Juniorprofessorin** für Proteomics, Medizinische Fakultät, Ruhr-Universität Bochum
2002 – 2007	**Gruppenleiterin** der "Brain Proteomics" -Gruppe am Medizinischen Proteom-Zentrum der Ruhr-Universität Bochum
seit Aug 2002	**Projektleiterin** verschiedener abgeschlossener Projekte gefördert durch die DFG, das BMBF, die EU, die Alzheimer Forschung Initiative e.V., FoRUM Personalverantwortung für Post-Doktoranden, Doktoranden, Diplom-/Masterstudenten und technische Assistentinnen

LEHRE

seit 2003	Betreuung von mehr als 30 Doktoranden und Absolventen
seit 2001	Organisation und Durchführung mehrerer Vorlesungen / Seminare / Praktika an der Medizinischen Fakultät, Fakultät für Biologie und Fakultät für Chemie der Ruhr-Universität Bochum

Lehraufträge

2005 - 2007	Lehre an der Fachhochschule Bonn-Rhein-Sieg, Praktikum und Seminar "Instrumental Analytics

FORSCHUNGSINTERESSEN

Funktionellle Proteomik, Proteinchemie, Massenspektrometrie, post-translationale Modifikationen von Proteinen, Methodenentwicklung, neurodegenerative Erkrankungen, neuromuskuläre Erkrankungen

AWARDS/GRANTS/HONORS:

2004	HUPO Young Investigator Award
2009	Lore Agnes Award

MITGLIEDSCHAFTEN

Mitgliedschaften

- DGMS (Deutsche Gesellschaft für Massenspektrometrie)
- DGPF (German Society for Proteome Research)
- EuPA (European Proteomics Association)
- GBM (Society for Biochemistry and Molecular Biology)
- FEBS (Federation of European Biochemical Societies)
- DPG (German Parkinson Association)
- DHV (German Academy Association)
- Research Department Protein (Ruhr-University Bochum)
- International Graduate School of Neurosciences (Ruhr-University Bochum)
- International Graduate School of Biosciences (Ruhr-University Bochum)

WEITERE AUFGABEN UND AKTIVITÄTEN

Funktionelle Aufgaben

- Stellv. Vorsitzende des Ausschusses für Wissenschaftliche Geräte und Informationstechnik der DFG (seit 2019)
- Vorsitzende der Gleichstellungskommission der RUB (seit 2018)
- Stellv. Vorsitzende des HUPO Human Brain Proteome Projects (2018)
- Vorsitzende des HUPO Human Brain Proteome Projects (2017)
- Vorstandsmitglied des HUPO Human Brain Proteome Projects (seit 2015)
- Mitglied des Fakultätsrats (seit 2017)
- Mitglied des Apparateausschusses der DFG (seit 2017)
- Stellvertretendes Mitglied im Fakultätsrat (seit 2015)
- Redaktionsmitglied “Journal of Proteomics” (seit 2011) und „Frontiers in Molecular Neuroscience“ (seit 2017)
- Generalsekretärin, des HUPO Brain Proteome Projects (seit 2009)
- Mentorin im Programm „m2[at]RUB“ – Mentoring für weibliche Wissenschaftlerinnen an der Medizinischen Fakultät, Ruhr-Universität Bochum (seit 2008)
- Mentorin im Programm „Tandem plus MED“ - Mentoring für weibliche Wissenschaftlerinnen an der Medizinischen Fakultät, RWTH Aachen (2009-2010)
- Gleichstellungsbeauftragte der Medizinischen Fakultät (2006 - 2019)
- Leiterin des DGPF-Arbeitskreises „Membranproteine“ (2008-2012)
- Stellvertretende Vorsitzende des „Technology Platforms & Standardization Committee“ im HUPO Human Brain Proteome Project (2005-2009)

Organisatorisches

- Verantwortliche Planung und Durchführung des Programms „m2[at]RUB“ – Mentoring für weibliche Wissenschaftlerinnen an der Medizinischen Fakultät, Ruhr-Universität Bochum (seit 2008)
- Durchführung und Organisation der Europäischen Summer School Serien „Proteomic Basics“ & „Advanced Proteomics“, gefördert durch die Volkswagenstiftung und FEBS (2007-2019), in Brixen, Südtirol, Italien)
- Durchführung und Organisation von drei Sommerschulen „Proteomic Basics“, gefördert durch das BMBF und die DGPF, 2004 in Opatija, Croatia; 2005 und 2006 in Brixen, Südtirol, Italien Co-Organisation einer PENS Summer School “Neuroproteomics in animal models for neurodegenerative disorders” (Juni 2010 in Smolenice, Slovakei)
- Co-Organisation des Workshops "Computational Proteomics", Schloß Dagstuhl, 2.3.-7.3.2008
- Co-Organisation von drei “DIGE”-Workshops (2006, 2007, 2010, Bochum)

Edition und Begutachtung

- Eingeladene Editorin des Buches „Quantitative Methods in Proteomics“, 2. Auflage, Methods in Molecular Biology, Humana Press, 2019
- Gutachterin im BMBF-Programm „KMUinnovativ“ (2011 - 2017)
- Eingeladene Editorin des Sonderbandes „Neuroproteomics“, Expert reviews of Proteomics, Future Drugs, London, 2007
- Eingeladene Editorin des Buches „Quantitative Methods in Proteomics“, Methods in Molecular Biology, Humana Press, 2012
- Eingeladene Editorin des Sonderbandes Proteomics/Genomics, Journal of Neural Transmission, Springer-Verlag, Wien, 2005
- Eingeladene Editorin des Buches „Proteomics in Drug Research“, Methods and Principles in Medicinal Chemistry, Wiley-VCH, 2004
- Gutachterin verschiedener Journale (Proteomics, J Prot Res, JNT, BBA, FEBS, J Proteomics, J Chr A etc.)

Publikationen

Insgesamt 196 PubMed-gelistete Publikationen, H-Index: 35

Peer-reviewed Manuskripte

Originalartikel

1. Homozygous expression of the myofibrillar myopathy-associated p.W2710X filamin C variant reveals major pathomechanisms of sarcomeric lesion formation, Schuld J, Orfanos Z, Chevessier F, Eggers B, Heil L, Uszkoreit J, Unger A, Kirfel G, van der Ven P, **Marcus K**, Linke WA, Clemen CS, Schröder R, Fürst DO, eingereicht bei Acta Neuropathol Commun.
2. Comparative proteomic analysis of osteogenic differentiated human adipose tissue and bone marrow-derived stromal cells, Dadras M, May C, Wagner J, Wallner C, Becerikli M, Dittfeld S, Serschnitzki B, Schilde L, Guntermann A, Köller M, Sengstock C, Köller, M, Seybold C, Geßmann J, Schildhauer TA, Lehnhardt M, **Marcus K**, Behr B, eingereicht bei J Cell Mol Med.
3. Human cerebrospinal fluid data for use as spectral library for biomarker research, Schilde L, Steinbach S, Serschnitzki B, Bähr M, Lingor P, **Marcus K**, May C, eingereicht bei Data in Brief
4. Find More from Less – Improved Protein Detection in Minimum Quantities of Human Postmortem Brain Tissue, Kösters S, Rettel M, Eggers B, Riederer P, Gerlach M, Savitski M, **Marcus K*** & May C*, eingereicht bei Proteomes
5. Multiomic elucidation of a coding 99-mer repeat-expansion skeletal muscle disease, Ruggieri A, Naumenko S, Smith MA, Iannibelli E, Blasevich F, Bragato C, Gibertini S, Barton K, Vorgerd M, **Marcus K**, Wang P, Maggi L, Mantegazza R, Dowling JJ, Kley RA, Mora M, Minassian BA, Acta Neuropathol., im Druck
6. microRNA-129 and microRNA-130 regulate VEGFR-2 expression in sensory and motor neurons during development, Glaesel K, May C, **Marcus K**, Matschke V, Theiss C, Theis V, Int J Mol Sci, im Druck
7. A patient-based model of RNA mis-splicing uncovers treatment targets in Parkinson's disease, Boussaad I, Obermaier CD, Hanss Z, Bobbili DR, Bolognin S, Glaab E, Wołyńska K, Weisschuh N, De Conti L, May C, Giesert F, Grossmann D, Lambert A, Kirchen S, Biryukov M, Burbulla LF, Massart F, Bohler J, Cruciani G, Schmid B, Kurz-Drexler A, Parkinson Disease Genetic Sequencing Consortium (PDGSC), May P, Duga S, Klein C, Schwamborn JC, **Marcus K**, Woitalla D, Vogt DM, Weisenhorn J, Wurst W, Baralle M, Krainc D, Gasser T, Wissinger B, Krüger R (2020), Science Transl Med, im Druck
8. Glucocorticoid receptor complexes form cooperatively with the Hsp90 co-chaperones PPH-5 and FKB 6, Kaziales A, Barkovits K, **Marcus K**, Richter K, eingereicht bei Sci Rep.
9. The process of somatic hypermutation increases polyreactivity for CNS antigens in primary CNS lymphoma, Montesinos-Rongen M, Terrao M, May C, **Marcus K**, Blümcke I, Hellmich M, Küppers R, Brunn A, Deckert M, Haematologica, im Druck
10. CalibraCurve: A Tool for Calibration of Targeted MS-Based Measurements, Kohl M, Stepath M, Bracht T, Megger DA, Sitek B, **Marcus K**, Eisenacher M (2020) Proteomics, e1900143
11. The Parkin-coregulated gene PACRG promotes TNF signaling by stabilizing the linear ubiquitin chain assembly complex, Meschede J, Šadić M, Furthmann N, Miedema T, Sehr DA, Nastase MV, Müller-Rischart AK, Bader V, Berlemann LA, Pilsl A, Schlierf A, Barkovits K, Kachholz B, Rittinger K, Ikeda F, **Marcus K**, Schaefer L, Tatzelt J, Winklhofer KF (2020) Science Signalling, 13(617), pii: eaav1256
12. Quantification of artificial blood contamination in CSF and its impact on the quantitative analysis of alpha-synuclein, Barkovits K, Kruse N, Uszkoreit J, Linden A, Tönges L, Pfeiffer K, Mollenhauer B, **Marcus K** (2020) 5;9(2). pii: E370
13. Chaperones in sporadic inclusion body myositis-Validation of proteomic data, Güttsches AK, Jacobsen F, Schreiner A, Mertens-Rill J, Tegenthoff M, **Marcus K**, Vorgerd M, Kley RA (2020) Muscle & Nerve, 61(1), 116-121

14. Reproducibility, specificity and accuracy of relative quantification using spectral library-based data-independent acquisition, Barkovits K, Pacharra S, Pfeiffer K, Steinbach S, Eisenacher M, **Marcus K*** & Uszkoreit J* (2020) Mol Cell Proteomics, 19(1),181-197
15. A spiked human proteomic dataset from human osteogenic differentiated BMSCs and ASCs for use as a spectral library, for modelling pathways as well as protein mapping, Dadras M, Marcus K Wagner JM, Wallner C, Becerikli M, Jaurich H, Dittfeld S, Lehnhardt M, Serschnitzki B, Guntermann A, Schilde L, Berh B, May C (2019) Data in Brief, 27:104748
16. CRN2 binds to TIMP4 and MMP14 and promotes perivascular invasion of glioblastoma cells, Solga R, Behrens J, Ziemann A, Riou A, Berwanger C, Becker L, Garrett L, Hrabe de Angelis M, Fischer L, Coras E, Barkovits K, **Marcus K**, Mahabir E, Eichinger L, Schröder R, Noegel AA, Clemen CS (2019) Eur J Cell Biol, 98(5-8), 151046
17. A metastable subproteome underlies inclusion formation in muscle proteinopathies, Ciryam P, Antalek M, Cid F, Tartaglia GG, Dobson CM, Guettsches AK, Eggers B, Vorgerd M, **Marcus K**, Kley RA, Morimoto RI, Vendruscolo M, Weihl CC (2019) Acta Neuropathol Commun. 7(1), 197
18. Let me infuse this for you - A way to solve the first YPIC challenge, Eggers B, Pacharra S, Eisenacher M, **Marcus K**, Uszkoreit J (2019) EuPA Open Proteom., 22-23, 19-21
19. Human tear fluid proteome dataset for usage as a spectral library and for protein modelling, Guntermann A, Steinbach S, Serschnitzki B, Grotegut P, Reinerh S, Joachim SC, Schargus M, **Marcus K**, May C (2019) Data in brief, 23, 103742
20. Spiked human substantia nigra proteome data set for use as a spectral library for protein modelling and protein mapping Steinbach S, Serschnitzki B, Gerlach M, **Marcus K**, May C (2019) Data in Brief, 23, 103711
21. The microRNA miR-375-3p and the Tumor Suppressor NDRG2 are Involved in Sporadic Amyotrophic Lateral Sclerosis, Rohm M, May C, **Marcus K**, Steinbach S, Theis V, Theiss C, Matschke V (2019) Cell Physiol Biochem., 52(6), 1412-1426
22. Effects of 12 Weeks of Hypertrophy Resistance Exercise Training Combined with Collagen Peptide Supplementation on the Skeletal Muscle Proteome in Recreationally Active Men, Oertzen-Hagemann V, Kirmse M, Egger s B, Pfeiffer K, **Marcus** K, de Marées M, Platen P (2019) Nutrients, 11(5). pii: E1072
23. Noninvasive diagnosis of urothelial cancer in urine using DNA hypermethylation signatures-Gender matters, Köhler CU, Bonberg N, Ahrens M, Behrens T, Hovanec J, Eisenacher M, Noldus J, Deix T, Braun K, Gohlke H, Walter M, Tannapfel A, Tam Y, Sommerer F, **Marcus K**, Jöckel KH, Erbel R, Cantor CR, Käfferlein HU, Brüning T (2019) Int J Cancer, 145(10), 2861-2872
24. Imbalances in protein homeostasis caused by mutant desmin, Winter L, Unger A, Berwanger C, Spörrer M, Wellhausen M, Türk M, Chevessier F, Strucksberg KH, Schlötzer-Schrehardt U, Wittig I, Goldmann WH, **Marcus K**, Linke WA, Clemen CS*, Schröder R* (2019) Neuropathology and Applied Neurobiology, 45:476-494
25. Protein inference using PIA workflows and PSI standard file formats, Uszkoreit J, Perez-Riverol Y, Eggers B, **Marcus K**, Eisenacher M (2019) J Proteome Res., 8(2):741-747
26. IgA autoantibodies against native myelin basic protein in a patient with MS. Schumacher H, Wenke NK, Kreye J, Höltje M, **Marcus K**, May C, Prüss H (2019) Neurol Neuroimmunol Neuroinflamm., 6(4):e569
27. Quantifying changes in the bacterial thiol redox proteome during host-pathogen interaction, Xie K, Bunse C, **Marcus K**, Leichert L (2019) Redox Biology, 21:101087
28. Integrated Fourier Transform Infrared Imaging and Proteomics for Identification of a Candidate Histochemical Biomarker in Bladder Cancer, Witzke KE, Großerueschkamp F, Jütte H, Horn M, Roghmann F, von Landenberg N, Bracht T, Kallenbach-Thieltges A, Käfferlein H, Brüning T, Schork K, Eisenacher M, **Marcus K**, Noldus J, Tannapfel A, Sitek B &Gerwert K (2019) Am J Pathol., 189(3):619-631

29. Intricate crosstalk between lipopolysaccharide, phospholipid and fatty acid metabolism in Escherichia coli modulates proteolysis of LpxC, Thomanek N*, Arends J, Lindemann C, Barkovits K, Meyer H.E., **Marcus K*** & Narberhaus F* (2019) Front Microbiol., 9:3285
30. Landscape of pain in Parkinson's disease: impact of gender differences, Zella MA, May C, Müller T, Ahrens M, Tönges L, Gold R, **Marcus K**, Woitalla D (2019) Neurol Res., 41(1):87-97
31. Protein variability in cerebrospinal fluid and its possible implications for neurological protein biomarker research, Schilde LM*, Kösters S*, Steinbach S*, Schork K, Eisenacher M, Galozzi S, Turewicz M, Barkovits K, Mollenhauer B, **Marcus K*** & May C* (2018) PlosOne, 13(11):e0206478
32. Characterization of cerebrospinal fluid via data-independent acquisition mass spectrometry, Barkovits K, Linden A, Galozzi S, Schilde L, Pacharra S, Mollenhauer B, Stoepel N, Steinbach S, May C, Uszkoreit J, Eisenacher M, **Marcus K** (2018) J Proteome Res., 17(19):3418-3430
33. A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects, Mayer G, Quast C, Felden J, Lange M, Prinz M, Pühler A, Lawerenz C, Scholz U, Glöckner FO, Müller W, **Marcus K**, Eisenacher M (2017) Brief Bioinform., 20(4):1215-1221
34. Molecularly imprinted polymers synthesized via template immobilization on fumed silica nanoparticles for the enrichment of phosphopeptides, Duarte M, Subedi P, Yilmaz E, **Marcus K**, Laurell T, Ekström S (2018) J Molec Recognit., 31(3)
35. Label-free identification of myopathological features with coherent anti-Stokes Raman scattering, Niedieker D, Grosserüschkamp F, Schreiner A, Barkovits K, Kötting C, **Marcus K**, Gerwert K, Vorgerd M (2018) Muscle Nerve, 58(3):456-459
36. Editorial: Breakthroughs in top-down proteomics, Penque D, **Marcus K**, Torres VM (2018) J Proteomics, 175:1-2
37. Autophagy inhibition promotes alpha-synuclein release and transfer via extracellular vesicles with a hybrid autophago/exosome-like phenotype, Minakaki G, Menges S, Kittel A, Emmanouilidou E, Schaeffner I, Barkovits K, Bergmann A, Rockenstein E, Adame A, Marxreiter F, Mollenhauer B, Galasko D, Irén Buzá E, Schlötzer-Schrehardt U, **Marcus K**, Xiang W, Chichung Lie D, Vekrellis K, Masliah E, Winkler J Klucken J (2018) Autophagy 14(1):98-119
38. One gene, two proteins: Coordinated production of a copper chaperone by differential transcript formation and translational frameshifting in Escherichia coli, Drees SL, Klinkert B, Helling S, Beyer DF, **Marcus K**, Narberhaus F, Lübben M (2017) Mol Microbiol., 106(4):635-645
39. Distinct metabolomic signature in cerebrospinal fluid in early parkinson's disease, Trezzi JP, Galozzi S, Jaeger C, Barkovits K, Brockmann K, Maetzler W, Berg D, **Marcus K**, Betsou F, Hiller K, Mollenhauer B (2017), Mov Disord., 32(10):1401-1408
40. Protective effects on the retina after ranibizumab treatment in an ischemia model, Joachim SC, Renner M, Reinhard J, Theiss C, May C, Lohmann S, Reinehr S, Stute G, Faissner A, **Marcus K**, Dick HB (2017) PLoS One, 12(8):e0182407
41. Hsp90-downregulation influences the heat-shock response, innate immune response and onset of oocyte development in nematodes, Eckl J, Sima S, **Marcus K**, Lindemann C, Richter K (2017) PLoS One, 12(10):e0186386
42. BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication, Turewicz M, Kohl M, Ahrens M, Mayer G, Uszkoreit J, Naboulsi W, Bracht T, Megger DA, Sitek B, **Marcus K**, Eisenacher M (2017) J Biotechnol., pii: S0168-1656(17)
43. Spatial and molecular resolution of diffuse malignant mesothelioma heterogeneity by integrating label-free FTIR imaging, laser capture microdissection and proteomics, Großerueschkamp F, Bracht T, Diehl HC, Kuepper C, Ahrens M, Kallenbach-Thieltges A, Mosig A, Eisenacher M, **Marcus K**, Behrens T, Brüning T, Theegarten D, Sitek B, Gerwert K (2017) Sci Rep., 7:44829
44. Metabolic profiling of body fluids and multivariate data analysis, Trezzi JP, Jäger C, Galozzi S, Barkovits K, **Marcus K**, Mollenhauer B, Hiller K, MethodsX (2017) 4:95-103

45. Morphological Plasticity of Emerging Purkinje Cells in Response to Exogenous VEGF, Herrfurth L, Theis V, Matschke V, May C, Marcus K, Theiss C (2017), Front Mol Neurosci., 10:2
46. Proteomics of rimmed vacuoles define new risk allele in inclusion body myositis., Güttsches AK, Brady S, Krause K, Maerkens A, Uszkoret J, Eisenacher M, Schreiner A, Galozzi S, Mertens-Rill J, Tegenthoff M, Holton JL, Harms MB, Lloyd, TE, Vorgerd M, Weihl CC*, Kley R*, **Marcus K*** (2017) Annals Neurol, 81(2):227-239
47. Proteomic characterization of neuromelanin granules isolated from human substantia nigra by laser-microdissection, Plum S, Steinbach S, Attems J, Keers S, Riederer P, Gerlach M, May C, **Marcus K** (2016) Sci Rep., 6:37139
48. In vivo trapping of FtsH substrates by label-free quantitative proteomics, Arends J, Thomanek N, Kuhlmann K, **Marcus K**, Narberhaus F (2016) Proteomics, 16(24):3161-3172
49. Validation of molecularly imprinted polymers for side chain selective phosphopeptide enrichment, Chen J, Shinde S, Subedi P, Wierzbicka C, Sellergren B*, Helling S*, **Marcus K*** (2016) J Chromatogr A, pii: S0021-9673(16)31350-4
50. Statically Adsorbed Coatings for High Separation Efficiency and Resolution in CE-MS Peptide Analysis: Strategies and Implementation, Pattky M, Barkovits K, **Marcus K**, Weiergräber OH, Huhn C (2016) Methods Mol Biol., 1483:53-75
51. Membrane tethering of APP c-terminal fragments is a prerequisite for T668 phosphorylation preventing nuclear sphere generation, Bukhari H, Kolbe K, Leonhardt G, Loosse C, Schröder E, Knauer S, **Marcus K**, Müller T (2016), Cellular Signalling, 28(11):1725-1734
52. Rab7 induces clearance of α-synuclein aggregates, Dinter E, Saridaki T, Nippold M, Plum S, Diederichs L, Komnig D, Fensky L, May C, **Marcus K**, Voigt, A, Schulz J.B, Falkenburger BH (2016), Journal of Neurochemistry, 138(5):758-774
53. Mutant desmin substantially perturbs mitochondrial morphology, function and maintenance in skeletal muscle tissue, Winter L, Wittig I, Peeva, V, Eggers B, Heidler J, Chessevier F, Kley RA, Barkovits K, Strecker V, Berwanger C, Herrmann H, **Marcus K**, Kornblum C, Kunz WS, Schröder R, Clemen CS (2016) Acta Neuropathol, 132(3):453-473
54. New insights into the protein aggregation pathology in myotilinopathy by combined proteomic and immunolocalization analyses, Maerkens A, Olivé M, Schreiner A, Feldkirchner S, Schessl J, Uszkoreit J, Barkovits K, Güttsches AK, Theis V, Eisenacher M, Tegenthoff M, Goldfarb LG, Schröder R, Schoser B, van der Ven PF, Fürst DO, Vorgerd M, **Marcus K*** & Kley RA* (2016) Acta Neuropathol Commun., 4(1):8
55. PAA: An R/Bioconductor package for biomarker discovery with protein microarrays, Turewicz M, Ahrens M, May C, **Marcus K**, Eisenacher M (2016) Bioinformatics, 32(10):1577-1579
56. Mitochondrial Defects and Neurodegeneration in Mice Overexpressing Wild Type or G399S Mutant HtrA2, Casadei N, Sood P, Ulrich T, Kieper N, Helling S, May C, Glaab E, Chen J, Nuber S, **Marcus K**, Rapaport D, Ott T, Riess O, Krueger R, Fitzgerald JC (2016) Hum Mol Genet., 25(3):459-471
57. Nuclear spheres modulate the expression of BEST1 and GADD45G, Loosse C, Pawlas M, Bukhari HS, Maghnouj A, Hahn S, **Marcus K**, Müller T (2016) Cell Signal.,100-109
58. Myofibrillar instability exacerbated by acute exercise in filaminopathy, Chevessier F, Schuld J, Orfanos Z, Plank AC, Wolf L, Maerkens A, Unger A, Schlötzer-Schrehardt U, Kley RA, von Hörsten S, **Marcus K**, Linke WA, Vorgerd M, van der Ven PF, Fürst DO, Schröder R (2015) Hum Mol Genet., 24(25):7207-7220
59. ProCon - PROteomics CONversion tool, Mayer G., Stephan C, Meyer H.E , Kohl M., **Marcus K**, Eisenacher M (2015) J Proteomics, 129:56-62
60. Primary Central Nervous System (CNS) Lymphoma B Cell Receptors Recognize CNS Proteins, Montesinos-Rongen M, Purschke FG, Brunn A, May C, Nordhoff E, **Marcus K**, Deckert M (2015) J Immunol., 195(3):1312-1319
61. PIA - An intuitive protein inference engine with a web-based user interface, Uszkoreit J, Maerkens A, Perez-Riverol Y, Meyer HE, **Marcus K**, Stephan C, Kohlbacher O, Eisenacher M (2015) J Proteome Res.,14(7):2988-2997

62. Enrichment of single neurons and defined brain regions from human brain tissue samples for subsequent proteome analysis, Molina M*, Steinbach S*, Park YM, Yun SY, Di Lorenzo Alho AT, Heinsen H, Grinberg LT, **Marcus K**, Paraizo Leite RE* & May C* (2015) Journal Neural Transm., 122(7):993-1000

63. Low-bias phosphopeptide enrichment from scarce samples using plastic antibodies, Chen J*, Shinde S*, Koch MH, Eisenacher M, Galozzi S, Lerari T, Barkovits K, Subedi P, Krüger R, Kuhlmann K, Sellergren B, Helling S, **Marcus K** (2015) Sci Rep., 5:1438

64. Indirect protein quantification of drug-transforming enzymes using peptide group-specific immunoaffinity enrichment and mass spectrometry, Weiß F*, Schnabel A*, Planatscher H, van den Berg BH, Serschnitzki B, Nuessler AK, Thasler WE, Weiss TS, Reuss M, Stoll D, Templin MF, Joos TO, **Marcus K*** & Poetz O* (2015) Sci Rep., 5:8759

65. Direct infusion-SIM for absolute protein quantification in complex samples: simple, fast, robust, Loosse C, Galozzi S, Debor L, Julsing MK, Bühler B, Schmid A, Barkovits K, Müller T***** & **Marcus K*** (2015) EuPA Open Proteomics

66. Improved preparation of nasal lavage fluid (NLF) as a noninvasive sample for proteomic biomarker discovery, Schoenebeck B & May C, Mollenhauer B, Meyer HE, Güldner C, Respondek G, Höglinger G, **Marcus K** (2015) BBA – Proteins and Proteomics, 1854(7):741-745

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Television

„Project Future: Proteomics“, Deutsche Welle, April 11th 2004, Report about the young scientist Dr. Katrin Marcus, Juniorprofessor for Proteomics, in the framework of the Human Brain Proteome Project

Laufende Projekte und Finanzierungen

Seit 2004 mehrere Einzel- und Netzwerkstipendien von der EU, BMBF (Bundesministerium für Bildung und Forschung), DFG (Deutsche Forschungsgemeinschaft), AFI (Alzheimer-Forschungsinitiative), Volkswagen Stiftung

MalK Massenspektrometrie basierte Identifizierung von Körperflüssigkeiten für forensische Zwecke
Projektleiterin, zusammen Landeskriminalamt, Nordrhein-Westfalen & Bayern
EU – Internal Security Fund 2014-2020
Förderung (eigener Anteil) 206.791 €

OsteoSys: Osteoporose – eine Volkserkrankung im Kontext von kardiovaskulärer Komplikationen und chronischer Inflammation: systemmedizinischer Ansatz zur personalisierten Therapie
Projektleiterin
Ministerium für Innovation, Wissenschaft und Forschung, Leitmarktagentur, Northrhein Westfalen
Förderung (eigener Anteil) 260.379 €

SepsisDataNet.NRW - Digitalisierte Mustererkennung für die personalisierte Behandlung von Sepsis-Patienten
Co- Projektleiterin
Ministerium für Innovation, Wissenschaft und Forschung, Leitmarktagentur, Northrhein Westfalen
Förderung (eigener Anteil)

NISCI – Antibodies against Nogo---A to enhance regeneration and functional recovery after acute spinal cord injury a multicenter European clinical proof of concept trial
Projektleiterin
EU Horizon 2020
Förderung (eigener Anteil) 295.000 €

Role of Cavβ2 splice variants in the association of L-type voltage-gated calcium channels to specific calcium signaling pathways in different subcellular microdomains of cardiac myocytes
Co-Projektleiterin
DFG
Förderung (eigener Anteil) 82.100 €

ValiBio – Validierung Marker-freier Imaging-Verfahren und neu identifizierter Biomarker unter Nutzung des PURE Konsortiums
Projektleiterin
Ministerium für Innovation, Wissenschaft und Forschung, Northrhein Westfalen
Förderung (eigener Anteil) 1.135.000 €

Isolierung von spezifischen Neuronenpopulationen und Gliazellen aus humaner Substantia nigra
Projektleiterin
Ministerium für Bildung und Forschung
Förderung (eigener Anteil) 154.875 €

German Network for Bioinformatics Infrastructure, deNBI
Co- Projektleiterin
Ministerium für Bildung und Forschung
Förderung (eigener Anteil) 2.097.482 €

Subcellular proteome analysis of neuromelanin-granules and Lewy-bodies of healthy controls and Parkinson's-diseased subjects
Projektleiterin
Verein zur Durchführung Neurowissenschaftlicher Tagungen e.V.
Förderung 34.500 €