

BIOGRAPHICAL SKETCH

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NAME OVERALL, Christopher M.		POSITION TITLE Professor & Canada Research Chair in Protease Proteomics and Systems Biology	
eRA COMMONS USER NAME CHRISOVERALL	ORCID IDENTITY 0000-0001-5844-2731		
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY
The University of Adelaide, South Australia, Australia	BDS	1979	Dental Surgery
The University of Adelaide, South Australia, Australia	BSc (Hons)	1980	Immunology/Oral Biology
The University of Adelaide, South Australia, Australia	MDS	1985	Oral Biology
The University of Toronto, Ontario, Canada		1984-1985	Post-Professional Fellowship, J.L. Eustace Fellow
The University of Toronto, Ontario, Canada	PhD	1991	Biochemistry
The University of British Columbia, B.C., Canada <i>Department of Biochemistry & Molecular Biology; Protein Engineering Network of Centres of Excellence; Faculty of Medicine</i>		1989-1992	Postdoctoral M.R.C. Centennial Fellow

A.1. Positions and Employment

1983 Lecturer, Department of Periodontics, The University of Adelaide; **1992-1997** Assistant Professor, Department of Oral Biology, The University of British Columbia (UBC); **1992-1995** Clinician Scientist, Medical Research Council of Canada (MRC); **1995-present** Associate Member, Department of Biochemistry & Molecular Biology, UBC; **1995-1998** Clinician Scientist, MRC; **1997-2000** Associate Professor, Department of Oral Biological & Medical Sciences, UBC; **1997-1998** Visiting Scientist, British Biotech, Oxford UK; **1999-2000** Canadian Institutes of Health Research (CIHR) Scientist; **1999-present** Member, Canadian Arthritis Network, Centres of Excellence; **2000-present** Full Professor, Department of Oral Biological & Medical Sciences, UBC; **2001-2005** Member, Protein Engineering Network, Centres of Excellence; **2001-present** Member, CIHR Group in Matrix Dynamics; **2001-present** Canada Research Chair (Tier I) in Metalloproteinase Proteomics & Systems Biology; **2002-present** Associate Member, UBC Prostate Centre; **2002-present** Member, UBC Centre for Blood Research; **2003-present** Internal VP, Canadian Proteomics Network; **2004-2005** Visiting Scientist, Protease Platform, Novartis Pharmaceuticals AG, Basel, Switzerland; **2004-present** Chair, Foreign Scientific Advisory Board, Australian Protease Network; **2005-present** External Consultant, Expert Protease Platform, Novartis Pharmaceuticals; **2005-2008** Director, Centre for Blood Research Proteomics Hub, UBC; **2005-2007**, External Advisor, Huntington Disease Society Protease Group; **2006-present** Executive Member, B.C. Proteomics Network; **2008** Visiting Scientist, Centre for Proteomic Chemistry, Novartis, Basel, Switzerland; **2010-2012** External Senior Fellow, Freiburg Institute of Advanced Studies, Albert-Ludwigs University, Germany; **2011-present** Editorial Board, Molecular Cellular Proteomics; **2013** Consultant, Proteases in Apoptosis Division, Genentech; **2013-present** Editorial Board, Biological Chemistry; **2015-present** Associate Editor, Journal of Proteome Research; **2014-present** Honorary Professor, Albert-Ludwigs-Universität Freiburg, Germany; **2015** Chief Scientific Officer (CSO) interfeRx antivirals; **2016** Editor of *mSystems*.

A.2. Honors and Awards

1984-1989 Postdoctoral Fellowship, Medical Research Council of Canada (MRC); **1987** Edward H. Hatton Award, 1st Place Postdoctoral, International Association for Dental Research (IADR); **1987** 1st Place Postdoctoral Research Award, CADR; **1988** Young Investigator Award, 3rd International Conference on Chemistry & Biology Mineralized Tissues; **1989** William J. Gies Award for best publication in 1988, AADR; **1989** 1st Place Award, Canadian Dental Research Foundation; **1989** Young Investigator Award, Matrix Metalloproteinase (MMP) Conference; **1989-1992** Centennial Fellowship (1st place), MRC; **1991** Young Investigator Award for best scientist under 35 years old, IADR; **1999** Scientist Award, MRC; **2001** Tier 1 Canada Research Chair in Metalloproteinase Proteomics & Systems Biology; **2002** **Researcher of the Year**, Canadian Institutes of Health Research (CIHR); **2003** Award for Research Excellence in Oral Health, CIHR; **2003** Chairman, MMP Gordon Research Conference (GRC); **2004** Listed in the Contemporary Who's Who; **2005** Fellow, Canadian Academy of Health Sciences; **2005** International Proteolysis Society Council; **2006** Killam Research Award, Senior Science Category, UBC; **2010** Chairman, Protease GRC; **2011** **Lifetime Achievement Award**, International Proteolysis Society; **2012** Barry Preston Award (**Lifetime Achievement Award** in Matrix Biology), Matrix Biology Society of Australia & New Zealand; **2013** **Distinguished Scientist Award** in Oral Biology, IADR; **2014** Tony Pawson Award for outstanding contribution and leadership to the Canadian proteomics community, Canadian National Proteomics Network; **2017** **Proteomass Scientific Society Award**, for "outstanding contribution in pioneering the understanding of the processes that explain the architecture of living organisms"; **2017** **HUPO Discovery Award**, Human Proteome Organization.

B.1. Selected peer-reviewed publications

Career total 256 papers (H-index 83, >24,700 citations). Trainees are underlined.

1. Fortelny, N., **Overall, C.M.**, Pavlidis, P., and Cohen Freue, G.V. 2017. Can we Predict Protein from mRNA Levels? **Nature** **547**, E19-E22. doi: 10.1038/nature23293.
2. Eckhard, U., Bandukwala, H., Mansfield, M.J., Marino, G., Cheng, J., Wallace, I., Holyoak, T., Charles, T.C., Austin, J., **Overall, C.M.***, and Doxey, A.C.* 2017. Discovery of a Proteolytic Flagellin Family in Diverse Bacterial Phyla that Assembles Enzymatically Active Flagella. **Nature Communications** **8**, 1-9. doi: 10.1038/s41467-017-00599-0. * *Joint Shared Senior Authors.*
3. Dufour, A., Bellac, C.L, Eckhard, U., Solis, N., Klein, T., Kappelhoff, R., Fortelny, N., Jobin, P., Rozmus, J., Mark, J., Pavlidis, P., Dive, V., Barbour, S.J., and **Overall, C.M.** Post-translational Truncation of IFN- γ Dampens Proinflammatory Macrophage Responses and is Reduced in Autoimmune Disease. **Nature Communications**, *Conditional Acceptance*, NCOMMS-17-07856.
4. Kappelhoff, R., Puente, X.S., Wilson, C.H., Seth, A., Lopez-Otin, C., and **Overall, C.M.** 2017. Overview of Transcriptomic Analysis of all Human Proteases, Non-proteolytic Homologs and Inhibitors: Organ, Tissue and Ovarian Cancer Cell Line Expression Profiling of the Human Protease Degradome by the CLIP-CHIPTM DNA Microarray. **Biochimica et Biophysica Acta Molecular Cell Research**, <http://dx.doi.org/10.1016/j.bbamcr.2017.08.004>.
5. Omenn, G.S., Lane, L., Lundberg, E.K., **Overall, C.M.**, and Deutsch, E.W. 2017. Progress on the Draft Human Proteome: 2017 Metrics of the Human Proteome Project. **Journal of Proteome Research** **16**, *in press*, pr-2017-003756.
6. Schwenk, J.M., Omenn, G.S., Sun, Z., Baker, M.S., **Overall, C.M.**, Ruedi Aebersold, R., Moritz, R.L., and Deutsch, E.W. 2017. The Human Plasma Proteome Draft of 2017: Building on the Human Plasma Peptide Atlas and Alternative Assays. **Journal of Proteome Research** **16**, *in press*.
7. Panwar, P., Butler, G.S., Jamroz, A, Azizi, P, **Overall C.M.**, and Brömme, D. Aging-associated Modifications of Collagen Affect its Degradation by Matrix Metalloproteinases. **Matrix Biology** 2017 Jun 17; [Epub ahead of print] PMID: 28634008.
8. Jobin, P.G., Butler, G.S., **Overall, C.M.** 2017. New Intracellular Activities of Matrix Metalloproteinases Shine in the Moonlight. **Biochimica et Biophysica Acta - Molecular Cell Research**, *in press*.
9. Fortelny, N., Butler, G.S., **Overall, C.M.*** and Pavlidis, P.* 2017. Protease-inhibitor Interaction Predictions: Lessons on the Complexity of Protein-protein Interactions. **Molecular Cellular Proteomics** **16.6**, 1038-1051, **Joint Shared Senior Authors. Featured Editors Pick.*
10. Marshall, N.C., Finlay, B.B., and **Overall, C.M.** 2017. Sharpening Host Defenses During Infection: Proteases Cut to the Chase. **Molecular Cellular Proteomics** **16**, S161-S171.
11. Scott, N.E., Rogers, L.D., Prudova, A., Brown, N.F., Fortelny, N., **Overall, C.M.**, and Foster, L.J. 2017 Interactome Disassembly During Apoptosis Occurs Independent of Caspase Cleavage. **Molecular Systems Biology** **13**, 906, 1-22, doi: 10.15252/msb.20167067.
12. Butler, G.S., Connor, A.R., Sounni, N.-E., Tam, E.M., Morrison, C.J., Dean, R.A., Noël, A., **Overall, C.M.** 2017. Degradomic and Yeast 2-Hybrid Inactive Catalytic Domain Substrate Trapping Identifies New Membrane-type 1 Matrix metalloproteinase (MMP14) Substrates: CCN3 (NOV) and CCN5 (WISP2). **Matrix Biology** **59**, 23-38 Doi: 10.1016/j.matbio.2016.07.006.
13. Goth, C.K., Tuhkanen, H.E., Khan, H., Lackmann, J.J., Wang, S., Narimatsu, Y., Hansen, L.H., **Overall, C.M.**, Clausen, H., Schjoldager, K.T., Petäjä-Repo, U.E. 2017. Site-Specific O-Glycosylation by Polypeptide GalNAc-Transferase T2 Co-Regulates Beta1-adrenergic Receptor N-Terminal Cleavage. **Journal of Biological Chemistry** **392**, 4,714-4,726.
14. Tsiatsiani, L., Giansanti, P., Scheltema, R., van den Toorn, H., **Overall, C.M.**, Altelaar, A. F. M., and Heck, A. 2017. Opposite ETD/HCD Fragmentation Characteristics of Proteolytic K/R(X)_n and (X)_nK/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. **Journal of Proteome Research** **16**, 852-861.
15. Poreba, M., Szalek, A., Rut, W., Kasperkiewicz, P.K., Rutkowska, I., Snipas, S.S., Itoh, Y., Turk, D., Turk, B., **Overall, C.M.**, Kaczmarek, L., Salvesen, G.S., Marcin Drag, M. 2017. ACC-DNP as an Efficient Fluorophore-Quencher Pair for the Investigation of Proteolytic Enzyme. **Scientific Reports** **23** (7:43135). doi: 10.1038/srep43135.
16. Taggart, C., Mall, M., Lalmanach, G., Cataldo, D., Ludwig, A., Janciauskiene, S., Heath, N., Meiners, S., **Overall, C.M.**, Schultz, C., Turk, B., Borensztajn, K. 2017. Proteases at the Cutting Edge: Friends or Foes in Chronic Lung Diseases? **European Respiratory Journal** **49**, pii: 1501200. doi: 10.1183/13993003.01200-2015.
17. Abdul-Muneer, P.M., Conte, A.A., Haldar, D., Long, M., Patel, R.K., Santhakumar, V., **Overall, C.M.**, and Pfister, B.J. 2017. Traumatic Brain Injury Induced Matrix Metalloproteinase 2 Cleaves CXCL12 α (Stromal Cell Derived Factor 1 α) and Causes Neurodegeneration. **Brain, Behavior and Immunity** **59**, 190-199. doi: 10.1016/j.bbi.2016.09.002.
18. Solis, N., and **Overall, C.M.** 2017. Characterizing the Termini of Recombinant Proteins. *in Analytical Characterization of Biotherapeutics, 1st Edition*. Edited by Lil, J.R., and Sandoval, W. John Wiley and Sons Inc., 43-71
19. Solis, N., and **Overall, C.M.** 2017. Identification of Protease Cleavage Sites and Substrates in Cancer by Carboxy-TAILS. *in Proteases and Cancer: Methods and Protocols* (Methods in Molecular Biology). Edited by Obaya, A., and Cal, S. Springer-Nature. *In press*.
20. Prudova, A., Gocheva, V., Keller, U. a-d, Eckhard, U., Olson, O., Akkari, L., Butler, G.S., Fortelny, N., Lange, P.F., Mark,

- J., Joyce, J., and **Overall, C.M.** 2016. TAILS N-terminomics and Proteomics Show Protein Degradation Dominates Over Proteolytic Processing by Cathepsins in Pancreatic Tumors. **Cell Reports** **16**, 1762-1773, **Featured cover**.
21. Klein, T., Viner, R.I., and **Overall, C.M.** 2016. Quantitative Proteomics Techniques to Elucidate the Role of Ubiquitination and Proteolysis in Adaptive Immunity. **Philosophical Transactions A** **374**, 20150372: 1-16.
22. Paik, Y.K., **Overall, C.M.**, Deutsch, E.W., Hancock, W.S., and Omenn, G.S. 2016. Progress in the Chromosome-Centric Human Proteome Project as Highlighted in the Annual Special Issue IV. **Journal of Proteome Research** **15**, 3,945-3,950.
23. Omenn, G.S., Lane, L., Lundberg, E., Beavis, R.C., **Overall, C.M.**, and Deutsch, E.W. 2016. Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. **Journal of Proteome Research** **15**, 3,951-3,960.
24. Deutsch, E.W., **Overall, C.M.**, Van Eyk, J.E., Baker, M.S., Paik, Y-K., Weintraub, S.T., Lane, L., Martens, L., Vandembrouck, Y., Kusebauch, U., Hancock, W.S., Hermjakob, H., Aebersold, R., Moritz, R.L., and Omenn, G.S. 2016. Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. **Journal of Proteome Research** **15**, 3,961-3,970.
25. Anania, V.G., Yu, K., Gnad, F., Pferdehirt, R.R., Li, H., Ma, T., Jeon, D., Forrest, W., Ashkenazi, A., Fortelny, N., **Overall, C.M.**, and Jennie R. Lill, J.R. 2016. Uncovering a Dual Regulatory Role for Caspases During Endoplasmic Reticulum Stress-induced Cell Death. **Molecular Cellular Proteomics** **7**, 2,293-2,307.
26. Hamey, J.J., Winter, D.L., Yagoub, D., **Overall, C.M.**, Hart-Smith, G., Wilkins, M.R. 2016. Novel N-terminal and Lysine Methyltransferases that Target Translation Elongation Factor 1A in Yeast and Human. **Molecular Cellular Proteomics** **15**, 164-176.
27. Eckhard, U., Huesgen, P.F., Schilling, O., Bellac, C.L., Butler, G.S., Cox, J.H., Dufour, A., Goebeler, V., Kappelhoff, R., auf dem Keller, U., Klein, T., Lange, P.L., Marino, G., Morrison, C.J., Prudova, A., Rodriguez, D., Starr, A.E., Wang, Y., and **Overall, C.M.** 2016. Active Site Specificity Profiling Datasets of Matrix Metalloproteinases (MMPs) 1, 2, 3, 7, 8, 9, 12, 13 and 14. **Data in Brief** **7**, 299-310.
28. Eckhard, U., Marino, G., Butler, G.S., and **Overall, C.M.** 2016. Positional Proteomics in the Era of the Human Proteome Project on the Doorstep of Precision Medicine. **Biochimie** **122**, 110-118.
29. Eckhard, U., Huesgen, P.F., Schilling, O., Bellac, C.L., Butler, G.S., Cox, J.H., Dufour, A., Goebeler, V., Kappelhoff, R., auf dem Keller, U., Klein, T., Lange, P.F., Marino, G., Prudova, A., Rodriguez, D., Starr, A.E., Wang, Y., and **Overall, C.M.** 2016. Active Site Specificity of the Matrix Metalloproteinase Family: Proteomic Identification of 4,300 Cleavage Sites by Nine MMPs Explored with Structural and Synthetic Peptide Cleavage Analyses. **Matrix Biology** **49**, 37-60.
30. Delolme, F., Anastasi, C., Alcaraz, L.B., Mendoza, V., Vadon-Le Goff, S., Talantikite, M., Capomaccio, R., Mevaere, J., Fortin, L., Mazzocut, D., Damour, O., Zanella-Cléon, I., Hulmes, D.J., **Overall, C.M.**, Valcourt, U., Lopez-Casillas, F., and Moali, C. 2015. Proteolytic Control of TGF- β Co-receptor Activity by BMP-1/Tolloid-like Proteases Revealed by Quantitative iTRAQ Degradomics. **Cellular and Molecular Life Sciences** **72**, 1,009-1,027.
31. Klein, T., Fung, S.Y., Renner, F., Blank, M.A., Dufour, A., Kang, S., Bolger-Munro, M., Scurll, J.M., Priatel, J.J., Schweigler, P., Melkko, S., Gold, M.S., Viner, R.I., Régnier, S.H., Turvey, S.E., and **Overall, C.M.** 2015. The Paracaspase MALT1 Cleaves HOIL1 Reducing Linear Ubiquitination by LUBAC to Dampen Lymphocyte NF- κ B Signalling. **Nature Communications** **6**, 8777. 1-17. **Featured Article and Featured in Nature Immunology**
32. Huesgen, P.F., Lange, P.F., Rogers, L.D., Solis, N., Eckhard, U., Kleifeld, O., Gomis-Rüth, F.X., and **Overall, C.M.** 2015. LysargiNase Mirrors Trypsin for Protein C-Termini and Methylation Sites Identification. **Nature Methods** **12**, 55-58.
33. Eckhard, U., Marino, G., Abbey, S.R., Matthew, I., and **Overall, C.M.** 2015. TAILS N-terminomic and Proteomic Datasets of Healthy Human Dental Pulp. **Data in Brief** **5**, 542-548.
34. Fortelny, N., Yang, S., Pavlidis, P., Lange, P.F., and **Overall, C.M.** 2015. Proteome TopFIND 3.0 and TopFINDER: Database and Analysis Tools for the Association of Protein Termini to Pre- and Post-Translational Events. **Nucleic Acids Research** **43** (Database Issue), D290-D297.
35. Zelanis, A., Huesgen, P.F., Oliveira, A.K., Tashima, A.K., Serrano, S.M.T., **Overall, C.M.** 2015. Snake Venom Serine Proteinases Specificity Mapping by Proteomic Identification of Cleavage Sites. **Journal of Proteomics** **113**, 260-267.
36. Jagdeo, J., Dufour, A., Fung, F., Luo, H., Kleifeld, O., **Overall, C.M.** and Jan, E. 2015. Heterogeneous Nuclear Ribonucleoprotein M Facilitates Enterovirus Infection. **Journal of Virology** **89**, 14, 7064-7078.
37. Fortelny, N., Pavlidis, P., and **Overall, C.M.** 2015. The Path of No Return—Truncated Protein N-termini and Current Ignorance of Their Genesis. **Proteomics** **15**, 2,547-2,552.
38. Marino, G., Eckhard, U., and **Overall, C.M.** 2015. Protein Termini and their Modifications Revealed by Positional Proteomics. **ACS Chemical Biology** **10**, 1,754-1,764.
39. Eckhard, U., Marino, G., Abbey, S.R., Tharmarajah G., Matthew, I., and **Overall, C.M.** 2015. The Human Dental Pulp Proteome and N-terminome: Levering the Unexplored Potential of Semi-tryptic Peptides Enriched by TAILS to Identify Missing Proteins in the Human Proteome Project in Underexplored Tissues. **J. Proteome Research** **14**, 3,568-3,582.
40. Paik, Y-K., Omenn, G.S., **Overall, C.M.**, Deutsch, E.W., and William S. Hancock, W.S. 2015. Towards a Critical Turning Point of Phase I in the Chromosome-Centric Human Proteome Project: No More Missing the Target. **Journal of Proteome Research** **14**, 3,409-3,414.

41. Solis, N. and **Overall, C.M.** 2015. Mass Spectrometry-based Methodologies for Studying Proteolytic Networks and the Degradome. **Encyclopedia of Cell Biology**, Edited by Bradshaw, R. and Stahl, P. by Academic Presse, Elsevier Inc, Waltham, MA, USA, Vol.1, 568-581.
42. Marchant, D., Bellac, C., Wadsworth, S., Dufour, A., Butler, G.S., Cheung, C., Ng, J., Luo, Z., Garmaroudi, F.S., Heilbron, K., Karpov, A., Devel, L., Georgiadis, D., Hegele, R.G., Luo, H., Dive, V., McManus, B.M., Overall, C.M. 2014. Transcriptional Upregulation of I κ B α by a Moonlighting Extracellular Metalloprotease is Essential for Antiviral Immunity. **Nature Medicine**, **20**, 493-502. doi 10.1038/nm.3508. (Featured Article in News and Views).
43. Fahlman, R.P., Chen, W., and Overall, C.M. 2014. Absolute Proteomic Quantification of Proteases and Proteolytic Processing in Proteomes Using Proteolytic Signature Peptides. **Journal of Proteomics** **100**, 79-91
44. Eckhard, U., Huesgen, P.F., Brandstetter, H. and Overall, C.M. 2014. Proteomic Protease Specificity Profiling of Clostridial Collagenases Reveals their Intrinsic Nature as Matrix Degraders. **Journal of Proteomics** **100**, 102-114.
45. Lange, P., Huesgen, P.F., Nguyen, K., and Overall, C.M. 2014. Annotating N termini for the Human Proteome Project: N termini and N ν -acetylation Status Differentiate Stable Cleaved Protein Species from Degradation Remnants in the Human Erythrocyte Proteome. **Journal of Proteome Research** **13**, 2028–2044.
46. auf dem Keller, U., Prudova, A., Eckhard, U., Fingleton, B., and Overall, C.M. 2013. Systems-Level Analysis of Proteolytic Events in Increased Vascular Permeability and Complement Activation in Skin Inflammation. **Science Signaling** **6**, rs2, 1-15: DOI: 10.1126/scisignal.2003512.
47. Dufour, A. and Overall, C.M. 2013. Missing the Target: Matrix Metalloproteinase Anti-Targets in Inflammation and Cancer. **Trends in Pharmacological Sciences** **34**, 233-242. Invited Review (Cover).
48. Wilson, C.H., Indarto, D., Doucet, A., Pogson, L.D., Pitman, M.R., McNicholas, K., Menz, R.I., Overall, C.M.*, and Abbott, C.A.* 2013. Identifying Natural Substrates for Dipeptidyl Peptidases 8 and 9 using Terminal Amine Isotopic Labeling of Substrates (TAILS) Reveals in Vivo Roles in Cellular Homeostasis and Energy Metabolism. *Joint Senior Authors. **Journal of Biological Chemistry** **288**, 13,936-13,949 **Paper of the Week**.
49. Starr, A.E., Dufour, A., Maier, J., and Overall, C.M. 2012. Biochemical Analysis of Matrix Metalloproteinase Activation of Chemokines CCL15 and CCL23 and Increased Glycosaminoglycan Binding of CCL16. **J Biol Chem** **287**, 5,848-60.
50. Lange, P., Huesgen, P. and Overall, C.M. 2012. TopFIND 2.0—Linking Protein Termini with Proteolytic Processing and Modifications Altering Protein Function. **Nucleic Acids Research**, **40**, D351-61.
51. auf dem Keller, U. and Overall, C.M. 2012. CLIPPER—An Add-on to the Trans-Proteomic Pipeline for the Automated Analysis of TAILS N-terminomics Data. **Biological Chemistry** **39**, 1477-1483.
52. Lange, P.F. and Overall, C.M. 2011. TopFIND, a Knowledgebase Linking Protein Termini with Function. **Nature Methods** **8**, 703-704.
53. Kleifeld, O., Doucet, A., Prudova, A., a.d. Keller, U., Kizhakkedathu, J., and Overall, C.M. 2011. Proteomic Identification of Protease Cleavage Products by Terminal Amine Isotopic Labeling of Substrates. **Nature Protocols** **6**, 1578-1611.
54. Schilling, O., Huesgen, P.F., Barré, O., auf dem Keller, U., and Overall, C.M. 2011. Characterization of the Prime and Non-Prime Active Site Specificities of Proteases by Proteome-derived Peptide Libraries and Tandem Mass Spectrometry. **Nature Protocols** **6**, 111-120.
55. Doucet, A., and Overall, C.M. 2011. Broad Coverage Identification of Multiple Proteolytic Cleavage Sites in Complex High Molecular Weight Proteins Using Quantitative Proteomics as a Complement to Edman Sequencing. **Molecular Cellular Proteomics** **10**, M110.003533 1-12.
56. Becker-Pauly, C., Barré, O., Schilling, O., auf dem Keller, U., Broder, C., Schütte, A., Kappelhoff, R., Stöcker, W. Overall, C.M. 2011. Proteomic Analyses Reveal an Acidic Prime Side Specificity for the Astacin Metalloprotease Family Reflected by Physiological Substrates. **Mol Cell Proteomics** **10**, M111.009233 1-19.
57. Morrison, C.J., Mancini, S., Kappelhoff, R., Cipollone, J., Roskelley C., and Overall, C.M. 2011. Microarray and Proteomic Analysis of Breast Cancer Cell and Osteoblast Co-cultures: The Role of Osteoblast Matrix Metalloproteinase (MMP)-13 in Bone Metastasis. **Journal of Biological Chemistry** **286**, 34,271-34,285.
58. Schilling, O., a.d. Keller, U., and Overall, C.M. 2011. Factor Xa Subsite Mapping by Proteome-Derived Peptide Libraries Improved Using WebPICS, a Resource for Proteomic Identification of Cleavage Sites. **Biol. Chem** **392**, 1031-1037.
59. Schilling, O., Barré, O., Huesgen, P.F., and Overall, C.M. 2010. Proteome-wide Analysis of Protein Carboxy Termini: C Terminomics. **Nature Methods** **7**, 508-511. Featured in C&EN.
60. Kleifeld, O., Doucet, A., auf dem Keller, U., Prudova, A., Schilling, O., Kainthan, R.K., Starr, A.E., Foster, L.J., Kizhakkedathu, J.N., and Overall, C.M. 2010. Isotopic labeling of Terminal Amines in Complex Samples Identifies Protein N-termini and Protease Cleavage Products. **Nature Biotechnology** **28**, 281-288.
61. Cox, J.H., Starr, A.E., Kappelhoff, R., Yan, R., Roberts, C.R., Overall, C.M. 2010. Matrix Metalloproteinase-8 Deficiency Exacerbates Inflammatory Arthritis Through Delayed Neutrophil Apoptosis and Reduced Caspase-11 Expression. **Arthritis and Rheumatism** **62**, 3,645-3,655. Editorial Highlighted.
62. auf dem Keller, U., Bellac, C.L., Li, Y., Lou, Y., Lange, P., Ting, R., Harwig, C., Kappelhoff, R., Dedhar, S., Adam, M., Ruth, T.J., Bernard, F., Perrin, D., Overall, C.M. 2010. Novel Matrix Metalloproteinase Inhibitors: [18 F]-Marimastat-Aryltrifluoroborate as a Probe for in vivo Positron Emission Tomography Imaging in Cancer. **Cancer Res** **70**, 7,562-69.
63. Prudova, A., auf dem Keller, U., Butler, G.S., and Overall, C.M. 2010. Multiplex N-Terminome Analysis of MMP-2 and

- MMP-9 Degradomes by iTRAQ-TAILS Quantitative Proteomics. **Molecular Cellular. Proteomics** **9**, 894-911.
64. A.d. Keller, U., Prudova, A., Gioia, M., Butler, G.S., and Overall, C.M. 2010. A Statistics Based Platform for Quantitative N-Terminome Analysis and Identification of Protease Cleavage Products. **Molecular Cellular. Proteomics** **9**, 912-27.
 65. Butler, G.S. and **Overall, C.M.** 2009. Proteomic Identification of Multitasking Proteins in Unexpected Locations Complicates Drug Targeting. **Nature Reviews Drug Discovery** **8**, 935-948. Featured Cover.
 66. Schilling, O. and **Overall, C.M.** 2008. Proteome-derived Database Searchable Peptide Libraries for Identifying Protease Cleavage Sites. **Nature Biotechnology** **26**, 685-694.
 67. Dean, R.A., Cox, J.H., Bellac, C.L., Doucet, A., Starr, A.E., and Overall, C.M. (2008). Macrophage-specific Metalloelastase (MMP-12) Truncates and Inactivates ELR⁺ CXC Chemokines and Generates CCL2, 7, 8, and 13 Antagonists: Potential Role of the Macrophage in Terminating PMN Influx. **Blood** **112**, 3444-3453.
 68. **Overall, C.M.** and Blobel, C.P. 2007. In Search of Partners: Linking Extracellular Proteases to Substrates. **Nature Reviews Molecular Cell Biology** **8**, 245-257.
 69. Wolf, K., Wu, Y.I., Liu, Y., Geiger, J., Tam, E., Overall, C.M., Stack, M.S., Friedl, P. 2007. Multi-step Pericellular Proteolysis Controls for the Transition from Individual to Collective Cancer Cell Invasion. **Nature Cell Biol** **9**, 893-904.
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B.2. Invention Disclosures, Patents and Trademarks (selected from a total of 21)

1. "LysargiNase a novel thermophilic digestion protease for Proteomics" by Overall CM, Huesgen PF, Gomis-Rüth FX, Disclosure 15-099, **2015**
2. "Inhibitors of MMP12 as Antiviral Agents" by **Overall CM**, McManus BM, Dive V, and Marchant D. International Patent 14 305192.8, February **2014**, Disclosure 14-131 ("Metalloproteinase inhibition for broadspectrum antiviral treatment").
3. CLIP-CHIP® trademarks in Canada and the US are 1,260,571 and 78/656,391, respectively.
4. "Proteome-wide Isolation of Carboxy Terminal Peptides by Proteolytic Removal of Internal and Amino Terminal Peptides" by **Overall CM** and Schilling O, Disclosure 08-090, October 13, 2007.
5. "Methods for the Composition of High Molecular Weight Hyperbranched Polymeric Supports, with Binding Functionalities and Applications Thereof" by Kizhakkedathu J, and **Overall CM** US provisional application No. 60/960,904, 2008.
6. "Synthesis and Application of Reversible Metalloproteinase Inhibitors for Proteomic Analysis and MALDI-MS Imaging" by **Overall CM**, Perrin D, Harwig C, Ting R, and auf dem Keller U, Disclosure 09-056, July 2008.
7. "Synthesis and Application of Reversible Metalloproteinase Inhibitors for *in vivo* PET Imaging" by **Overall CM**, Perrin D, Ting R, and auf dem Keller U, Disclosure 09-052, July 2008.
8. "Substituted Aryl-Fluorides as Imaging Agents" by Perrin D, Ting R, and **Overall CM**. International Patent Application PCT/CA2008/001368 and US patent application 12/670,108,2010.

C. Ongoing Research Support

Tier 1 Canada Research Chair: Metalloproteinase Proteomics & Systems Biology	Overall (PI)	2015-2021
CIHR Foundation Grant FDN-148408: From Proteolytic Networks to Human Biology and Disease: Protease Regulation of Signal Transduction in Chronic Inflammatory Diseases	Overall (PI)	2016-2023