

Publications 2016-2018

1. Yu J, Schorlemer M, Alejandro Gomez-Toledo A, Pett C, Sihlbom C, Larson G, Westerlind U and Nilsson J. (2016) Distinctive MS/MS fragmentation pathways of glycopeptide-generated oxonium ions provide evidence of the glycan structure. *Chemistry Eur J* 22 (3): 1114–1124., DOI: 10.1002/chem.201503659 (GUP 228774) **Impact factor 5.160 (2017)**
2. Nasir W, Toledo AG, Noborn F, Nilsson J, Wang M, Bandeira N and Larson G. (2016) SweetNET: A Bioinformatics Workflow for Glycopeptide MS/MS Spectral Analysis. *J. Proteome Res.* 2016, 15, 2826–2840. DOI: 10.1021/acs.jproteome.6b00417 (GUP) **Impact factor 4.268 (2016)**
3. Noborn F, Gomez Toledo A, Green A, Nasir W, Sihlbom C, Nilsson J and Larson G (2016). Site-specific identification of heparan and chondroitin sulfate glycosaminoglycans in hybrid proteoglycans. *Sci. Rep.* 6, 34537; doi: 10.1038/srep34537 (GUP) **Impact factor 4.12**
4. Nilsson J, Noborn F, Gomez Toledo A, Nasir W, Sihlbom C and Larson G (2017) Characterization of glycan structures of chondroitin sulfate-glycopeptides facilitated by sodium ion-pairing and positive mode LC-MS/MS. *J Am Soc Mass Spectrometry*, 28(2):229-241, DOI:10.1007/s13361-016-1539-1 (GUP) **Impact factor 2.786 (2016)**
5. Noborn F, Gomez Toledo A, Nasir W, Nilsson J, Dierker T, Kjellén L, Larson G. Expanding the chondroitin glycoproteome of *Caenorhabditis elegans*. *J Biol Chem.* 2018 Jan 5;293(1):379-389. doi: 10.1074/jbc.M117.807800. **Impact factor 4.01 (2018)**
6. Guzzi N, Ciesla M, Ngoc PCT, Lang S, Arora S, Dimitriou M, Pimkova K, Sommarin MNE, Munita R, Lubas M, Lim Y, Okuyama K, Soneji S, Karlsson G, Hansson J, Jonsson G, Lund AH, Sigvardsson M, Hellstrom-Lindberg E, Hsieh AC, Bellodi C. Pseudouridylation of tRNA-derived fragments steer translational control in stem cells. *CELL* 2018 May 17; 173(5) 1204-1216. Doi 10.1016/j.cell.2018.03.008 **Impact factor 31.4 (2017)**
7. Westman JS, Stenfeldt L, Vidovic K, Moller M, Hellberg A, Kjellström S, Olsson ML. Allele-selective RUNX1 binding regulates P1 blood group status by transcriptional control of A4GLAT. *BLOOD* 2018 Apr 5; 131:1611-1616. Doi 10.1182/blood-2017-08-803080 **Impact factor 15.132 (2017)**
8. Saravanan R, Holdbrook DA, Petrlova J, Singh S, Berglund, NA, Chong YK, Kjellström S, Bond PJ, Malmsten M, Schmidtchen A. Structural basis for endotoxin neutralization and anti-inflammatory activity of thrombin-derived C-terminal peptides. *Nature Communications* 2018 Jul 17; 9. Doi 10.1038/s41467-018-05242-0 **Impact factor 12.124 (2016)**
9. Gaetani M, Zubarev RA. Functional Identification of Target by Expression Proteomics (FITeXP). *Book Chapter of "Mass Spectrometry-Based Chemical Proteomics"* edited by WILEY. *In Press.*

10. Azimi A, Caramuta S, Seashore-Ludlow B, Boström J, Robinson JL, Edfors F, Tuominen R, Kemper K, Krijgsman O, Peeper DS, Nielsen J, Hansson J, Egyhazi Brage S, Altun M, Uhlen M, and Maddalo G. Targeting CDK2 overcomes melanoma resistance against BRAF and Hsp90 inhibitors. *Molecular Systems Biology* (2018) 14, e7858 **Impact factor 8.447 (2017)**
11. Matic LP, Jesus Iglesias M, Vesterlund M, Lengquist M, Hong MG, Saieed S, Sanchez-Rivera L2, Berg M, Razuvaev A, Kronqvist M, Lund K, Caidahl K, Gillgren P, Pontén F, Uhlén M, Schwenk JM, Hansson GK, Paulsson-Berne G, Fagman E, Roy J, Hultgren R, Bergström G, Lehtiö J, Odeberg J, Hedin U. Novel Multiomics Profiling of Human Carotid Atherosclerotic Plaques and Plasma Reveals Biliverdin Reductase B as a Marker of Intraplaque Hemorrhage. *JACC Basic Transl Sci.* 2018 Aug 1;3(4):464-480. **Impact factor does not yet qualify for Impact Factor consideration**
12. Sork H, Corso G, Krjutskov K, Johansson HJ, Nordin JZ, Wiklander OPB, Lee YXF, Westholm JO, Lehtiö J, Wood MJA, Mäger I, El Andaloussi S. Heterogeneity and interplay of the extracellular vesicle small RNA transcriptome and proteome. *Sci Rep.* 2018 Jul 17;8(1):10813. doi: 10.1038/s41598-018-28485-9. **Impact factor 4.12**
13. Schmidt A, Marabita F, Kiani NA, Gross CC, Johansson HJ, Éliás S, Rautio S, Eriksson M, Fernandes SJ, Silberberg G, Ullah U, Bhatia U, Lähdesmäki H, Lehtiö J, Gomez-Cabrero D, Wiendl H, Lahesmaa R, Tegnér J. Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. *BMC Biol.* 2018 May 7;16(1):47. doi: 10.1186/s12915-018-0518-3. **Impact factor 6.779 (2016)**
14. Zhu Y, Orre LM, Johansson HJ, Huss M, Boekel J, Vesterlund M, Fernandez-Woodbridge A, Branca RMM, Lehtiö J. Discovery of coding regions in the human genome by integrated proteogenomics analysis workflow. *Nat Commun.* 2018 Mar 2;9(1):903. **Impact factor 12.124 (2016)**
15. Nassa G, Giurato G, Cimmino G, Rizzo F, Ravo M, Salvati A, Nyman TA, Zhu Y, Vesterlund M, Lehtiö J, Golino P, Weisz A, Tarallo R. Splicing of platelet resident pre-mRNAs upon activation by physiological stimuli results in functionally relevant proteome modifications. *Sci Rep.* 2018 Jan 11;8(1):498. **Impact factor 4.12**
16. Murie C, Sandri B, Sandberg AS, Griffin TJ, **Lehtiö J**, Wendt C, Larsson O. Normalization of mass spectrometry data (NOMAD). *Adv Biol Regul.* 2018 Jan;67:128-133. **Impact factor 6.15**
17. Gaetani M, Zubarev RA. New Promises of Chemical Proteomics for Drug Development. *Novel Approaches in Drug Designing and Development*, 2017, June 23; 2(1): 555579 **Impact factor 3.40**
18. Zhu Y, Engström PG, Tellgren-Roth C, Baudo CD, Kennell JC, Sun S, Billmyre RB, Schröder MS, Andersson A, Holm T, Sigurgeirsson B, Wu G, Sankaranarayanan SR, Siddharthan R, Sanyal K, Lundeberg J, Nystedt B, Boekhout T, Dawson TL Jr, Heitman J, Scheynius A, **Lehtiö J**. Proteogenomics produces comprehensive and highly accurate protein-coding gene annotation in a complete genome assembly of *Malassezia sympodialis*. *Nucleic Acids Res.* 2017 Mar 17;45(5):2629-2643. **Impact factor 11.561 (2017)**

19. Warpman U., Berglund K, Sanjiv H., Gad C., Kalderén T., Koolmeister T., Pham C., Gokturk R., Jafari G., Maddalo B., Seashore-Ludlow A., Chernobrovkin A., Manoilov I. S., Pateras A., Rasti A.-S., Jemth I., Almlöf O., Loseva T., Visnes B. O., Einarsdottir F. Z., Gaugaz A., Saleh B., Platzack O. A., Wallner K. S. A., Vallin M., Henriksson P., Wakchaure S., Borhade P., Herr Y., Kallberg P., Baranczewski E. J., Homan E., Wiita V., Nagpal T., Meijer N., Schipper S. G., Rudd L., Bräutigam A., Lindqvist A., Filppula T-C., Lee P., Artursson J. A., Nilsson V. G. Gorgoulis Lehtiö J., Zubarev R. A. Scobie M., Helleday T. Validation and development of MTH1 inhibitors for treatment of cancer. *Annals of Oncology*, Volume 27, Issue 12, 1 Dec 2016, Pages 2275–2283 **Impact factor 13.926 (2017)**
20. Konasani VR, Jin C, Karlsson NG, Albers E. A novel ulvan lyase family with broad-spectrum activity from the ulvan utilisation loci of *Formosa agariphila* KMM 3901. *Sci Rep.* 2018 Oct 2;8(1):14713. doi: 10.1038/s41598-018-32922-0. PubMed PMID: 30279430; PubMed Central **Impact factor 4.12**
21. Mirgorodskaya E, Karlsson NG, Sihlbom C, Larson G, Nilsson CL. Cracking the Sugar Code by Mass Spectrometry : An Invited Perspective in Honor of Dr. Catherine E. Costello, Recipient of the 2017 ASMS Distinguished Contribution Award. *J Am Soc Mass Spectrom.* 2018 Jun;29(6):1065-1074. doi: 10.1007/s13361-018-1912-3. Epub 2018 Apr 11. PubMed PMID: 29644549; PubMed Central PMCID: PMC6003999. **Impact factor 2.786 (2016)**
22. Shadnezhad A, Naegeli A, Sjögren J, Adamczyk B, Leo F, Allhorn M, Karlsson NG, Jensen A, Collin M. EndoSd: an IgG glycan hydrolyzing enzyme in *Streptococcus dysgalactiae* subspecies *dysgalactiae*. *Future Microbiol.* 2016 Jun;11:721-36. doi: 10.2217/fmb.16.14. Epub 2016 May 20. PubMed PMID: 27200457. **Impact factor 3.374 (2016)**
23. Hykollari A, Malzl D, Eckmair B, Vanbeselaere J, Scheidl P, Jin C, Karlsson NG, Wilson IBH, Paschinger K. Isomeric separation and recognition of anionic and zwitterionic N-glycans from royal jelly glycoproteins. *Mol Cell Proteomics.* 2018 Aug 13. pii: mcp.RA117.000462. doi: 10.1074/mcp.RA117.000462. PubMed PMID: 30104209. **Impact factor 5.232**
24. Pett C, Nasir W, Sihlbom C, Olsson BM, Caixeta V, Schorlemer M, Zahedi RP, Larson G, Nilsson J, Westerlind U. Effective Assignment of α 2,3/ α 2,6-Sialic Acid Isomers by LC-MS/MS-Based Glycoproteomics. *Angew Chem Int Ed Engl.* 2018 Jul 20;57(30):9320-9324. doi: 10.1002/anie.201803540. Epub 2018 Jun 20. PubMed PMID: 29742324. **Impact factor 11.994 (2016)**
25. Muthusamy S, Lundin D, Mamede Branca RM, Baltar F, González JM, Lehtiö J, Pinhassi J. Comparative proteomics reveals signature metabolisms of exponentially growing and stationary phase marine bacteria. *Environ Microbiol.* 2017 Mar 30 **Impact factor 4.974**
26. Kifer I, Branca RM, Ben-Dor A, Zhai L, Xu P, Lehtio J, Yakhini Z. Optimizing Analytical Depth and Cost Efficiency of IEF-LC/MS Proteomics. *IEEE/ACM Trans Comput Biol Bioinform.* 2017 Mar-Apr;14(2):272-281. **Impact factor 2.428**

Submitted manuscripts

27. Amir Ata Saei, et al. ProTargetMiner: A proteome signature library of anticancer molecules for functional discovery. - bioRxiv 421115; doi: <https://doi.org/10.1101/421115> **Impact factor** *bioRxiv is not a journal but a repository*
28. Xuepei Zhang et al. Anticancer effect of deuterium depleted water - comprehensive proteomics analysis suggests a redox disbalance mechanism. (*submitted to Molecular & Cellular Proteomics*)
29. Amir Ata Saei, et al. Proteome signatures of anticancer molecules for functional and mechanistic discoveries. (*Submitted to Nature Chemical Biology*)
30. Leanderson K et al. Wnt5a is a TLR2/4-ligand that induces tolerance in human myeloid cells
Nature Immunology submitted
31. Svanborg C et al. Commensal Escherichia coli secrete RNA polymerase II inhibitors 2 that fine-tune host gene expression and create symbiosis
Nature Microbiology submitted