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**Chancellor’s Postdoctoral Research Fellowship Scheme 2017**

**1. EXPRESSION OF INTEREST COVERSHEET**

**This coversheet must be the first page of your EOI submission**

**Entries should be identical to your EOI registration details**

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| --- | --- | --- | --- |
| **APPLICANT INFORMATION** | | | |
| **Family name: Van Sluyter** | | **Given name(s): Steve** | |
| **Title** (e.g. Dr)**: Dr** | | **Email: steve.vansluyter@gmail.com** | |
| **PROJECT TITLE**  *Please provide a short, descriptive title for your proposed project (maximum* ***12 words****). Avoid discipline-specific terms and abbreviations. This can be a working title which may be changed later.* | | | |
| **Title: Continent-scale leaf protein mapping: how and why do photosynthesis proteins vary across Australia?** | | | |
| **PROJECT SUMMARY**  *Please provide a summary outlining the proposed project (maximum* ***100 words****).* | | | |
| Photosynthesis is driven by groups of proteins that are similar across the plant kingdom. But, the *amounts* of those proteins across species, plant types, and environmental gradients are unknown because measuring them has been technically impossible until now. I have recently developed methods that quantify leaf proteins on a per leaf area basis. I will adapt those methods to resources at UTS in order to analyse leaves of native plants from across Australia. Leaf protein amounts will be linked to remote sensing imagery in order to create an Australian map of leaf proteins. | | | |
| **FELLOWSHIP SUPERVISOR** | | | |
| **Family name: Andrea** | | **Given name: Leigh** | |
| **Title** (e.g. Dr)**: A/Prof** | | **Email: Andrea.Leigh@uts.edu.au** | |
| **UTS FACULTY (or equivalent)** – tick [X] | | | |
| [ ] Engineering & IT  [ X ] Science  [ ] Business  [ ] Law | [ ] Arts & Social Sciences  [ ] Health (Faculty)  [ ] Graduate School of Health  [ ] Design, Architecture & Building | | [ ] Institute for Sustainable Futures  [ ] IPPG  [ ] Jumbunna |
| **PHD QUALIFICATION** | | | |
| **Institution:** | | **University of Melbourne** | |
| **Country:** | | **Australia** | |
| **IF AWARDED – PhD award date:** | | (dd/mm/yyyy): 26/05/2012 | |
| **IF NOT YET AWARDED – PhD submission date (past or prospective):** | | (dd/mm/yyyy): | |

**2. Curriculum Vitae**

**Education**

* Ph.D., The University of Melbourne, School of Botany, 26 May 2012, thesis: “Grape and *Botrytis cinerea* proteases: characterization and utilization in winemaking”
* University of North Carolina at Wilmington
  + B.A. *Cum Laude* Philosophy, minor in Environmental Sciences, 2001
  + B.S. *Magna Cum Laude* Biology (Honors), minor in Chemistry, 2002, thesis: “Comparison of grape chitinase activities in Chardonnay and Cabernet Sauvignon with *Vitis rotundifolia* cv. Fry”

**Employment history**

* Current: Postdoctoral Fellow, Macquarie University. Projects: ARC Discovery Project on leaf proteomics; Wine Australia project on modeling vineyard yields.
* 2013-16: SIEF Postdoctoral Fellow, Macquarie University.
* 2010-12: Research Associate, Macquarie University. Maintained and operated two mass spectrometers, conducted grape and wine proteomics research.
* 2009-10: Research Fellow, The Australian Wine Research Institute. Researched wine proteins, grape and fungal enzymes for improved winemaking, and the chemistry of white wine mouth feel.
* 2005: Occupational Trainee, The Australian Wine Research Institute.
* 2004: Seasonal lab technician, Nobilo Drylands Estate Winery, Blenheim, New Zealand.
* 2003: Seasonal lab technician, Buena Vista Winery, Sonoma, California.
* 2003-04: Casual research assistant, Department of Chemistry and Biochemistry, University of North Carolina at Wilmington. Purified, modified, and characterized an enzyme implicated in human cancers.

**Scholarships and awards**

* 2008: German Academic Exchange Service (DAAD), €3275. Conducted grape enzyme research at the Max Planck Institute for Plant Breeding Research.
* 2008: The University of Melbourne, School of Botany, Gietria Weste Pathology and Mycology Scholarship, $500.
* 2007: The Australian Society of Plant Scientists and International Society for Plant Molecular Biology postgraduate travel award, $2700
* 2007: The University of Melbourne, Melbourne Abroad Travelling Scholarship, $1250
* 2007: The University of Melbourne, School of Botany travel grant $1250. Travelled to the Laboratory of Phytopathology, Wageningen University to research molecular plant-pathogen interactions.
* 2006-09: Endeavour International Postgraduate Research Scholarship, ca. $100,000; Melbourne International Research Scholarship, ca. $70,000; School of Botany and The Australian Wine Research Institute Studentship, ca. $27,000.
* 2002: University of North Carolina at Wilmington, Carl and Janice Brown Merit Scholarship, US$2500.

## Reviewer for journals

## *Proteomics*, *Environmental and Experimental Botany*, *Journal of Agricultural and Food Chemistry*, *European Food Research and Technology*, *Australian Journal of Grape and Wine Research*, *International Journal of Food Science and Technology*, *FEMS Yeast Research*, and *Biotechnology Progress*

**3. Research record relative to opportunity**

**a) Research achievements, skills, and evidence of impact in your research field**

My areas of expertise are plant protein chemistry and proteomics. I worked and conducted my PhD research at the Australian Wine Research Institute (AWRI), producing two new winemaking technologies (publications 3 & 6) and findings on the texture of white wines directly useful to industry (e.g. publication 8). My work was often promoted as AWRI research highlights in annual reports and reports to the funding agency and AWRI board.

Since moving to Macquarie University I’ve shifted my research to basic plant ecophysiology, although I’ve continued wine industry research, raising substantial funds in both areas ($1.1m since my PhD).

My approach to using proteomics in large-scale plant ecophysiology experiments (ARC Discovery Project) is an entirely new way of answering longstanding important questions. In the process of answering those questions I’ve developed new proteomics methods that I expect will set the new standard of excellence in plant proteomics.

I’m self-funded and I run my own research group of 2 postdocs, 3 technicians, and I co-supervise a PhD student. Grant 1 (below) pays my salary; grant 2 pays operating costs.

To UTS I will bring: funds from industry and the ARC; expertise in proteomics applicable to any organism; an imaginative and entirely new way of thinking about ecosystems.

**b) Research funding (\*I wrote most of the proposal; \*\*I wrote all of the proposal)**

1) \*\*Awarded. [Wine Australia](http://research.wineaustralia.com/research-development/current-projects/accurate-and-early-yield-predictions-through-advanced-statistical-modelling/). Van Sluyter (Chief Investigator), Beaumont, Dunn (DPI NSW), Small (Treasury Wine Estates). *Accurate and early yield predictions through advanced statistical modelling.* 2014-17. Macquarie University. $356,026.

2) \*Awarded. [ARC Discovery Project](http://www.arc.gov.au/discovery-projects) DP140101875. Westoby, Van Sluyter (2nd Chief Investigator, project manager), Haynes, Gygi (Harvard Medical School). *Answering longstanding plant ecology questions with new technology: the effects of changes in leaf proteins with age*. 2014-16. Macquarie University. $408,000.

3) Awarded. [Macquarie University Research Infrastructure Block Grant](http://www.mq.edu.au/research/research-opportunities-at-macquarie/funding-fellowships-and-partnerships/internal_funding/mq-research-infrastructure-block-grants). Molloy, Nevalainen, Packer, Haynes, Westoby, Van Sluyter (6th Chief Investigator). *Proteomics sample preparation systems*. 2013. Macquarie University. $54,177.

4) \*\*Awarded. [Science and Industry Endowment Fund John Stocker Postdoctoral Fellowship](http://www.sief.org.au/FundingActivities/What-Has-Been-Funded_POS.html#Postdoc). Westoby (supervisor), Van Sluyter (fellow). *Building better climate change vegetation models: How do leaves allocate nitrogen among photosynthesis and stress proteins in future climate scenarios?* 2013-16. Macquarie University. $276,000.

5) \*\*Awarded. [Grape Research Coordination Network](http://www.vitaceae.org/index.php/Grape_Research_Coordination_Network) travel stipend. Van Sluyter (Chief Investigator). Travel to conduct grapevine proteomics research at University of Nevada-Reno and Harvard Medical School. 2012. University of Nevada-Reno. US$9200.

6) \*\*Awarded. [Wine Australia](http://research.wineaustralia.com/completed_projects/cold-active-proteases-from-antarctic-fungi-as-alternatives-to-heat-stabilisation-with-bentonite/). Nevalainen, Van Sluyter (2nd Chief Investigator), T’eo. *Cold-active proteases from Antarctic fungi as alternatives to heat-stabilisation with bentonite*. 2011-12. Macquarie University. $37,430.

7) \*\*Awarded. [Grape Research Coordination Network](http://www.vitaceae.org/index.php/Grape_Research_Coordination_Network) travel stipend. Van Sluyter (Chief Investigator). Travel to conduct grapevine proteomics research at Nanjing Agricultural University and University of California-San Diego. 2011. University of Nevada-Reno. US$9500.

8) \*\*Awarded. [Macquarie University New Staff grant](http://www.mq.edu.au/research/research-opportunities-at-macquarie/funding-fellowships-and-partnerships/internal_funding/mqns). Van Sluyter (Chief Investigator). *Characterization of enzymatic protein modifications during plant cell death*. 2011. Macquarie University. $7931.

**c) Career Disruptions (none)**

**4. Publications**

**a) Bibliometrics**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Item | Scholarly books | Scholarly book chapters | Refereed journal articles | Refereed conference papers | TOTAL |
| # of publications | 0 | 1 | 20 | 0 | **21** |
| # of citations *(excluding self-citations)* | 0 | 6 | 557 | 0 | **563** |
| # of publications as *leading* author | 0 | 0 | 4 | 0 | **4** |
| # of publications since PhD award date | 0 | 1 | 11 | 0 | **12** |

Source of publication and citation count – tick [X]:

[X] Scopus

[ ] Web of Science

[ ] Microsoft Academic *not permitted for applicants in**FEIT, FoH, GSH and SCI*

[ ] Google Scholar *not permitted for applicants in FEIT, FoH, GSH and SCI*

Date of bibliometrics data retrieval: **19/05/16**

Additional commentary (100 words maximum):

I have 6 additional articles in non-refereed wine industry trade publications.

Seven journal articles and my book chapter had students as first authors. For those I provided substantial technical assistance in mass spectrometry, protein chemistry, or proteomics data analysis (with the exception of one review article that I helped write).

My current proteomics methods are not yet published because they have commercial value. I am exploring adoption options with the MQ Office of Commercialisation and Innovation and three biotech companies.

My current grape yield modelling research is intended to produce a resource for Australian industry and will not be published.

**b) ‘Top 10’ Career-best Publications**

1. Van Sluyter, S.C., J.M. McRae, R.J. Falconer, P.A. Smith, A. Bacic, E.J. Waters and M. Marangon (2015) Wine protein haze: mechanisms of formation and advances in prevention. *Journal of Agricultural and Food Chemistry* 63:4020-4030.

IF 2.9, 7 cites. This review summarized the previous 10 years of wine protein research. The ToC figure is being used in an upcoming textbook, [*Understanding Wine Chemistry*](http://au.wiley.com/WileyCDA/WileyTitle/productCd-1118627806.html).

1. \*Van Sluyter, S.C., M. Marangon, S.D. Stranks, K.A. Neilson, Y. Hayasaka, P.A. Haynes, R.I. Menz and E.J. Waters. (2009) Two-step purification of pathogenesis-related proteins from grape juice and crystallization of thaumatin-like proteins. *Journal of Agricultural and Food Chemistry* 57:11376-11382.

IF 2.9, 13 cites. This describes wine protein purification and crystallization methods that made possible several key advances in wine protein chemistry.

1. Van Sluyter, S.C., N.I. Warnock, S. Schmidt, P.A. Anderson, J.A.L. van Kan, A. Bacic and E.J. Waters (2013) An aspartic acid protease from *Botrytis cinerea* removes haze forming proteins during white winemaking. *Journal of Agricultural and Food Chemistry* 40:9705-9711.

IF 2.9, 3 cites. This describes the first enzyme to destroy nuisance proteins during winemaking; a challenge since the 1960s and AWRI research highlight [reported to the Australian Productivity Commission](http://www.pc.gov.au/inquiries/completed/rural-research/submissions/sub082.pdf).

1. \*Cramer, G.R., S.C. Van Sluyter, D.W. Hopper, D. Pascovici, T. Keighley, and P.A. Haynes. (2013) Proteomic analysis indicates massive changes in metabolism prior to the inhibition of growth and photosynthesis of grapevine (*Vitis vinifera* L.) in response to water deficit. *BMC Plant Biology* 13:49.

IF 3.8, 26 cites. This convincingly demonstrated that plant proteins respond to stress more quickly than physiological traits. Computational methods are similar to the proposed project.

1. \*Neilson, K.A., N.A. Ali, S. Muralidharan, M. Mirzaei, M. Mariani, G. Assadourian, A. Lee, S.C. Van Sluyter and P.A. Haynes. (2011) Less label, more free: approaches in label-free quantitative mass spectrometry. *Proteomics* 11:535-553.

IF 3.8, 268 cites. This review is a comprehensive summary of different quantitative proteomics methods, including computational method similar to those in the proposed project.

1. Marangon, M., S.C. Van Sluyter, E.M.C. Robinson, R.A. Muhlack, H.E. Holt, P.A. Haynes, P.W. Godden, P.A. Smith, E.J. Waters. (2012) Degradation of white wine haze proteins by Aspergillopepsin I and II during juice flash pasteurization. *Food Chemistry* 135:1157-1165.

IF 3.4, 11 cites. [I conceived](http://research.wineaustralia.com/wp-content/uploads/2012/04/R_D_WorkJun11.pdf) this new winemaking technology shortly before leaving the Australian Wine Research Institute and then performed the proteomics. The technology has been [promoted heavily](http://www.awri.com.au/information_services/awitc-workshop-reference-lists/s4-1/) to industry.

1. Marangon, M., S.C. Van Sluyter, E.J. Waters and R.I. Menz (2014) Structure of haze forming proteins in white wines: *Vitis vinifera* thaumatin-like proteins. *PLoS ONE* 9:e113757.

IF 3.2, 5 cites. This presented the first crystal structures for wine proteins and proposed a structural explanation for why some wine proteins are less stable than others.

1. Gawel, R., M. Day, S.C. Van Sluyter, H.E. Holt, E.J. Waters and P.A. Smith (2014) White wine taste and mouth-feel as affected by juice extraction and processing. *Journal of Agricultural and Food Chemistry* 62:10008-10014.

IF 2.9, 1 cite. This was a combination of real-world winery experiments and cutting edge analytical methods that I helped develop. The results are directly relevant to industry.

1. \*Chapman, B., N. Castellana, A. Apffel, R. Ghan, G.R. Cramer, M. Bellgard, P.A. Haynes and S.C. Van Sluyter. "Plant Proteogenomics: From Protein Extraction to Improved Gene Predictions." In Methods in Molecular Biology, Vol. 1002, Proteomics for Biomarker Discovery, Eds. M. Zhou and T. Veenstra. Humana Press, 2013.

6 cites. This book chapter provides clear step-by-step protocols for complex protein extraction and mass spectrometry sample preparation methods similar to those in the proposed project.

1. \*Marangon M., S.C. Van Sluyter, K.A. Neilson, C. Chan, P.A. Haynes, E.J. Waters and R.J. Falconer. (2011) Roles of grape thaumatin-like protein and chitinase in white wine haze formation. *Journal of Agricultural and Food Chemistry* 59:733-740.

IF 2.9, 24 cites. This combined experiments with real wine, purified proteins in a model system, and proteomics to conclusively demonstrate dramatic differences among wine haze proteins.

**5. Selection of Supervisor and UTS**

**Supervisors at UTS.** A/Profs Andrea Leigh and Stella Valenzuela will supervise my fellowship, which is a combination of plant ecophysiology (Leigh) and biochemistry (Valenzuela). Valenzuela has held ARC funding continuously since 2005, has >$5.3m in competitive funding in the past 5 years, and is a CI on the UTS ARC Industry Transformation Research Hub for biomedical devices.

For a 25% teaching position I need a strong teaching mentor like Leigh. Leigh is only 8 years from her PhD and is already an A/Prof. She has received teaching awards and is Associate Head of School, Teaching and Learning. I believe strongly in my approach to science and I want to be great at teaching it to others; Leigh is the perfect mentor for helping me achieve that.

My proposed project was developed in consultation with Prof Alfredo Huete, a senior researcher with the C3 Institute, and Dr Matt Padula, UTS Proteomics Core Facility. Both Huete and Padula will contribute resources and expertise.

**Plant science at UTS.** I’ve gotten to know UTS plant scientists through Sydney Plant Ecophysiology Group seminars I organise, often at UTS. Through that I’ve started working with Leigh and Valenzuela and their student, Kirsty Milner, on an exciting trans-disciplinary project closely related to my plant proteomics research.

My proposed project will involve fieldwork across Australia, which would normally be very expensive and logistically challenging. However, my fieldwork will be doable because I will coordinate it with the work that Leigh already conducts across Australia. Also, she is a leading plant physiologist and expert in Australian native plants and, because I’m mainly a protein chemist, I will learn a lot from her in those areas.

**Proteomics at UTS.** A goal for my proposed fellowship is to make my proteomics methods platform-independent. UTS has suitable Agilent instruments and Padula tells me that UTS will likely acquire one or two extremely capable Thermo mass spectrometers. Also, Padula already uses the free version of the expensive data analysis software that is currently required for my proteomics methods.

**Ecology at UTS.** In order to map proteins on a continental scale I will express protein amounts on a per land area basis, which means using remote sensing data. Huete is clearly a world leader in linking satellite data with plant physiology. He is the perfect person to work with to develop new methods and he already has on hand the imaging resources I’ll need.

Beyond the direct scope of my proposed work, which is entirely terrestrial, I’ve discussed coastal and marine plant proteomics possibilities with C3 Institute Director Prof Peter Ralph and DECRA fellow Dr Manoj Kumar. I plan to eventually map leaf proteins globally and Ralph and Kumar’s work on coastal systems and seagrasses will be an important part of that.

**Sustainability at UTS.** I have conducted research in industrial microbiology, plant physiology, plant pathology, and biochemistry, which combine under the themes of Food Security and Food Biotechnology. These are increasingly important areas for Australian undergraduate learning and postgraduate research in sustainability.

My proposed plant research relates to sustainability because of the central role photosynthesis plays in carbon cycles. Our current knowledge of photosynthesis is based on a handful of crop and model species grown under artificial conditions. The biochemistry of native leaves is critically important to carbon cycles, but is currently hardly understood.

Although not a part of my proposed project, I will contribute to UTS sustainability research by raising industry funds through collaborations with crop researchers. I’ve discussed research possibilities using my proteomics methods with barley, rice, and cotton researchers, with enthusiastic responses. I have industry connections through my wine research and DPI NSW and I have a strong track record in industry funding and outcomes.

**6. Proposed Fellowship Project**

**Background**

Photosynthesis is driven by a group of protein complexes and enzymes that are similar in their compositions across the plant kingdom (Allen et al 2011). But, the *amounts* of those proteins across species, plant types, and environmental gradients are unknown because measuring them has been technically impossible until now. Proteomics is the field of identifying large numbers of proteins using mass spectrometry. However, the usefulness of proteomics in plant research has been limited by methods that estimate quantitative differences using *only relative, arbitrary units*. In contrast to that, I have developed proteomics methods that measure leaf proteins in *absolute terms*; e.g. milligrams of individual proteins or protein complexes per leaf area.

The significant advantages of my methods are that comparisons can be made across experiments and species, and using real units of measurement makes it possible to quantitatively link protein amounts to physiological traits. Those advantages make proteomics much more useful to crop researchers, plant physiologists, and ecologists.

My overall research strategy is to conduct method development and basic plant ecology research as my UTS fellowship project, and to simultaneously build new collaborations and raise funds through applied crop research. The broad goal of the basic research is to make it possible to answer global-scale questions that would be competitive for ARC funding, and to produce high impact outputs that showcase my technologies in order to encourage their adoption. *The two-pronged basic/applied research strategy has worked for me already*: my current research at Macquarie University has been funded by industry (Wine Australia), an ARC Discovery Project grant, and a Science and Industry Endowment Fund fellowship.

**Aims**

The three aims of my proposed research at UTS are to: 1) adapt my methods to the mass spectrometry resources at UTS, which would make them platform independent; 2) determine the main drivers of variation in leaf protein composition across a range of species sampled across Australia; 3) link remote sensing data to leaf protein data in order to create an Australian leaf protein map.

To achieve those aims at UTS I will work with A/Prof Leigh, a plant physiologist who routinely samples plants across Australia, A/Prof Valenzuela, a biochemist already working with Leigh on leaf stress proteins, Dr Padula, a proteomics expert who has already used the software my project will require, and Prof Huete, a world leading expert in linking remote sensing data to plant physiology.

**Outcomes and impact**

The outcomes of my proposed UTS fellowship project will be:

1) New mass spectrometry methods that are more accessible to plant researchers and that produce real-world results. Absolute quantification of proteins--using real units of measurement as opposed to relative quantification--will soon be the standard for proteomics and I intend to be a world leader in the field.

2) Basic knowledge into the composition of the ‘average’ leaf and how environmental factors shape leaf composition and function. These advances in knowledge will be so fundamental to plant science that I expect them to be included in plant physiology textbooks.

3) Linking leaf proteins to remote sensing data will make it possible to map proteins at landscape, continent, and even global scales. It will enable a new way of thinking about ecosystems as collections of functional molecules.

Many scientists have likely imagined life on Earth as collections of molecules. But, in my case, mapping them on a continent scale is technically feasible in a 4-year project. Also, the molecules that I will map, enzymes, actually do things—they catalyse the reactions of photosynthesis, which are critically important to better understand because of the role plants play in ecosystem responses to climate change.

**Significance, innovation, and benefit to UTS**

Proteomics is only about 15 years old and innovation in the field is driven mostly by medical research. According to market research commissioned by Macquarie Uni to assess one of my methods, plant proteomics is a rapidly growing globally, although it technologically lags behind medical proteomics. My general approach to plant proteomics is to adapt cutting edge medical proteomics methods to plants, to develop my own new methods, and to make them accessible to plant researchers.

The proposed project falls under the Government research priority of Environmental Change because it will answer fundamental questions about how Australia’s native plants work. In addition to my proposed fellowship project, the collaborations I anticipate with crop researchers will address the Government’s Food Priority.

The methods I will adapt to resources at UTS will be in high demand by plant researchers, particularly crop researchers, because they are fast, they produce easy to understand results, and the results are quantitatively meaningful. I know of no other group that quantifies leaf proteins on a per leaf area basis—the ability to do that sets me apart and opens up a range of new questions in plant science that can be answered at UTS.

**Approach and methodology**

**Aim 1.** The leaf protein extraction method will be similar to Chapman et al (2012). The mass spectrometry method will be similar to Liu et al (2013), but will use the free software Skyline (MacLean et al 2010), in collaboration with Padula.

**Aim 2.** Data will come from: 1) existing data from ~1000 evergreen leaf samples from my current Discovery Project; 2) from new samples that represent plant types absent from the Discovery Project. Leigh and I will collect leaf samples from grasses, herbaceous species, confers, etc., in order to capture a cross section of Australian land plants. Environmental data will be acquired from resources such as the Terrestrial Ecosystem Research Network (TERN). Data analysis will be performed with Leigh and Valenzuela.

**Aim 3.** At each field site I will take overhead images with a multi-spectral camera provided by Huete, who will also help with data analysis. The camera collects data in the same wavelengths as satellites used for global vegetation mapping. I will collect all the leaves within a given area of each image and quantify the proteins of the multi-species samples.

**Data publication and visualisation.** Mass spectrometry data will be made publicly available in a repository such as ProteomeXchange. Protein data, in combination with spatial data, will be visualised in collaboration with Dr Adam Carroll (ANU) through his current MONSTERS project (Metadata, Ontology and Standards-based Experimental Reporting System).

Allen, J.F., de Paula, W.B.M., Puthiyaveetil, S., and Nield, J. (2011). A structural phylogenetic map for chloroplast photosynthesis. Trends in Plant Science *16*, 645–655.

Chapman, B., Castellana, N., Apffel, A., Ghan, R., Cramer, G., Bellgard, M., Haynes, P., and Van Sluyter, S. (2013). Plant Proteogenomics: From Protein Extraction to Improved Gene Predictions. In Proteomics for Biomarker Discovery, M. Zhou, and T. Veenstra, eds. (Humana Press), pp. 267–294.

Liu, Y., Hüttenhain, R., Surinova, S., Gillet, L.C., Mouritsen, J., Brunner, R., Navarro, P., and Aebersold, R. (2013). Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS. Proteomics *13*, 1247–1256.

MacLean, B., Tomazela, D.M., Shulman, N., Chambers, M., Finney, G.L., Frewen, B., Kern, R., Tabb, D.L., Liebler, D.C., and MacCoss, M.J. (2010). Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. Bioinformatics *26*, 966–968.