Dear ISAC Members,

I still remember my first CYTO congress in Montpellier in 2004. I was only months into cytometry, and Bob Murphy and Jim Wood pulled up folding chairs in an empty room to hear my ideas about data standards for flow cytometry. That moment defined ISAC for me: a place where senior leaders make time for newcomers, and where someone who cares about improving how the field works can actually make it happen, not just locally, but globally. I have attended every CYTO congress since, and each one has deepened my commitment to this Society.

In the twenty-two years since, I have tried to live up to that belief.I chaired the Data Standards Task Force, helped create FlowRepository, launched FlowCAP, and worked with the community to release open-source tools like flowCore that remain part of the field's everyday toolkit. I served on Council and as an Associate Editor for Cytometry Part A, and founded Cytapex on the same open principles. Each of these efforts has been driven by the same goal: to make cytometry more reproducible, more comparable, and more useful to the broader scientific and clinical community. It was a CYTO meeting that ultimately led me to leave academia and join Dotmatics, where I now serve as VP and Research Director of Flow Cytometry. Every major milestone in my career traces back to this Society, and any success I have had is directly connected to it. I was grateful to receive ISAC's Distinguished Service Award; there is no recognition from this field that I value more. I would be honoured to serve this community as President.

Cytometry's technical capabilities have never been greater, yet our ability to compare, reproduce, and build on each other's work has not kept pace. Without a common language for cell populations, the promise of AI-driven analysis, cross-lab reproducibility, and regulatory acceptance of cytometry data cannot be fully realized. These challenges are not unique to any one society. They are shared across ISAC, ICCS, ESCCA, IUIS, and FOCIS, and the solutions must be shared too. Since I presented SOULCAP at CYTO 2025, it has grown from a vision into a registered foundation with five societies, major pharmaceutical partners, instrument manufacturers, and reagent vendors working together to address exactly this. It is governed by a board drawn from across academia, industry, and society leadership, and driven forward by a global corps of subject-matter expert volunteers who have made the work their own. What has made this effort work is not any one idea, but the model: bringing the right people to the same table, aligning around a shared problem, and building practical, open solutions together. That is the approach I would bring to the presidency.

As President, I would focus on three priorities. These priorities are grounded in ISAC's Strategic Plan, particularly its commitments to equity in access, diverse leadership, transparency with membership, and the highest quality educational programming. They reflect where I believe I can contribute most.

First, strengthening ISAC's role as the convening force for the field. No single society can solve cytometry's biggest challenges alone, and no President can solve every problem. Bioinformatics has been the focus of my research career and it is where my scientific strength lies, but what I have also demonstrated, repeatedly including within this Society, is an ability to bring large groups together around shared goals and lead them to tangible results. SOULCAP is now doing the same for cell annotation terminology, with a volunteer corps that spans academia, industry, and clinical practice across multiple continents and a governance structure designed from the start to reflect that breadth. Our citizen science collaborations have shown that this approach can reach far beyond the traditional cytometry community, bringing entirely new audiences into contact with our data. A common thread in all of this work has been lowering barriers: to data, to tools, and to participation in the field. From FlowCAP to FlowRepository to SOULCAP, the pattern has been the same: identify a problem the field cannot solve in silos, build a coalition, and deliver something open and practical. As President, I would extend that approach to working with sister societies, with organizations like CDISC, NIST, and the NIH, and with publishers to improve the quality and reproducibility of science across the field. I would also prioritize clear, regular communication with the membership about how the Society operates and where its resources go, not as a bureaucratic exercise, but because transparency builds the trust that makes everything else possible. Having served on Council, I understand how it functions and I am committed to ensuring it operates as a truly representative body where every voice is heard. I have been part of ISAC long enough to know its people and its workings well, and I have built relationships with leaders in these partner organizations as well. I have never been afraid to say what I believe is the right thing to do. I have also learned from every one of these efforts that the best outcomes come from working as a team to get to the right solution.

Second, connecting research, clinical, and regulatory cytometry. Already, the data standards and annotation work that SOULCAP and others are building has direct implications for regulatory submission, clinical trial design, and diagnostic reproducibility, but those connections will not happen on their own. ISAC is uniquely positioned to bridge these worlds, and as President I would work to bring regulatory and clinical voices more actively into our conversations, not as an afterthought but as partners in shaping where the field goes next.

Third, investing in the next generation of cytometrists. As a professor of Medical Genetics at UBC, I spent years training the next generation of computational cytometrists, supervising graduate students and postdoctoral fellows, contributing to a national bioinformatics training program, and developing an online course in flow cytometry bioinformatics that reached students around the world. What these experiences taught me is that the best students need mentorship, not just coursework. This is something ISAC is uniquely positioned to provide. ISAC invested in me as a Scholar early in my career, and I have seen firsthand how that support shapes a scientific life. I have since had the privilege of serving as an ISAC Scholar mentor, and closing that loop from recipient to guide is one of the most meaningful things I have done, both in this Society and in my professional career. I am committed to expanding and strengthening those pathways, and to ensuring that ISAC's leadership and volunteer structures reflect the full diversity of its membership.

ISAC gave me folding chairs and an audience of two, and that was enough to change the course of my career. I would be honoured to help ensure this Society continues to offer those moments, and to build on them.

With thanks for your consideration,
Ryan R. Brinkman

THE UNIVERSITY OF BRITISH COLUMBIA
Curriculum Vitae for Faculty Members

1. **SURNAME**: Brinkman **FIRST NAME**: Ryan **Initials**: RRB
MIDDLE NAME(S): Remy **Date:** 3/24/2026

2. **DEPARTMENT/SCHOOL:** Medical Genetics

3. **FACULTY**: Medicine

4. **PRESENT RANK**: Professor (Emeritus) **SINCE**: January 1, 2023

5. POST-SECONDARY EDUCATION

(a)

University or Institution	Degree	Subject Area	Dates
Carleton University	BSc	Biology and Biotechnology	09/86-05/92
University of British Columbia	PhD	Genetics	01/97-06/01

(b) Title of Dissertation and Name of Supervisor

“Prediction of age of onset and penetrance and its application to clinical trial design for Huntington Disease”.
[Dr. Michael Hayden, Medical Genetics, UBC]

Special Professional Qualifications

6. EMPLOYMENT RECORD

University, Company or Organization	Rank or Title	Dates
Banting Research Institute, Ottawa, ON, Canada	Laboratory Technician	05/90-09/90
National Laboratory for Sexual Transmitted Diseases, Ottawa, ON, Canada	Database Entry	11/90-05/91
National Laboratory for Sexual Transmitted Diseases, Ottawa, ON, Canada	Laboratory Technician	05/91-09/91
Children’s Hospital of Eastern Ontario, Ottawa, ON, Canada	Database Developer	05/92-10/92

Washington University Genome Sequencing Center, St. Louis, MO, USA	Bioinformatician	11/92-12/95
University of British Columbia, Michael Hayden Laboratory, Vancouver, BC, Canada	Database Developer	01/96-01/97
University of British Columbia, Vancouver, BC, Canada	Graduate Student	01/97-06/01
Outreach Lipid Clinics, Vancouver, BC, Canada	Database Developer and Statistician	09/97-01/01
MedPed, St. Paul's Hospital, Vancouver, BC, Canada	Database Developer	10/97-10/00
Xenon Pharmaceuticals Inc., Burnaby, BC, Canada	Bioinformatics Consultant	02/98-01/01
Clinical Genetics, Vancouver, BC, Canada	Database developer	05/99-01/00
Xenon Pharmaceuticals Inc., Burnaby, BC, Canada	Bioinformatics Group Leader	06/01-10/03
Terry Fox Laboratory British Columbia Cancer Research Centre, Vancouver, BC, Canada	Research Associate	11/03-06/05
Terry Fox Laboratory British Columbia Cancer Agency (Full institutional support for this position is provided by the BC Cancer Agency), Vancouver, BC, Canada	Senior Scientist	07/05-06/15
Medical Genetics, University of British Columbia, Vancouver, BC, Canada	Assistant Professor	07/05-07/10
Genetics Program, University of British Columbia, Vancouver, BC, Canada	Assistant Professor	11/05-06/10 (program closed)
Bioinformatics Centre, University of British Columbia, Vancouver, BC, Canada	Associate Faculty Member	08/05-12/22
CIHR/MSFHR Bioinformatics Training Program, Vancouver, BC, Canada	Associate Faculty Member	08/05-12/22
Canada's Michael Smith Genome Sciences Centre, BC Cancer Agency, Vancouver, BC, Canada	Associate Faculty Member	06/07-12/22
Department of Molecular Biology and Biochemistry, Faculty of Science, Simon Fraser University, Burnaby, BC, Canada	Adjunct Faculty	08/09-09/14
Department of Medical Genetics, Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada	Associate Professor	07/10-06/15
School of Computing Science, Faculty of Applied Science, Simon Fraser University, Burnaby, BC, Canada	Adjunct Faculty	01/13-12/22
Terry Fox Laboratory	Distinguished Scientist	07/15-12/22

British Columbia Cancer Agency		
Department of Medical Genetics, Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada	Professor	07/15-12/22
Cytapex Bioinformatics Inc	CEO	08/16-05/20
Cytapex Bioinformatics Inc	Managing Director	05/20-12/22
Terry Fox Laboratory British Columbia Cancer Agency	Distinguished Scientist (Emeritus)	01/2023-present
Department of Medical Genetics, Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada	Professor (Emeritus)	01/2023-present
Dotmatics Inc.	Vice President & Research Director, Flow Cytometry	01/2023-present
SOULCAP Foundation (501(c)(3) nonprofit)	Founding Director	01/2024-present

(c) *Date of granting of tenure at U.B.C.:*

N/A

7. LEAVES OF ABSENCE

I experienced significant delays in my independent scientific career due to absence related to diagnosis of cancer in 2007, followed by surgeries to remove tumor material in 2007, 2008 and 2009.

8. TEACHING

(a) *Areas of special interest and accomplishments*

I enjoy teaching, especially in those areas of my specialized experience where I have the most to offer. I am most proud of developing and the Canadian Bioinformatics Workshop on-line course on flow cytometry bioinformatics. It has been wonderful to get emails from students around the globe who have found it through Google and enjoyed the content. In 2005, I received both an “A” grade from a peer review of teachings from the Medical Genetics Department of UBC, and the highest facilitator score (9.3/10) from the 2005 PBL in Bioinformatics ranked versus nine other faculty, including five faculty from UBC. BIOF501A and BIOF520 are participatory/problem-solving courses and operate through student flexibility and my facilitation versus traditional lecturer-controlled instruction.

(b) *Courses Taught*

Synopsis: I have been teaching BIOF 520 Problem-Based Learning In Bioinformatics and BIOF 501A Special Topics in Bioinformatics each of the last 6 years, these are UBC courses that are available to bioinformatics students from SFU as well, as they are the two core-required courses for the CIHR-funded Bioinformatics Training Program co-led by faculty at UBC and SFU (including myself), and are team taught by faculty from both Universities. 501A is a student led discussion course (functioning much like a journal club) where each week students present recent papers in the field of bioinformatics of their choice and followed by a Q&A session where the students are also marked on their participation. I have co-coordinated the Special Topics course with one SFU faculty each year and we each marked the students**.** I have been requested to present “Data standards and integration” each year for the BIOF520 PBL course and was responsible for all content, presentation and marking for this component. All other courses I was responsible for developing, presenting and marking for my component of the course.

Year	**Course Number**	**Scheduled Hours**	**Class Size**	**Hours Taught**				
				Lectures	**Tutorials**	**Labs**	**Other**	
							PBL	**Student led discussion**
1998	BIOL 334	26	15			32 (TA)		
1999	BIOL 334	26	16			32 (TA)		
2005	MEDG 548C	2	12	2				
2005	MEDG 420	1	15	1				
2006	GENE501 (UBC)/$^{/}$MBB50	26	8				26	
2006	MEDG 430	4	15	4				
2007	MBB505(SFU)	26	12				26	
2007	MBB659(SFU)/ MEDG584C	4	12				4	
2008	BIOF501A (UBC)/ [1]MBB505(SFU)	26	11					26
2008	BIOF520(UBC) / MBB659(SFU	4	11				4	
2009	BIOF501A (UBC)/ MBB505(SFU)	26	12					26
2009	BIOF520(UBC) /MBB659(SFU	4	12				4	
2010	BIOF501A (UBC)/ MBB505(SFU)	26	9					26
2010	BIOF520(UBC) / MBB659(SFU	4	9				4	
2011	BIOF 501A/ MBB505(SFU)	26	12					26
2011	BIOF 520/ MBB659(SFU	4	12				4	
2011	STAT540 (UBC)	2	30	2				
2012	BIOF501A (UBC)/MBB505 (SFU)	32.5	9					26

2012	BIOF520(UBC) /MBB659(SFU	4	12				4	
2013	BIOF501A (UBC)/ MBB505(SFU)	26	13					26
2013	BIOF520(UBC) /MBB659(SFU)	4	13				4	
2014	BIOF501A (UBC)/MBB505 (SFU)	26	14					26
2014	BIOF520(UBC) /MBB659(SFU)	4	12				4	
2015	PATH 711	1	13					
2015	BIOF 501A	18	8					
2016	BIO 501A	22	8					
2017	BIO 501A	22	15					
2018	BIOF520(UBC) /MBB659(SFU)	4	13					
2020	BIOF520(UBC) /MBB659(SFU)	4	15					
2021	BIOF520(UBC) /MBB659(SFU)	4	18					

Brief Descriptions of the Principal Courses Taught:

BIOL 334 (Basic Genetics): Mendelian genetics, chromosome theory of heredity, linkage, mutation, mapping, gene structure and function, gene interaction, quantitative genetics, population genetics.

MEDG 548C (Directed Studies): A series of laboratory sessions, directed readings and directed counselling interviews related to selected areas of Medical Genetics.

MEDG 420 (Human Genomics and Medical Genetics): Sequence and structure of the human genome. Human genetic evolution. Identification of genes affecting normal and pathological variation. Molecular mechanisms of genetic diseases and disorders. Medical applications of human genetics.

BIOF 501A/MBB505 (SFU) (previously MBB659(SFU)/MEDG584C) (Special Topics in Bioinformatics)
This discussion-based bioinformatics course expose students to the latest developments in bioinformatics analysis and algorithms. It runs in conjunction with VanBug Seminar Series (http://vanbug.org), in which the students will have the opportunity to meet and discuss their work with guest speakers, both local and international scientists.

MBB659(SFU)/BIOF 520 (previously MBB505(SFU)/BIOF 501A) Problem Based Learning in Bioinformatics: The problem-based learning course will develop students' ability to exchange ideas in small groups focused on real but simplified problems in bioinformatics. Problems will be carefully selected to cover multiple areas of bioinformatics research. This is an advanced bioinformatics course that assumes the student has previous bioinformatics training. This course is identical to CMPT 505 and students cannot take both courses for credit. Prerequisite: MBB 741 or equivalent bioinformatics course (undergraduate or graduate). My section is on "Data standards and data integration".

STAT540 (Statistical Methods for High Dimensional Biology): The objectives of this course are to provide students from the computational sciences, especially statistics, an introduction to the exciting problems arising in genomic research; and to provide students with a primary background in molecular biology and biochemistry with an introduction to the statistical techniques that are particularly relevant for genomic data. Emphasis is on gene expression profiling, but I provided a lecture on high dimensional flow cytometry data analysis.

(c) Other Teaching of Undergraduates, Graduates and Postgraduates

N/A

(d) Students Supervised

Synopsis:

MSc Total = 7; 1 current; 6 completed
PhD Total = 12; 2 current; 9 completed, 1 withdrew
PDF Total = 7; 0 current; 7 completed
Additional HQP = 51; 5 current

Graduate Students and Supervised and/or Co-Supervised

Student Name	Program Type	Start	Finish	Duration (months	Principal Supervisor	Co-Supervisor	Current Position/ Trainee Awards
Shang-Jung (Jessica) Lee	*MSc, Genetics (thesis) "Prediction of Graft-versus-Host Disease based on Supervised Temporal Analysis on High-Throughput Flow Cytometry"*	01/2005	06/2007	29	**R. Brinkman**		Teacher at Kahnawake Learning Centre
Kenneth Lo	PhD, Statistics *"Statistical Methods for High Throughput Genomics"*	05/2006	07/2009	38	R. Gottardo	**R. Brinkman**	Data Scientist, Mobile Services Platform at eBay

Parisa Shooshtari	PhD, Computer Science *"Computational Techniques For Flow Cytometry. The Application for Automated Analysis of Innate Immune Response Flow Cytometry Data"*	06/2007	04/2012	58	**R. Brinkman**	A. Gupta (UBC)	Assistant Professor (tenure track) at Schulich School of Medicine & Dentistry
Kieran O'Neill	PhD, Bioinformatics *"Leukemia Diagnosis by Automated Analysis of Flow Cytometry Data"*	09/2008	09/2014	60	**R. Brinkman**		Bioinformatics process development coordinator at BC Cancer
Adrian Cortes	MSc, Bioinformatics (thesis) *"Automated Analysis of High-Throughput Flow Cytometry Data from Hemoatopoietic Stem Cell Experiments"*	09/2008	03/2010	18	**R. Brinkman**		Scientific Director GlaxoSmithKline
Habil Zare	PhD, Computer Science *"Automatic Analysis of Flow Cytometry Data and its Application to Lymphoma Diagnosis"*	04/2009	10/2011	30	**R. Brinkman**	V. Kabanets (UBC)	Tenure Track Assistant Professor, Computer Science Department at Texas State University.
Nima Aghaeepour	PhD, Bioinformatics *"Computational analysis of flow cytometry data for diagnosis, biomarker discovery, and marker panel design"*	09/2009	12/2012	39	**R. Brinkman**	H. Hoos (UBC)	Assistant Professor at Stanford University

Radina Nikolic	MSc, Bioinformatics (Department of Continuing Education & Department of Statistics Oxford Bioinformatics Programme, St. Cross College, University of Oxford; thesis) *“Automated Semi-supervised Cell Population Identification in Flow Cytometry Data”*	12/2009	05/2010	5	**R. Brinkman**	A. Dalby (Oxford)	Research Associate, British Columbia Institute of Technology
Melanie Courtot	PhD, Bioinformatics *“Adverse events following immunization: metadata standardization, automatic case classification and signal detection”*	09/2009	04/2014	49	**R. Brinkman**		Director of Genome Informatics & Principal Investigator at Ontario Institute for Cancer Research
Adrin Jalali	PhD, Bioinformatics *“Automated Cell Population Analysis in Flow Cytometry Data”*	09/2011	12/2012 (withdrew from program)	15	**R. Brinkman**		Machine Learning EngineerMachine Learning Engineer Hugging Face
Marjan Farahbod	MSc, Bioinformatics (Department of Computing Science, Chalmers University of Technology, Göteborg University, Sweden; thesis) *“Comparison of Clustering Methods in Flow Cytometry*	09/2011	09/2012	12	**R. Brinkman**		Postdoctoral Researcher, Simon Fraser University

	Analysis Including Ensemble Clustering”						
Benedikt Brink	PhD, Technology (German-Canadian DFG International Research Training Group (1906/1), Faculty of Technology, Bielefeld University Bielefeld, Germany *“Polyomics Visualization"*	04/2015	10/2015	6	T. Nattkemper	**R. Brinkman**	Bioinformatician, Cytapex Bioinformatics Inc.
Alice Yue	MSc, MADD-Gen, SFU “*Feature-based Comparison of Flow Cytometry Data*”	09/2015	08/2017	24	**C. Chauve**	**R. Brinkman**	Bioinformatician, METAFORA
Markus Lux	PhD, MADD-Gen, SFU (Rotation student) “*Efficient Grouping Methods for the Annotation and Sorting of Single Cells*”	05/2016	12/ 2016	6	**R. Brinkman (PhD rotation supervisor)**		Software Architect, QAware
Albina Rahim	PhD, Bioinformatics	09/2016	Present (on medical leave of absence till May 2026)	-	**R. Brinkman**		
Alice Yue	PhD Candidate, Computer Science, SFU	09/2017	04/2022	-	**C. Chauve**	**R. Brinkman**	METAFORA Biosystems
Sherrie (Xue) Wang	MSc, Bioinformatics “*Flow Cytometry Data Analysis Pipeline:*	01/2018	04/2020	27	**R. Brinkman**		UBC Medical School

	Data Quality Control Tool Development and Biomarker Discovery”						
Sebastiano Montante	PhD, Bioinformatics	10/2018	04/2024	-	**R. Brinkman**		NSERC CREATE scholarship 2019
Yixuan (Eve) Chen	MSc, Bioinformatics	08/2020	06/2024	-	**R. Brinkman**		

Graduate Student Supervisory Committees

Student Name	**Program Type**	**Start**	**Finish**	**Supervisor**	**Department or Program**
Benjamin Good	PhD	2006	2009	M. Wilkinson	Bioinformatics
Daniel Horspool	PhD	2008	2009	R. Holt	Bioinformatics
Ying Zhang	PhD	2005	2012	D. Mager	Genetics
Niels Hanson	PhD	2011	2015	S. Hallam	Bioinformatics
Paul Miller	PhD	2011	2016	C. Eaves	Experimental Medicine
Adriana Sedeno	PhD	2012	2015	P. Pavlidis	Bioinformatics
Rebecca De Souza	PhD	2010	2015	B. Leavitt	Medical Genetics
Dean Attali	MSc	2015	2016	J. Bryan	Bioinformatics
Oscar Urtatiz	PhD	2015	2019	C. Van Raamsdonk	Medical Genetics
Abdur Rahman M. A. Basher	PhD	2015	2020	I. Birol	Bioinformatics
Allen Zhang	PhD	2016	2019	S. Shaw, W. Wasserman	Bioinformatics
Elijah Willie	MSc	2018	2020	S. Mostafavi	Bioinformatics
Uyen Nguyen	MSc	2019	2020	M. Levings	Experimental Medicine
Yue (Will) Huang	MSc	2020	Present	K. Haas, P. Pavlidis	Bioinformatics
Cecilia Yang	MSc	2022	Present	I. Birol	Bioinfoirmatics

Postgraduate Students Supervised

Name	**Program Type**	**Start**	**Finish**	**Supervisor**	**Current Position**
Sumitra Nair	Post-doctoral Fellow	Jul 2008	May 2009	**R. Brinkman**	Post Doctoral Fellow, Center for the Environmental Implications of Nanotechnology, California Nanosystems Institute, University of California

Ali Bashashati	Post-doctoral Fellow	Mar 2007	Mar 2010	**R. Brinkman**	Staff Scientist/Director of Operation (Computational Biology group, Molecular Oncology Dept)
Alireza Khodabakhshi	Post-doctoral Fellow	Sept 2008	May 2010	**R. Brinkman**	Staff Scientist, BC Cancer Agency/Genome Sciences Center
Emad Ramadan	Post-doctoral Fellow	Aug 2010	Aug. 2011	**R. Brinkman**	Unknown (left without notice to return to Egypt during its period of unrest to be with family)
Faysal El Khettabi	Post-doctoral Fellow	Aug 2010	Aug. 2013	**R. Brinkman**	(left Science)
Josef Spidlen	Post-doctoral Fellow, 2008 Research Associate, 2014 Staff Scientist, II	Oct 2005	Oct 2016	**R. Brinkman**	International Society for the Advancement of Cytometry Scholar; Bioinformatics Software Engineer, FlowJo
Stepan Grinek	Postdoctoral Fellow	Oct 2016	Oct 2018	**C. Chauve** **R. Brinkman (co-supervisor)**	Maurano Lab, Institute for Systems Genetics, NYU Langone Health
Razzi Movassaghi Jorshari	Postdoctoral Fellow	Mar 2020	Mar 2022	**R. Brinkman**	Data Scientist. Tutela

Other Students Supervised and/or Co-Supervised

Name	**Program Type**	**Year**	**Principal Supervisor**	**Program**
Ben Smith	Summer Student	2005	**R. Brinkman**	BSc, Engineering
Simon Chen	Co-op Student Supervisor	2002	**R. Brinkman**	BSc, Computer Science
Linda Lei	Co-op Student Supervisor	2005	**R. Brinkman**	BSc, Statistics
Jessica Lee	Research Rotation Supervisor	2005	**R. Brinkman** (co-supervised with P. Lansdorp)	MSc, CIHR/MSFHR Bioinformatics Training Program
Tysen Li	Co-op Student Supervisor	2005-2006	**R. Brinkman**	BSc, Statistics
Wendy Zhang	Co-op Student Supervisor	2005-2006	**R. Brinkman**	BSc, Statistics
Simon Claret	Co-op Student Supervisor	2006	**R. Brinkman**	BSc, Computer Science
Morgan Langille	Research Rotation Supervisor	2006	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program

Eng-Liang Ch’ng	Co-op Student Supervisor	2006	**R. Brinkman**	BSc, Computer Science
Di Wang	Research Rotation Supervisor	2006	**R. Brinkman**	MSc, CIHR/MSFHR Bioinformatics Training Program
Anna Krasnova	Co-op Student Supervisor	2007	**R. Brinkman**	BSc, Statistics
Stanley Wong	Co-op Student Supervisor	2007	**R. Brinkman**	PhD, Statistics
Yun-Feng Dai	Co-op Student Supervisor	2008	**R. Brinkman**	PhD, Statistics
Donghong Wu	Co-op Student Supervisor	2008	**R. Brinkman**	MSc, Statistics
Miao (Maggie) Yu	Co-op Student Supervisor	2009	**R. Brinkman**	MSc, Statistics
Settimo Szliske	BCIT Practicum Supervisor	2006-2007	**R. Brinkman**	Bachelors of Technology (Computer Systems)
Jeffrey Chu	Undergraduate Directed Studies Supervisor	2005-2006	**R. Brinkman**	BSc, Computer Science
Evengy Maksakov	Undergraduate Directed Studies Supervisor	2006	**R. Brinkman**	BSc, Computer Science
Nancy Weng	Undergraduate Directed Studies Supervisor	2006	**R. Brinkman**	BSc, Computer Science and Biology
Xiaohui Chen	Research Rotation Supervisor	2007	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
James Wagner	Research Rotation Supervisor	2007	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Nick Wiebe	Research Rotation Supervisor	2007	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Kenneth Lo	Research Rotation Supervisor	2007	**R. Brinkman**	PhD, MITACS Internship
Denil Wickrama	Research Rotation Supervisor	2008	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Nima Aghaeepour	Research Rotation Supervisor	2008	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Nima Aghaeepour (2nd rotation)	Research Rotation Supervisor	2009	**R. Brinkman** (co-supervised with C. Eaves)	PhD, CIHR/MSFHR Bioinformatics Training Program
Timothy Au-Yeung	Research Rotation Supervisor	2009	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program

Andrew Roth	Research Rotation Supervisor	2010	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Patrick Tang	Research Rotation Supervisor	2010	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Laura Cheung	Research Rotation Supervisor	2013	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training Program
Lisa Wei	Research Rotation Supervisor	2014	**R. Brinkman**	Summer student
Beryl Zhuang	Research Rotation Supervisor & Mentor	2014	**R. Brinkman**	PhD, CIHR/MSFHR Bioinformatics Training
Sibyl Drissler	Supervisor	2016	**R. Brinkman**	NSERC URSA summer studentship (UBC)
Justin Meskas	HSA Bioinformatician	2013 - 2019	**R. Brinkman**	Cytapex Bioinformatics
Mehrnoush Malek	HSA Biostatistical Analysis	2012 - 2022	**R. Brinkman**	Senior Statistical Programmer at Cytel
Albina Rahim	HSA Bioinformatition	2015 - 2016	**R. Brinkman**	PhD candidate, Brinkman Lab
Sibyl Drissler	Bioinformatics Technologist	2016 - 2018	**R. Brinkman**	Bioinformatics Technologist, Hoodless Lab, BC Cancer
Sherrie Wang	Research Student	2017 - 2018	**R. Brinkman**	MSc, Bioinformatics, UBC, Brinkman Lab
Daniel Yuzo Okada Yokosawa	Bioinformatics Technician	2018 - 2023	**R. Brinkman**	Staff
Dylan Whitney	Undergraduate Trainee	2018 - 2019	**R. Brinkman**	UBC undergraduate program
Rebecca Ruthven	NSERC URSA summer studentship	2019 - 2019	**R. Brinkman**	McGill , NSERC URSA summer studentship (UBC)
Marjan Najafabadipour	Visiting International Research Student	2019 - 2019	**R. Brinkman**	PhD student, Software, Systems and Computing , Universidad Politécnica de Madrid (UPM) in Madrid, Spain
Uyen Nguyen	Research Rotation Supervisor	2019	**R. Brinkman**	MSc, Experimental Medicine
Yixuan Chen	Visiting International Research Student	2019 - 2020	**R. Brinkman**	Biology Undergraduate student; Wuhan University, China Expected graduation 2020
Yuta Kawakami[1]	Visiting graduate student, JNIT program	Sept 2019	**R. Brinkman**	Japanese National Institute of Technology
Richard (Xukun) Chen	Internship	Jan 2020	**R. Brinkman**	MBA, Vancouver Island University; Master of Science

---

				of International Management, University of Hertfordshire
Leon Li	Internship + Co-op	Jan 2022 – May 2023	**R. Brinkman**	UBC Computer Science
Quentin Michalchuk	Internship	May 2022 – August 2022	**R. Brinkman**	UBC Computer Science
Jhannelle D Francis	Visiting Researcher	May 2022 – August 2022	**R. Brinkman**	University of Manitoba
Sameer Shankar	Co-op student	Aug 2022 – May 2023	**R. Brinkman**	UBC Computer Science
Alan Milligan	Research Student	Sep 2022– Dec 2022	**R. Brinkman**	UBC Computer Science

(e) Continuing Education Activities

1. Attendance at major flow cytometry meetings, especially International Society for Advancement of Cytometry (bi-yearly from 2004-2010, then yearly as conference switched to higher frequency).

2. Rounds regularly attended: Terry Fox Laboratory Work-In-Progress (once a week) 2003-present; presented 4 times.

(f) Lecturer (indicate university/organization and dates)

1. Bioinformatics (1 hour) Simon Fraser University, 2005

(g) Educational Leadership

N/A

(h) Curriculum Development & Innovation

1. Two-day hands-on course, I developed the entire content of the course and was the lecturer, Canadian Bioinformatics Workshop. Flow Cytometry Data Analysis Using R. Toronto ON, Jun 17-18, 2013. 6 lecture modules including code, data files, slides, and accompanying audio recordings of presented material are available at http://bioinformatics.ca/workshops/2013/flow-cytometry-data-analysis-using-r-2013.

2. Member, International Society for Advancement of Cytometry, E-learning Delivery Task Force (2014-2016). We are developing an extensive on-line lecture series covering all aspects of cytometry being delivered free to members of the society through cytou.org. 20 PIs responsible for all content, I regularly attended bi-weekly calls to review additional content

3. Bioinformatics Program Advisory Committee, Langara College. 2022-

(i) Other Teaching & Learning Activities

1. Canadian Bioinformatics Workshops (80 hours), 1999
2. The Canadian Bioinformatics Resource for Industry (CBRI) (27 hours), 2003
3. Tutorial co-developer and instructor. Algorithmic Analysis of Flow Cytometry Data; (Part 1 and 2; 3hours). Prepared curriculum and taught scientific tutorial session. Congress of the International Society for Advancement of Cytometry (CYTO2014).
4. Mentor, International Society for the Advancement of Cytometry, Shared resource Lab Emerging Leaders Program to Rob Salomon (2014-2016).
5. Guest Lecturer. Wellcome Trust Advanced Course: Immunophenotyping: Generation and Analysis of Immunological Datasets. Hinxton, Cambridge, UK, Feb 21-27, 2016.

9. SCHOLARLY AND PROFESSIONAL ACTIVITIES

(a) Areas of special interest and accomplishments

1. My research is focused on developing automated methods for flow cytometry data analysis and applying them to medical genetics related research programs, mainly for methodologies for correct and timely diagnosis of disease. Significant effort has been focused throughout my career on developing open data and metadata standards and open tools for the technology for the community to enable bioinformatics across the community. I coordinated these activities under the auspices of the International Society for Advancement of Cytometry (ISAC) for which I chaired the Data Standards Task Force from 2008-2020, leading the publication of several standards for the technology. ISAC recognized my contributions to the field by awarding me the distinction of ISAC Scholar in 2006. I continue to be an active member of the flow cytometry community, with various roles within the Society, culminating with my current position on ISAC Council. I was also awarded both a Michael Smith Foundation for Health Research (MSFHR) Scholar Award (and operating grant; 2007-2013) and a Terry Fox Research Institute New Investigator Award (and operating grant; 2010-2013) in recognition of my contributions to the field of flow cytometry informatics. In 2018, I was awarded the Distinguished Service award from the International Society for Advancement of Cytometry (ISAC) in recognition of my service and contributions of the success to the Society and the field of flow cytometry informatics. In 2020, I was acknowledged by the Department of Medical Genetics at UBC for Outstanding Academic Performance (OAP) for the 2019 and 2020 calendar years.
2. I was recognized by ScholarGPS as a Highly Ranked Scholar (Lifetime): top 0.02% of all scholars worldwide, ranked #2 globally in Flow Cytometry (5-year period), and #13 lifetime. A 2025 bibliometric network analysis of 283,000+ papers and 500,000+ authors identified me as one of the "most influential contributors" and "core network nodes" in flow cytometry, alongside Virginia Litwin, Andrea Cossarizza, and J. Paul Robinson.

(b) Research or equivalent grants (indicate under COMP whether grants were obtained competitively (C) or non-competitively (NC)). ***BOLD = current funding***

Synopsis:

61 research grants ($59,609,370 total; $7,721,992 to RB)
34 as PI ($5,545,881 total)
25 as co-PI of dual/multi-PI grants

Granting Agency	Subject/Title	COMP	$ per Year (CAD)	Years	Principal Investigator	Co-Investigators
OPERATING GRANTS						
Canadian Institutes of Health Research (CIHR)	Bioinformatics standards for flow cytometry	C	5,500	Jan 2004	**R. Brinkman**	
*National Institutes of Health (NIBIB)	Bioinformatics standards for flow cytometry	C	Y1:299,256 Y2:296,564 Y3:256,573 Y4:219,740 TOTAL: 1,072,133	May 2005 – Apr 2009	**R. Brinkman**	C. Smith P. Haaland R. Gentleman M. Ochs A. Treister
BC Transplant Foundation	Diagnosis of graft versus host disease using high throughput flow cytometry	C	30,000 TOTAL: 60,000	May 2006- Apr 2007	C. Smith	**R. Brinkman**
MITACS	Statistical methods for high throughput flow cytometry	C	15,000	Jul 2007	R. Gottardo	**R. Brinkman**
**Michael Smith Foundation of Health Research	Development and application of data standards for flow cytometry	C	62,500 TOTAL: 142,500	Jul 2007 –Jun 2010	**R. Brinkman**	
BCCA/ MSFHR Inter-disciplinary Recruitment Training Incentive	Flow cytometry bioinformatics	C	10,000	Sept 2008	**R. Brinkman**	
CIHR/HeRRO	Automatic bioinformatics pipeline for the analysis of clinical lymphoma flow cytometry data	C	5,000	Apr 2008 – Mar 2009	**R. Brinkman**	
National Institutes of Health (NIBIB)	The statistical and computational analysis of flow cytometry data	C	Y1: 468,120 Y2: 407,245 TOTAL: 1,686,994 (est)	Dec 2008- Nov 2012	R. Gottardo	**R. Brinkman**
Genome Canada/ Genome BC/ Genome Quebec	High throughput high-dimensional multi-parametric analysis of the immune system	C	Y1: 402,700 Y2: 365,699 TOTAL: 768,399	Sept 2008- Aug 2010	**R. Brinkman** R. Sekaly	R. Gottardo RL. Blanc L. Greller R. Somogyi P. Wilkinson
PHAC/CIHR	PHAC/CIHR influenza research network	C	TOTAL: 10,403,100 [1]	Sept 2009- Aug 2012	[2] See details below	[3] See details below
Canadian Institutes of Health	Statistical analysis of clinical lymphoma data for automated quality assurance of	C	68,228	Jul 2009 – Jun 2010	**R. Brinkman**	R. Gascoyne R. Gottardo A. Weng

	diagnosis and biomarker identification					
BCCA/ MSFHR Recruitment Training Incentive	Flow cytometry bioinformatics	C	10,000	Sept 2009	**R. Brinkman**	
Canadian Institutes of Health	CIHR-MOST team in CML treatment predictors - clinical trial to predict imatinib resistance (CML-CMT)	C	10,000	Jul 2009 – Jun 2009	C. Eaves	**R. Brinkman** Z. Chen, D. Forrest X. Jiang J. Li CA. Smith DP. Wu RC. Zhao Y. Zhao
National Institutes of Health	The statistical and computational analysis of flow cytometry data (administrative supplement)	C	83,800	Jun 2010- April 2011	**R. Brinkman** R. Gottardo (PI of Parent Grant; supplemental award is for work exclusively in my group)	
International Society for Advancement of Cytometry	International flow cytometry data repository	NC	94,436	June 2010- May 2011	**R. Brinkman**	
De Novo Software	Data standards for amnis image stream	NC	5,393	Nov 2010	**R. Brinkman**	
National Institutes of Health / National Institutes of Allergy and Infections Diseases	FlowCAP summit meeting	NC	29,193	Jul 2010	**R. Brinkman** R. Scheuremann	R. Gottardo J. Schoenfeld
National Institutes of Health / National Institutes of Allergy and Infections Diseases	FlowCAP-2 summit meeting	NC	40,000	Jul 2010	**R. Brinkman** R. Scheuremann	R. Gottardo J. Schoenfeld
Canadian Cancer Society Research Institute	Statistical and bioinformatics approaches to the classification of clinical lymphoma and leukemia data	C	Y1: 138,000 Y2: 123,280 Y3: 123.280 TOTAL: 384,560	Jul 2010 –Jun 2013	**R. Brinkman**	R. Gottardo A. Weng B. Dalal J. Kuruvilla R. Coupland S. Assouline P. Petrogiannis Haliotis
Terry Fox Research Institute	Flow informatics approaches for the identification of normal and malignant stem cells	C	Y1: 96,168 Y2: 112,667 Y3: 226,417 Y4: 83,417 TOTAL: 435,252	Nov 2010 – Oct 2013	**R. Brinkman**	C. Eaves P. Lansdorp A. Weng G. Krystal RK. Humphries
International Society for Advancement of Cytometry	International flow cytometry data repository	C	67,000	Jan 2011 – Jan 2012	**R. Brinkman**	

National Institutes of Health/ National Institutes of Allergy and Infections Diseases	Standardization of flow cytometry data analysis using lyoplates and FITMaN marker panels	C	Y1: 405,840 Y2: 405,840 (73,440/yr to RB) TOTAL: 811,680	Dec 2011 – Nov 2013	R. Gottardo	**R. Brinkman** R. Scheuermann D. Hafler H. Maecker
National Institutes of Health	Statistical and computational analysis of flow cytometry data (Renewal of above)	C	Y1: (48,600/yr to RB) TOTAL: 800,000	May 2012 - Apr 2016	R. Gottardo	**R. Brinkman**
International Society for Advancement of Cytometry	Flow cytometry data standards development	NC	50,000	Jan 2012-Jan 2013	**R. Brinkman**	
Prostate Cancer Canada	High-throughput discovery of prostate tumour initiating cells markers for prognosis and personalized medicine	C	Y1: 75,000 Y2: 75,000 (1,500/yr to RB)	Jul 2012-Jun 2014	R. Bristow	**R. Brinkman** L. Ailles
Wallace H. Coulter Foundation	International flow cytometry data repository	C	184,532	Apr 2012-Mar 2014	**R. Brinkman**	
International Society for Advancement of Cytometry	Flow cytometry data standards development	NC	$30,000 USD	Jan 2013-Jan 2014	**R. Brinkman**	
CytoBank Inc.	Flow Cytometry Data Standards	NC	$58,631	Sept 2012-June 2013	**R. Brinkman**	
Natural Sciences and Engineering Research Council of Canada (NSERC)	Automated analysis of high dimensional flow cytometry data	C	$43,500/yr CAD TOTAL: $215,000 CAD	Apr 2013-Mar 2018 (extended to Mar 2019)	**R. Brinkman**	
ISAC/Wallace H. Coulter Foundation	International flow cytometry data repository	NC	$115, 548 USD / yr TOTAL: $231,097 USD	May 2013-Dec 2014	**R. Brinkman**	
Leukemia and Lymphoma Society	Resolution of Intratumoral Heterogeneity in B-Cell NHL by Flow Cytometry	C	$383,518 USD/yr Total: $767,036 USD ($169,597 to RB)	Jan 2014-Dec 2015	A. Weng	**R. Brinkman** R. Gascoyne
Canadian Institutes of Health Research (CIHR)	The Canadian National Transplant Research Program	C	13,850,000 (10,000 to RB)	2014-2015 (RB component)	L. West (Leving)	105 investigators, 87 collaborators across 9 provinces
International Society for the Advancement of Cytometry	Flow Repository	NC	USD $100,000 plus $25,000	2015 (extended to Dec 2019)	**R. Brinkman**	
Genome BC	Defining the Mouse Cytome	C	CAD $200,000 CAD total	July 2015-Dec 2016	**R. Brinkman**	

BCCA Translational	Determining the role of donor-derived CD56$^{\text{bright}}$ regulatory NK (NK-reg) in chronic graft-vs-host disease	C	$30,000 CAD total $8,500 to RB	Sept 2015-Sept 2016	K. McNagny K. Shultz	**R. Brinkman**
Genome Canada Bioinformatics and Computational Biology Competition	Automated analysis of big Flow cytometry data	C	$249,994 CAD total $118,762 yr1, $131,232 yr2 ($64,566 to RB yr1, $66,666 to RB yr2)	Oct 01 2016 – Mar 31 2018	**R. Brinkman**	C. Chauve S. Mostafavi
Canadian Institutes of Health Research (CIHR)	Resolution of inter- and intra-tumoral heterogeneity in DLBCL using mass cytometry	C	$860,064 CAD total ($24,098 CAD per year to RB; $120,465 total)	Jul 2016 – June 2021	A. Weng	**R. Brinkman** C. Steidl
ALS Society of Canada (Discovery grant)	The role of peripheral inflammation in ALS: an exploratory study	C	$99,640 CAD($12,000 CAD total to RB)	Sept 2015 – Aug 2017	F. Rossi	**R. Brinkman**
Canadian Institutes of Health Research (CIHR)	Correlates of acquisition and immune control of primary Epstein-Barr virus infection in Ugandan infants	C	$326,233 CAD ($18,276.25 CAD total to RB)	Jul 2014 to Aug 2019	S. Gantt	C. Caspar, J. Cohen, T. Kollmann, P. Tang Collaborator: **R. Brinkman**
Providence Cancer Center	Improving work flow for peripheral blood immune phenotyping assays	NC	$28, 268 USD	Sept 2016 to May 2017	**R. Brinkman**	Yoshinobu Koguchi
National Institute of Allergy and Infectious Disease (U19) 1U19AI118608-01A1 F16-01098	Systems Biology to Identify Biomarkers of Neonatal Vaccine Immunogenicity (HIP-C)	C	Total (USD): $2,028,320 Y1 $1,959,643 Y2 $1.984.196 Y3 $2,057,593 Y4 $2,076,285 Y5 To RB: Project 2: 2,925 Y2 11,962 Y3 72,934 Y4 79,605 Y5 * DMC: 7,938 Y1 7,938 Y2 7,938 Y3 8, 573 Y4 7,938 Y5 * ** pending*	Dec 2016-Nov 2021	NPA: Ofer Levy Boston Children’s Hospital (BCH) Project 002 Lead: Ofer Levy DMC Lead: Alexander Ozonoff (BCH)	Tobi Kollman (co-PI on overall grant) **R. Brinkman** **(co-PI on Project 2 and Database Management Core - DMC)**
NIH (IOF) F17-02666 NIH Project Number 5U19AI118610-03	Dengue Human Immunology Project Consortium (DHIPC) Continued and Expanded Computational Analysis and	C	$5,350,863 USD award total; $311,372 yr1 $67,440 USD to RB yr1	May 2017 – May 2020 RB subaward Jul 2017 – Jun 2018	A. Fernandez-Sesma (Mount Sinai) R. Scheuermann (JVCI)	**R. Brinkman**

	Integration of Flow and Mass Cytometry Data Across HIP-C Centers (Renewal)					
NIH Common Fund	KOMP2 (Knockout Mouse Phenotyping Program) Production and phenotyping by the DTCC consortium	C	$90,000 CAD	Jun 2017 – Mar 2018	K. Lloyd (UC Davis)	L. Nutter (SickKids)
NIH F17-02270	Big Flow Cytometry Data: Reproducible Discovery and Statistical Modeling	C	$1,760,408 USD award total to RB: $72,900 USD/yr $364,500 USD total	Jul 2017 – (Jun 2022) Terminated Jan 31, 2021 by Finak (left FHCRC)	G. Finak (Fred Hutchinson Cancer Research Center)	**R. Brinkman (Consortium PI)** R. Gottardo C. Chauve
CIHR Team Grant: Human Immunology Initiative: Standardization Core	**Canadian Autoimmunity Standardization Core (CAN-ASC)**	**C**	**$ 1,500,000 CAD award total** **To RB:** **$10,000 Y2** **$10,000 Y3**	**Mar 2018 – Mar 2023**	**M. Levings (BC Children's Hospital Research Institute)**	**J.L. Bramson** **C. Des Rosiers** **JP. Dutz** **E. Haddad** **SM. Ivison** **J. Kimmelman** **SP. Lesage** **A. Prat** **JD. Rioux** **SA. Ritz** **SE. Turvey** **SM. Vercauteren** **JE. Wither** **(RB – collaborator)**
NIH Common Fund	KOMP2 (Knockout Mouse Phenotyping Program) Production and phenotyping by the DTCC consortium	C	$247,382 USD award total to RB : $64,920 USD total	Aug 2018 – Jul 2021	K. Lloyd (UC Davis)	L. Nutter (SickKids)
Canadian Institutes of Health Research (CIHR) Project Grant _* commercialization_	Machine Learning for Flow Cytometry Clinical Data and Trial Analysis	C	$317,475 CAD Award total	Apr 2020 – Jan 2022	**R. Brinkman**	A. Weng
Natural Sciences and Engineering Research Council of Canada (NSERC)	**Automated analysis of high dimensional flow cytometry data**	**C**	**$33,600/yr CAD** **TOTAL: $168,000 CAD**	**Apr 2020- Mar 2025**	**R. Brinkman**	
Cytapex Bioinformatics Inc. partnered with the BC Cancer Foundation, Ignite Campaign	Project Discovery	N	$30,000/ partner, CAD TOTAL: $60,000 CAD	Nov 2020	**R. Brinkman**	
BD Investigator Sponsored Study (ISS)	Developing an automated analysis pipeline for multiparametric flow cytometry based Acute myeloid	C	$51,000 total $0 to RB	Sep 2021 – Aug 2022	X. Wang (VCH)	Collaborators: A. Weng **R. Brinkman**

	leukemia MRD detection					
New Frontiers in Research Fund – Special Call	**A mobile gaming platform to accelerate flow cytometry data analysis**	**C**	**$237,970 total** **$60,000 to RB + $15K indirects**	**Mar 2022 – Feb 2023**	**J. Waldisphul (McGill)**	**R. Brinkman**
EQUIPMENT GRANTS						
CFI Leading Edge Fund (LEF)	Systems Analysis of Single Stem Cells	**C**	$7,488,178	2013	F Rossi	S Aparicio, **R Brinkman,** C Eaves, C Hansen, M Hirst, RK Humphries, T Keiffer, J Piret, TM Underhill.
TRAINING GRANTS						
CIHR Training Grant	Bioinformatics training for health research	C	$325,000 ($0 to RB) TOTAL: $2,367,222	Sept 2009-Aug 2015	S. Jones F. Brinkman	R Abugharbieh, C Chauve, M Ester, M Marra, C Sahinalp, D Baillie, N Chen, J Graham, I Meyer, W Wasserman, **R. Brinkman,** C Cherkasov, A Gupta, P Pavlidis, M Wilkinson, J Bryan, A Condon, P Hieter, F Pio
Natural Sciences and Engineering Research Council of Canada & SFU	CREATE: Computational Methods for the Analysis of Diversity and Dynamics of Genomes	C	$300,000 (NSERC) $100,000 (SFU) Total: $400,000 ($0 to RB)	Mar 2013-Feb 2018	C. Cenk Sahinalp	R. Brinkman P. Unrau, F. Brinkman, C. Chauve, M. Ester, J. Chen, C. Collins, S. Shah; A, Shriraman, N. Rajapakse
CFI Innovation Fund 2017	Multimodal Development of the CHIMERA Platform of Trauma	C	4, 549, 881	2017	C. Wellington	R. Brinkman P. Cripton D. Namjoshi W. Tetzlaff W. Panenka I. Welch P. Kozloeski D. Lampron S. Motafavi S. Salcudean

1. Value of award incorrect in CIHR database
2. SA Halperin, RA Bortolussi, JP Collet, G De Serres, MM Johnson, JC Kwong, SA McNeil, DW Scheifele, BJ Ward
3. UD Allen, MK Andrew, JM Ansermino, ME Appleton, JA Bettinger, GL Bjornson, G Boivin, EA Bone, T. F. Booth; **R. Brinkman**, DL Buckeridge, SG Campbell, LW Chambers, AU Chandran, CL Cooper, M Courtot, NS Crowcroft, JA Dickinson, M Dionne, SR Dobson, R Elliott, MS Finkelstein, K Fonseca, DM Gallant, IM Gemmill, JE Graham, S Grono, M Guay, GJ Gubitz, DA Haase, BA Halperin, GW Hammond, A Hanrahan, TF Hatchette, E Henderson, BL Johnston, TM Karnauchow, JD Kellner, FE Kolbe, TR Kollmann, M Landry, JM Langley, BJ Law, NM Le Saux, MB Loeb, AJ Loewen, JC MacDonald, NE MacDonald, AE McCarthy, JE McElhaney, AJ McGeer, HR McKim, DL Moore, AK Petrich, M Petric, GN Predy, MN Primeau, C Quach-Thanh, K Rockwood, VR Roth, E Rubinstein, ML Russell, BH Sander, LJ Sauve, C Sikora, CD Skedgel, MJ Smieja, BR Smith, KN Suh, JA Talbot, B Tapiero, G Trudeau, OG Vanderkool

* NIH grant scored at the 11th percentile (Priority Score 162) on the first application.
** Top ranked application, peer review conducted by the Michael Smith Foundation for Health Research

(c) Research or equivalent contracts, including funding for clinical trials (indicate under COMP whether grants were obtained competitively (C) or non-competitively (NC). ***BOLD = current funding.***

Granting Agency	Subject/Title	COMP	$ per Year (CAD)	Years	Principal Investigator	Co-Investigators
Vancouver Coastal Health Authority	Statistical and bioinformatics support and development	NC	90,000 TOTAL: 120,000	Jan 2006 –Dec 2009	**R. Brinkman**	
Bristol-Myers Squibb	A predictive test of tyrosine kinase inhibitor resistance in newly diagnosed patients with CML	C	100,000 (0 to RB)	Dec 2010-Nov 2012	C. Eaves	**R Brinkman** X. Jiang C. Smith D. Forrest L. Foltz
Bristol Myers Squibb (BMS)	Automated analysis of high dimensional flow cytometry data	C	58,052	Jan 2014-Dec 2015	**R. Brinkman**	
Celgene	Automated analysis of high dimensional flow cytometry data	C	36, 753	Sep 2014-August 2015	**R. Brinkman**	
Genocea	Analysis of Large Datasets	C	32,083.87	06/2015-11/2015	**R. Brinkman**	

(d) Invited Presentations

Synopsis:

- **134 invited talks (national and international). Since 2011 I have increasingly received unsolicited requests for invited talks in which the hosting organization fully supported all travel, including within Canada, US, EU as well as in China, New Zealand, Switzerland, South Africa and Australia**

1. Using age of onset predictions to design clinical trials for Huntington's Disease. 1999 Huntington Study Group Meeting, Palm Beach FL, Jan 21-24, 1999.
2. Using age of onset predictions to design clinical trials for Huntington's Disease. 1999 Genetic Testing Group Meeting, San Francisco CA, Feb 15, 1999.
3. Developing a bioinformatics pipeline for gene discovery. Canada's Michael Smith Genome Sciences Centre, Vancouver BC, Sep 21, 2003.
4. Developing a bioinformatics pipeline for gene discovery. BC Cancer Research Centre, Vancouver BC, Sep 28, 2003.
5. Bioinformatics standards and data integration: impact on clinical research. Department of Molecular Biology and Biochemistry, Simon Fraser University, Vancouver BC, Mar 17, 2005.
6. Bioinformatics standards for flow cytometry. 15th Cytometry Development Workshop: Technologies for Cell Analysis, Pacific Grove CA, Oct 27-29, 2005.
7. Minimum information for a fluorescence activated cell experiment. 1st Functional Genomics Ontology (FuGO) Meeting. Philadelphia PA, Feb 13-15, 2006.

8. What aspects of software should be standardized. Standards, Numbers, and New Technology: Flow Cytometry Evolving. 2006 Northwest Regional Cytometry Meeting, Portland OR, Mar 17-18, 2006.
9. Data standards for flow cytometry. 23rd Annual International Congress of the International Society for Analytical Cytology, Quebec City PQ, May 20-24, 2006.
10. Opening the gate to high throughput flow cytometry: A Graft versus Host Disease example. 23rd Annual International Congress of the International Society for Analytical Cytology, Quebec City PQ, May 20-24, 2006.
11. Data standards for flow cytometry. 1st Flow Informatics and Computational Cytometry Society Meeting, Fred Hutchinson Cancer Research Center, Seattle WA, Sep 20-21, 2006.
12. Bioinformatics data standards for flow cytometry. 16th Cytometry Development Workshop, Pacific Grove CA, Oct 20-23, 2006.
13. Data standards for flow cytometry. 2nd Flow Informatics and Computational Cytometry Society Meeting, Fred Hutchinson Cancer Research Center, Seattle WA, Nov 7-8, 2006.
14. Gates to the road forward: data standards for high throughput flow cytometry - order in cytometric complexity: quantitation, inference, and data management. 2007 Northwest Regional Cytometry Meeting, Fred Hutchinson Cancer Research Center, Seattle WA. Mar 23-24, 2007.
15. Bioinformatics for flow cytometry and its application to Graft versus Host Disease (GvHD). BC Cancer Agency Seminar Series, Vancouver BC, Apr 2, 2007.
16. Data standards for flow cytometry. NIH/DAIT Bioinformatics Summit, Gaithersburg MD, May 7-8, 2007.
17. Minimum information about a flow cytometry experiment. NIAID Annual Centers Program Progress Meeting, Mount Sinai School of Medicine, New York NY, Jun 8, 2007
18. MIFlowCyt: Minimum Information about a Flow Cytometry experiment. DAIT/NIAID/NIH Immune Modeling Information Sharing Meeting, Bethesda MD, Nov 7, 2007.
19. Minimum information about a flow cytometry experiment. Northwest Regional Cytometry Meeting, Portland OR, Mar 13, 2008.
20. Minimal information about a flow cytometry experiment. 1st Minimum Information for Biological and Biomedical Investigations, European Bioinformatics Institute, Hinxton, United Kingdom, Apr 2-3, 2008.
21. Flow informatics and computational cytometry Society and NCIC-CTG: opportunities for collaborative science. NCIC Clinical Trials Group Meeting, Toronto ON, May 1-4, 2008.
22. Automated analysis of clinical flow cytometry data for novel biomarker identification. NCIC Clinical Trials Group Meeting. Toronto ON, May 1-4, 2008.
23. The Analytical Cytometry Standard (ACS). A New Standard for Cytometry Data Being Developed by ISAC's Data Standards Task Force. 24th Annual International Congress of the International Society for Analytical Cytology, Budapest Hungary, May 17-21, 2008.
24. The Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) ISAC Standard. 24th Annual International Congress of the International Society for Analytical Cytology, Budapest Hungary, May 17-21, 2008.
25. An automatic pipeline for the analysis of flow cytometry data: preliminary results on lymphoma. 24th Annual International Congress of the International Society for Analytical Cytology, Budapest Hungary, May 17-21, 2008.

26. Data standards and computational approaches to facilitate high-throughput flow cytometry. Bioinformatics in immunology, vaccinology and cohort studies Symposium. Vancouver BC, Dec 4, 2008.
27. An open source software framework for high throughput flow cytometry data analysis. Flow Cytometry High Content Analysis. Simon Fraser University. Burnaby BC, Jul 24, 2009.
28. An open source software framework for high throughput flow cytometry data analysis. Flow Cytometry High Content Analysis. VanBUG (Vancouver Bioinformatics Users Group). Vancouver BC, Sept 17, 2009.
29. An open source software framework for high throughput flow cytometry data analysis. Flow Cytometry High Content Analysis. Cambridge Healthtech Institute. Boston MA. Sept 22-23, 2009.
30. The analytical cytometry standard. ISAC Image Data Standards Workshop. Seattle WA, May 13, 2010.
31. Estimating the number and initial position of cell populations for automated gating. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010.
32. FlowCAP: Flow Cytometry: Critical Assessment of Population identification methods. Twentieth Cytometry Development Workshop: Technologies for Cell Analysis. Pacific Grove CA, Oct 20-24, 2010.
33. FlowCAP, FlowSuite, FlowSite. FICCS. Fred Hutchinson Cancer Research Center. Seattle WA, Nov 30, 2010.
34. **Invited speaker.** FLOSSflow: free/libre/open source software for high volume & high dimensional flow cytometry data. Becton Dickension Bioscience Bioinformatics Symposium. San Jose CA, Mar 3, 2011.
35. Opening the floodgates through automated flow cytometry analysis. King’s College London, London UK, Mar 11, 2011.
36. **Invited Keynote speaker**, Automated gating and analysis: state of the art and prospects. Northwest Regional Cytometry Meeting. Portland OR, Mar 24-26, 2011.
37. **Invited Keynote speaker**, Opening the floodgates through automated flow cytometry analysis. 2nd International Conference on Transplantomics and Biomarkers in Organ Transplantation. Barcelona Spain, Mar 13-15, 2011.
38. **Invited speaker.** Opening the floodgates through automated flow cytometry analysis. Transplantomics and Biomarkers in Organ Transplantation: Bioinformatics and Biostatistics. Barcelona Spain, Mar 13-15, 2011.
39. Automated gating and analysis: State of the art and prospects. 2011 Northwest Regional Cytometry Meeting. Portland OR, Mar 24-26 2011.
40. Computational analysis of flow cytometry data with R/BioConductor. CYTO 2011 XXVI Congress of the International Society for the Advancement of Cytometry, Baltimore MD, May 20-25, 2011.
41. Clustering on clusters: diagnosis and discover on the WestGrid. Ribbon cutting special guest speaker for WestGrid UBC High-Performance Computing launch, Vancouver BC, Jun 30, 2011.
42. **Invited speaker.** How I learned to stop gating and love the R. Western New York Flow Users Group. University of Rochester Medical Centre. Rochester NY, Jul 13, 2011.
43. Managing high throughput flow cytometry data. Institute for System Biology. Seattle WA, Sept 8-10, 2011.

44. Automated flow cytometry data analysis: we're loving' it. STEMCELL Inc, Vancouver BC, Sept 15, 2011.
45. **Invited speaker.** Automated flow cytometry data analysis: we're lovin' it. Great Lakes International Imaging and Flow Cytometry Association. Oconomowoc WI, Sept 30-Oct 3, 2011.
46. **Invited speaker.** Managing high throughout data. West Coast Association of Shared Resource Directors (WSASRD). Seattle WA, Oct 27-28, 2011.
47. **Invited speaker.** Gating is not enough: automate and let go. Canadian Cytometry Association, Cytometry and Microscopy Symposium. Toronto ON, Nov 24-26, 2011.
48. A simple tool to use, online tool for improving discrimination between mantle cell and small lymphocytic lymphoma. CLL Day. Vancouver BC, Dec 3, 2011.
49. **Invited speaker.** Data in Discovery Out: Automated High-dimensional Flow Cytometry Data Analysis. University of Pennsylvania, Philadelphia PA, Jun 6, 2012
50. **All travel expenses covered speaker,** ***State of the art lecture***. Computational analysis of high-dimensional data. XXVII Congress of the International Society for Advancement of Cytometry 2012, Leipzig Germany, Jun 23-27, 2012.

    This lecture on my work was invited by the ISAC leadership as part of the traditional the opening series of 3 lectures for the annual meeting of 1,500+ attendees highlighting the cutting edge of research being done in the field, and "setting the stage" for the rest of the week long meeting.

51. **Invited speaker.** Advanced Data Analysis Pre-Congress Course: Automated Data Analysis - A Broad Overview. XXVII Congress of the International Society for Advancement of Cytometry 2012, Leipzig Germany, Jun 23-27, 2012
52. An Overview of Data Analysis in High-throughput High-content Flow Cytometry, Single Cell Systems Biology and Cytomics: The Future Has Just Begun. Society for Industrial and Applied Mathematics (SIAM) Conference on the Life Sciences. San Diego CA. August 7-10, 2012.
53. **Invited speaker.** Automated analyses for diagnosis and discovery of clinically relevant biomarkers. 27th Annual Clinical Cytometry Meeting 7 Course. New Orleans LA, Oct 5-9, 2012.
54. **Invited speaker.** What's your MIFlowCyt Love Score? Take the Quiz at FlowRepository.org! 27th Annual Clinical Cytometry Meeting 7 Course. New Orleans LA, Oct 5-9, 2012.
55. **Invited speaker.** Automated Analysis of Flow Cytometry Data for Diagnosis and Discovery. 35th Annual Meeting of the Australasian Flow Cytometry Group (AFCG). Melbourne, Australia, Oct 15-17, 2012.
56. **Invited speaker.** Applying Bioinformatics Techniques to Flow Cytometry Data. 35th Annual Meeting of the Australasian Flow Cytometry Group (AFCG). Melbourne, Australia. Oct 15-17, 2012.
57. **Invited speaker.** Automated Analyses of Discovery and Diagnosis of Clinically Relevant Biomarkers. Ontario Cancer Institute. Toronto ON, Oct 31-Nov 1, 2012.
58. **All travel expenses covered speaker** Automated Analyses of Discovery and Diagnosis of Clinically Relevant Biomarkers. Myeloma Canada Scientific Roundtable, Montreal QC, Nov 1-3, 2012.
59. **Invited speaker.** Flow Cytometry Informatics: Mining FlowRepository.org Using Automated Analysis for Diagnosis and Biomarker Discovery. Chesapeake Cytometry Society. Rockville MD, Nov 5, 2012.

60. **Invited speaker.** Automated Analyses of Discovery and Diagnosis of Clinically Relevant Biomarkers. Ontario Cancer Institute, University of Virginia, Charlottesville VA, Nov 5, 2012.
61. **Invited speaker.** Automating Gating Hierarchies with flowDensity. FlowCAP-3, NIH, Bethesda MD, Nov 29-30, 2012.
62. **Invited speaker.** Advanced Data Analysis in Flow Cytometry Based on Open Source Software Solutions. Advanced Data Analysis in Flow Cytometry Based on Open-Source Software Solutions Conference, University of Zurich, Zurich Switzerland, Mar 25, 2013.
63. **Invited speaker.** Data analysis and quality assurance in R. Advanced Data Analysis in Flow Cytometry Based on Open-Source Software Solutions Conference, University of Zurich, Zurich Switzerland, Mar 26, 2013.
64. **Invited speaker.** Flow Cytometry Informatics: Automated Analysis for Diagnosis and Discovery. Advanced Data Analysis in Flow Cytometry Based on Open-Source Software Solutions Conference, University of Zurich, Zurich Switzerland, Mar 28, 2013.
65. **Invited speaker.** Reproducing Manual Gating of Flow Cytometry Data by Automating Cell Population Identification. XXVIII Congress of the International Society for Advancement of Cytometry (Cyto2013). San Diego CA, May 20, 2013.
66. **Invited speaker.** Automated analysis of flow data for diagnosis & discovery. Canadian Cytometry and Microscopy Association 2013 Annual Symposium. Montreal QC, Jun 15, 2013.
67. **Invited speaker.** Pan-Canadian initiative for harmonization of flow cytometry data for hematologic malignancies. Canadian Cytometry and Microscopy Association 2013 Annual Symposium. Montreal QC, Jun 14, 2013.
68. **Invited speaker.** FlowCAP Analysis of HIP-C Panels. The Cytome Meeting at FOCIS. Federation of Clinical Immunology Societies. Boston, MA, Jun 28-29, 2013.
69. **Invited speaker.** Automated Flow Cytometry Data Analysis for Diagnosis and Discovery. EMBO (European Molecular Biology Organization) practical course on Intravital Microscopy, Flow Cytometry and Cell Sorting. Berlin Germany, Jul 7-12, 2013.
70. **Invited speaker.** Free, open source data analysis pipelines for cytometry-based diagnosis and discovery. Institute national de la santé et de la recherche médicale (INSERM). Bordeaux France, Oct 2, 2013.
71. **Invited speaker.** Automated Flow Cytometry Data Analysis for Diagnosis and Discovery TFRI Symposium: New Frontiers in Cancer Research. Banff, Alberta. Oct. 21, 2013
72. **Invited speaker.** Automated Flow Cytometry Data Analysis for Diagnosis and Discovery FlowTex. Houston, Texas. Oct 23, 2013.
73. **Invited speaker.** Automated Flow Cytometry Data Analysis for Diagnosis and Discovery. MetroFlow Meeting. New York, New York, Oct 23, 2013.
74. **Invited speaker.** Automated Flow Cytometry Data Analysis for Diagnosis and Discovery, BMS, New Jersey, Oct 25, 2013
75. Standardization in Flow Cytometry: in silico Approaches. IMPC Flow Cytometry Meeting, Toronto, ON. Oct 28-Oct30, 2013.
76. **Invited speaker.** FlowCAP and other adventures in automated flow cytometry data analysis. Association for Cancer Immunotherapy (CIMT)/CIMT Immunoguiding Programme (CIP), Amsterdam, Netherlands, Jan 20,-22, 2014.

77. **Invited speaker.** Automated flow cytometry data analysis for clinical diagnosis and biomarker discovery, Terry Fox Research Institute's Annual Scientific Meeting. Montreal, QC, Canada, May 8-10, 2014.
78. **Invited Speaker**. FlowCAP-III: Results from Community Evaluation of Methods for Automated Analysis of Flow Cytometry Data, CYTO2014, ISAC International Congress, Fort Lauderdale, FL, USA, May 17-21, 2014
79. **Invited Speaker**. flowDensity automated cell population identification algorithm and CYTO2014, ISAC International Congress, Fort Lauderdale, FL, USA, May 17-21, 2014.
80. **Invited Speaker**. Automated flow cytometry data analysis for diagnosis and discovery. ImmunoBC (5th Annual BC Immunology Conference). Vancouver, BC June 5, 2014.
81. **Invited speaker.** Automated Flow Cytometry Data Analysis for Diagnosis and Discovery, Malaghan Institute of Medical Research, Wellington, New Zealand. Nov 7, 2014.
82. **Invited speaker.** Community-based standards development: The flow cytometry perspective. NIH Big Data to Knowledge (BD2K) sponsored meeting: Workshop on Community-Based Data and Metadata Standards. Bethesda, Maryland, February 25-26, 2015.
83. **Invited speaker.** Computational tools for flow cytometry and how well they work. 13th CIMT (Cancer Immunotherapy) Annual Meeting, Mainz, Germany, May 11 – 13, 2015.
84. **Invited speaker.** Data standards and algorithms supporting big flow cytometry data analysis for diagnosis and discovery. 21st International Society for Cellular Therapy (ISCT) Meeting, Las Vegas, NV, USA, May 27, 2015.
85. **Invited speaker.** Data Standards for Flow Cytometry. Canadian Cytometry and Microscopy Association Annual Meeting. Toronto, ON, Canada. June 18-20 2015.
86. **Invited speaker.** Sneak Peek at New Features in Flow Repository. CYTO 2015 Conference. Glasgow, Scotland. UK. June 26-30, 2015.
87. **Invited Keynote speaker.** Automated data analysis for diagnosis and discovery in single cell datasets**.** European Federation of Biotechnology 6th Annual “Analysis of Microbial Cells at the Single Cell Level” Symposium. Retz, Austria, July 19-22, 2015.
88. **Invited Instructor/Speaker.** Immunophenotyping: Generation and Analysis of Immunological Datasets. Wellcome Genome Campus, Hinxton, Cambridge, UK. Feb 21-27, 2016.
89. **Invited Speaker.** Automated Flow Cytometry Data Analysis for Clinical Diagnosis and Biomarker Discovery. Terry Fox Research Institute 7th Annual Scientific Meeting. Vancouver, BC, May 12-13, 2016.
90. **Invited speaker.** Supervised and unsupervised analysis of IMPC FCM data for cell population identification and phenodeviant identification. Knockout Mouse Phenotyping Program KOMP2-Phase2 Kick-off meeting**.** Bethesda, MD, Oct 12-14, 2016.
91. **Invited Speaker (Sponsored talk).** Belgian Society for the Advancement of cytometry. Oct 21, 2016. (Declined)
92. **Invited Speaker (Sponsored talk).** Automated flow cytometry data analysis. Bielefeld University, Germany. October 14, 2016 (Declined).

93. **Invited Speaker.**Automated analysis of big flow cytometry data. Ohio River Valley Cytometry Association. Cincinnati, Ohio. Sep 28, 2016.

94. **Invited Speaker.**Automated data analysis pipelines that drop-in replicate and extend manual analysis. Australian Cytometry Society Meeting. Sydney, Australia. Nov 2, 2016.

95. **Invited Speaker (Sponsored talk).** Big Flow Cytometry Data Analysis, Single Cell Analysis session, Pacific Symposium in Biocomputing. Jan 3-7, 2017. Kona, HI. (Declined)

96. **Invited Speaker.** Automated Analysis of EPIC Flow Cytometry data. Human Immunology Project Consortium (HIPC) Annual Meeting. EPIC Satellite meeting. Rockville, MD. Mar 22-23, 2017.

97. **Invited Speaker.** FCS 4.0. 32nd Congress of the International Society for Advancement of Cytometry (CYTO). Boston, MA. Jun 10-14, 2017.

98. **Invited Speaker,** Data-driven Cytometry. Boston Children's Hospital, Boston, MA. Jun 14, 2017.

99. **Invited Speaker.**Immunophenotyping Automated Analysis Pipeline. International Mouse Immunophenotyping Consortium (IMPC) Meeting. Nanjing, China. May 9-11, 2017.

100. **Invited Speaker.**Bioinformatic Approaches in Flow Cytometry**.** American Thoracic Society Conference (ATS2017). Washington, DC. May 19, 2017.

101. **Invited Speaker.**Automated Flow Analysis and Biomarker Discovery. 15th Transplantation Science Symposium (TTS 2017). Victoria, BC. May 24-26, 2017.

102. **Keynote Speaker.** "Bioinformatic approaches in flow cytometry. Flow cytometry in human and mouse lungs: From experimental design to analysis". 2017 ISAC Lecture Award, MASSCAUSAL2: Workshop in Computational Methods for Cytometry and Single-Cell Data meeting, University of Crete. Herkalion, Crete. Sep 1-3, 2017.

103. **Invited Speaker.** Data-driven Cytometry. University of Alberta. Edmonton, Alberta. Feb 15-16, 2018.

104. **Invited Speaker.** The Importance of Standardization and Harmonization. Is the Quality of Data Only as Good as the Weakest Control Planned? St. Anna Kinderkrebsforschung Children's Cancer Research Institute. Vienna, Austria. May 2-3, 2018.

105. **Invited Speaker.** New data analysis methods (Traditional knowledge-based approach vs. non-supervised, automated exploratory approaches; High-throughput analysis of high content data). The American Thoracic Society (ATS) Workshop on Improving the Quality and Reproducibility of Flow Cytometry in the Lung. San Diego, California. May 18, 2018.

106. **Invited Speaker.** Data-Driven Cytometry. Juno Therapeutics. Seattle, Washington. May 23-24, 2018.

107. **Invited Speaker.** Data-Driven Cytometry. The Joint Meeting of the Canadian Cancer Immunotherapy Consortium (CCIC) and ImmunoBC 2018. June 18-20, 2018.

108. **Invited Speaker.** Data-Driven Cytometry, Frontiers in Cytometry - Plenary Session 1: Frontiers in Flow Cytometry. 33rd Annual Clinical Cytometry Meeting & Course. Portland, Oregon. Sep 28 - Oct 2, 2018.

109. **Invited Speaker.** Data-Driven Cytometry. Cytometry Development Workshop: Cells, Sensors, and Systems Symposium. San Diego, California. Nov 7-11, 2018.

110. **Invited Speaker.** Automated vs manual gating: A comparison across cell populations, centres, instruments, and diseases. Cytometry Development Workshop: Cytometry Development Tutorials. San Diego, California. Nov 7-11, 2018.
111. **Invited Speaker.** Automated Data analysis for Large Scale Cytometry. Cytometry Development Workshop: Cytometry Development Workshop. San Diego, California. Nov 7-11, 2018.
112. **Invited Speaker.**Data-Driven Cytometry. TIMtalk, Becton Dickinson. San Jose, California. Jan 11, 2019.
113. **Invited Speaker.**Data-Driven Cytometry. Excellence in Genetics & Immunology lecture, McGill University. Montreal, QC. February 7, 2019.
114. **Invited Speaker.** Informatics in flow cytometry: Automated flow data analysis. International Society of Laboratory Hematology (ISLH) 2019 annual meeting. Vancouver, BC. May 9-11, 2019.
115. **Invited Speaker.**Algorithmic Analysis of High Dimensional Data. Icahn School of Medicine at Mount Sinai (ISMMS), Symposium. December 10, 2019.
116. **Invited Speaker.** The COVID Cytometry Project. COVID-19 Research Symposium: Understanding the Immune Response. Beckman-Coulter, Virtual Meeting. May 19-21, 2020.
117. **Invited Speaker.** Twitch Livestream. Project Discovery – Citizen Science Livestream. June 18, 2020.
118. **Invited Speaker.** The COVID Cytometry Project. BC Childrens Hospital Research Institute COVID-19 Seminar Series. Virtual Meeting. July 8, 2020.
119. **Invited Speaker.** Crowd Sourced Optimization of Visual Identification, Discovery and Data Sharing for COVID-19 Immunophenotyping Data: The COVID Cytometry Project. International Clinical Cytometry Society Annual Meeting - Plenary Session 5: Rules, Regulations and Reaching Beyond the Status Quo. Virtual Meeting, September 28-30, 2020.
120. **Invited Keynote Speaker.** Robust, reproducible & interactive QC, cell population identification and biomarker discovery. Glorbal Engage – The Research & Technology Series: Flow Cytometry. Virtual meeting, October 8-9, 2020.
121. **Invited Speaker.** Data Driven Cytometry. Data Analysis Educational Presentations and Roundtable. FlowTex 2021 Annual Meeting. Virtual meeting, February 3-4, 2021
122. **Invited Speaker.** COVID-19-Focused Citizen Science for Flow Cytometry Data Analysis and Machine Learning**.** CYTO2022 (Dotmatics break out session) , Philadelphia, PA, June 3-7, 2022.
123. **Invited Keynote Speaker.** COVID-19-focused citizen science for flow cytometry data analysis and machine learning. Flowcytometryuk 2022. Birmingham, United Kingdom. July 20-22, 2022.
124. **Invited Speaker.** Replacing Manual Gating of Flow Cytometry Data in Cell Therapy Manufacturing. Bioprocessing Summit Europe, Cambridge Healthtech Institute (CHI), Barcelona, Spain, March 14–17, 2023.
125. **Invited Workshop speaker**, AI in FC analytical tools guidelines-Philadelphia, CYTO 2023, May 21, 2023
126. **Invited Speaker.** Flow Repository and Flow Cytometry in the Informatics Space. FAIR Data and Flow Cytometry Panel, NERLSCD 2023, Burlington, VT, October 20, 2023.
127. **Invited speaker.** Project Discovery. Fan Fest 2025. Reykjavík, Iceland. September 20, 2023

128. **Invited speaker.** Project Discovery. FOCiS 2025. Cape Town, South Africa, December 2, 2023
129. **Invited Speaker.** SOULCAP initiative**,** Poster presentation. ICCS Annual Meeting, August 2024.
130. **Invited Speaker.** SOULCAP: Standardized Ontology and Universal Labeling for Cell Annotation and Population Identification. Discover Dotmatics, San Francisco, CA, October 8, 2025.
131. **Invited Plenary Speaker.** SOULCAP: Standardized Ontology and Universal Labeling for Cell Annotation and Population Identification. Rapid-fire plenary presentation (10 min), Global Health Plenary Session, CYTO 2025, International Society for Advancement of Cytometry (ISAC). June 3, 2025. Invited by ISAC President-Elect Virginia Litwin and CYTO 2025 Co-Chair Silas Leavesley.
132. **Invited Speaker.** NIST–FDA–NIAID Workshop: AI and Flow Cytometry. "SOULCAP: Enabling Trustworthy AI in Flow Cytometry Through Standardization and Objective Algorithm Evaluation" June 9, 2025
133. **Invited Speaker.** FOCiS Symposium. Role of AI in Immunology: Advancing Scientific Frontiers. "Fromm Dim Markers to Bright Futures: How SOULCAP's Standardization of Annotation will Transform Data Repositories into AI Discovery Powerhouses" June 12, 2025
134. **Invited Speaker.** Cell Annotation (SOULCAP). Workshop 291 — Multiparametric Cytometry Data Analysis: Stairway to High-Content. Montpellier, France, October 5–7, 2026. Pasteur Institute.

(e) Invited Participation

(f) Conference Participation (Organizer, Chair, Moderator, etc.)

1. Organizer and Chair, Bioinformatics Standards for Flow Cytometry. XXII International Society for Analytical Cytology Congress Side Meeting. Montpellier France, May 22-27, 2004. (15 attendees)
2. Chair, Statistics and Standardization Parallel Session. Northwest Regional Cytometry Meeting. Portland OR, Mar 17-18, 2006. (20 attendees)
3. Co-chair, Flow Instrumentation Session. 23rd Annual International Congress of the International Society for Analytical Cytology. Quebec City QC, May 20-24, 2006. (80 attendees)
4. Co-organizer and Co-Chair, 1st Flow Informatics and Computational Cytometry Society Meeting. Fred Hutchinson Cancer Research Centre. Seattle WA, Sep 20-21, 2006. (20 attendees)
5. Co-organizer and Co-Chair, 2nd Flow Informatics and Computational Cytometry Society Meeting. Fred Hutchinson Cancer Research Centre. Seattle WA, Nov 7-8, 2006. (40 attendees)
6. Organizer and Chair, 3rd Flow Informatics and Computational Cytometry Society Meeting. Fred Hutchinson Cancer Research Centre. Seattle WA, Mar 22, 2007. (40 attendees)
7. Organizer and Chair, Ontology for Biomedical Investigations International Workshop. Vancouver BC, Jan 28-Feb 1, 2008. (17 attendees)
8. Organizer and Chair, 4th Flow Informatics and Computational Cytometry Society Meeting. Fred Hutchinson Cancer Research Centre. Portland OR, Mar 13, 2008. (40 attendees)
9. Workshop Organizer, Cytometry Data Standards. 24th Annual International Congress of the International Society for Analytical Cytology. Budapest Hungary, May 17-21, 2008. (50 attendees)

10. Congress Program Committee, ISAC XXIV International Congress. Budapest Hungary, May 17-21, 2008. (1.306 attendees)
11. Poster Review Panel Member, ISAC XXIV International Congress. Budapest Hungary, May 17-21, 2008.
12. Organizer and Chair, Ontology for Biomedical Investigations. International Workshop. Vancouver BC, Feb 2-6, 2009 (16 attendees)
13. Organizer and Chair, 6th Flow Informatics and Computational Cytometry Society Meeting. Fred Hutchinson Cancer Research Centre. Seattle WA, Mar 13, 2009 (50 attendees)
14. Co-organizer, ISAC Image Cytometry Standards Workshop. Seattle WA, May 16, 2010.
15. Congress Program Committee, CYTO2010, ISAC International Congress. Seattle WA, May 17-21, 2010. (1,815 attendees)
16. Co-organizer and Co-chair, Informatics Issues in Primary Analysis of Enterprise Scale Flow Cytometry Experiments. ISAC International Congress. Seattle WA, May 17-21, 2010.
17. Chair, Assessing FRET response of fluorescent proteins in varying cellular microenvironments and equipment configurations. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010.
18. Poster Judge, Genome BC 8th Annual Genomics Forum. Vancouver BC, May 28, 2010.
19. Co-organizer, FlowCAP Summit, NIH campus. Bethesda MD, Sept 20-21, 2010. (70 attendees)
20. Co-organizer, Flow Informatics and Computational Cytometry Society. Seattle WA, Nov 30, 2010. (50 attendees)
21. Co-organizer, Bioinformatics Symposium, Becton Dickenson Biosciences. Boston MA, March 3, 2011.
22. Co-organizer, Flow Informatics and Computational Cytometry Society (FICCS7). Northwest Regional Cytometry Meeting. Portland OR, Mar 25, 2011.
23. Poster Judge, Research Exchange and Poster Competition. 9th Annual Genomics Forum, Genome BC and Student Biotechnology Network. Vancouver BC, May 6, 2011.
24. Workshop Organizer, Computational analysis of flow cytometry data with R/BioConductor. CYTO 2011 XXVI Congress of the International Society for the Advancement of Cytometry. Baltimore MD, May 20-25, 2011.
25. Congress Program Committee, CYTO 2011 XXVI Congress of the International Society for the Advancement of Cytometry. Baltimore MD, May 20-25, 2011. (1,375 attendees)
26. Poster Judge, Computational analysis of flow cytometry data with R/BioConductor. CYTO 2011 XXVI Congress of the International Society for the Advancement of Cytometry. Baltimore MD, May 20-25, 2011.
27. Lead Organizer, FlowCAP-2 Summit. NIH campus, Bethesda MD, Sept 22-23, 2011. (~70 attendees)
28. Congress Organizing and Program Committees, CYTO2012, ISAC International Congress. Leipzig Germany, Jun 23-27, 2012. (1,521 attendees)
29. Co-Organizer, FlowCAP-3 Summit. NIH campus, Bethesda MD, Sept 22-23, 2012. (~70 attendees)
30. Congress Organizing and Program Committees, CYTO2013, ISAC International Congress, San Diego CA, May 19-23, 2013. (1,621 attendees)

31. Organizing Committee, Terry Fox Research Institute, Scientific Annual Meeting, Ottawa ON, May 9 - 13, 2013.
32. Congress Organizing Committees, CYTO2014, ISAC International Congress, Fort Lauderdale, FL, May 17-21, 2014 (1,524 attendees)
33. Chair, Frontiers Session 1: Challenges in Data Evaluation, CYTO2014, ISAC International Congress, Fort Lauderdale, FL, May 17-21, 2014
34. Chair, Parallel Session 17: Flow Cytometry Data Analysis III, CYTO2014, ISAC International Congress, Fort Lauderdale, FL, May 17-21, 2014
35. Workshop Organizer, Flow Cytometry: Critical Assessment of Population Identification Methods (FlowCAP) IV: Results from Community Evaluation of Automated Analysis of Standardized Flow Cytometry. Fort Lauderdale, FL, May 17-21, 2014
36. Congress Organizing Committees, CYTO2015. ISAC International Congress, Glasgow, Scotland, June 26-30, 2015.
37. Program Committee, CYTO2017, Boston, MA, June 10-15, 2017.
38. Chair, Parallel Session 14: Data Management and Data Pipelines, CYTO2017, Boston, MA, June 10-15, 2017.
39. Workshop Organizer and Leader, Automating High-Volume Cytometry Data Analysis for Central Facilities, CYTO2017, Boston, MA, June 10-15, 2017.
40. Program Committee, CYTO2018, Prague, Czech Republic, April 28 – May 2, 2018.
41. Workshop Organizer and Leader, Workshop 11: Flow Cytometry Application in Multi-Center Global Clinical Studies: The Importance of Standardization and Harmonization. Is the Quality of Data Only as Good as the Weakest Control Planned? CYTO2018, Prague, Czech Republic, April 28 – May 2, 2018.
42. Workshop Organizer, Topic Session 4 - Data analysis, The American Thoracic Society (ATS) Workshop on Improving the Quality and Reproducibility of Flow Cytometry in the Lung, San Diego, California, May 18, 2018.
43. Poster Judge, BIG 19 - Bioinformatics Interdisciplinary Oncology Genome Science Research Day, Vancouver, BC. March 14, 2019.
44. Member, Youth Workshop Organizing Committee, CYTO2019, Vancouver, BC, June 22-26, 2019.
45. Session Co-chair, New Algorithms, CYTO2019, Vancouver, BC, June 22-26, 2019.
46. Workshop Organizer and Leader, WS10 – Flow Cytometry for Clinical Trials, Manual or Automated Analysis? CYTO2019, Vancouver, BC, June 22-26, 2019.
47. Session Moderator, Cutting Edge C: Tools. CYTO2020, Virtual Meeting, August 4-5, 2020.
48. Workshop Organizer and Leader, AI for flow cytometry diagnosis. CYTO2022, Philadelphia, PA, June 3-7, 2022.

(g) Other Poster Presentations and Oral/Poster Presentations by Trainees and Collaborators

1. Surh L, Hunter A, Kasaboski CA, **Brinkman R,** Damini J, Hastins V, Pluscauskas MP, Wright. Peeling R, Pennie R, Gautier M. Prevalence of chlamydial infection a post-secondary student population in Ottawa. Meeting of the Royal College of Physicians and Surgeons of Canada. Calgary AB, Sep 1992. *Oral presentation by Surh.*

2. Hillier L, Gish W, Green P, Dear S, **Brinkman R**, Cooper M, Chinwalla A, Ficenec D, Hodgson D, Holman M, Maffitt D, Marth G, Parsons J, Platt D, Wendl M, Waterston R, and Genome Sequencing Consortium. Software for large-scale DNA sequencing projects. Genome Mapping & Sequencing. Cold Spring Harbor NY, May 1996. *Oral presentation by Hillier*
3. **Brinkman RR**, Mezei MM, Theilmann J, Almqvist E and *Hayden MR*. Likelihood of being affected with Huntington Disease by a particular age for a specific CAG Size. UBC Genetics Program Annual Retreat. Vancouver BC, Nov 1997. *Poster presented by self.*
4. **Brinkman RR**, Paulsen J and *Hayden MR*. Design of clinical trials for Huntington Disease. Canadian Genetic Diseases Network Annual Scientific Meeting. Montreal QC, May, 1998. *Poster presented by self.*
5. Almqvist E, **Brinkman R**, *Hayden MR*. Successful introduction of a community-based predictive testing protocol for Huntington Disease in British Columbia. American Society of Human Genetics 48th Annual Meeting. Denver CO, Oct 1998. *Oral presentation by Almqvist.*
6. **Brinkman RR**, Paulsen JS, *Hayden MR*. Pharmocogenomic approaches to the design of clinical trials for polyglutamine expansion diseases: Huntington Disease as a prototype. American Society of Human Genetics 48th Annual Meeting. Denver CO, Oct 1998. *Poster presented by self.*
7. **Brinkman RR**, Rossini AJ, Ochs MF, Treister AS, Smith CA, Haaland P. Bioinformatics standards for flow cytometry. XXII International Society for Analytical Cytology Congress. Montpellier France, May 22-27, 2004. *Poster presented by self.*
8. <u>Spidlen J</u>, Gentleman R, Haaland P, Moloshok T , Ochs M, Smith C, Treister A, **Brinkman RR.** Flow cytometry data standards for the semantic web. 23rd Annual International Congress of the International Society for Analytical Cytology. Quebec City QC, May 20-24, 2006. *Oral presentation by Spidlen.*
9. <u>Spidlen J</u>, Gentleman R, Haaland P, Ochs M, Schmitt C, Smith C, Treister A, **Brinkman RR**. Proposed gating standard for flow cytometry. 23rd Annual International Congress of the International Society for Analytical Cytology. Quebec City PQ, May 20-24, 2006. *Oral presentation by Spidlen.*
10. Le Meur, N, Rossini A, Gasparetto M, Smyth C, **Brinkman RR**, Gentleman R. Data quality assessment in flow cytometry experiment. 23rd Annual International Congress of the International Society for Analytical Cytology. Quebec City QC, May 20-24, 2006. *Oral presentation by Le Meur.*
11. <u>Lee S-J</u>, Gasparetto M, Smith C, **Brinkman RR**. Prediction of graft-versus-host disease based on supervised temporal analysis on high-throughput flow cytometry data. BCCA Annual Cancer Care Conference. Vancouver BC, Nov 24, 2006. *Poster presentation by Lee.*
12. <u>Lo K</u>, **Brinkman R**, Gottardo R. Model-based clustering for flow cytometry data. Northwest Regional Cytometry Meeting. Seattle WA, Mar 23, 2007. *Oral presentation by Lo.*
13. Tchuvatkina O, <u>Spidlen J</u>, **Brinkman R**, Wilkinson P, Goraczyk E, Manion F, Qian Y, Scheuermann R. Bioinformatics standards for flow cytometry. Northeast Regional Life Sciences Core Directors Meeting. Cornell University, Ithaca NY, Nov 7-9, 2007. *Oral presentation by Tchuvatkina.*
14. Power MM, Di Sauro G, Brooks-Wilson A, **Brinkman R**, Nevill TJ, Lavoie JC, Smith CA, Shepherd JD, Toze CL, Sutherland HJ, Barnett MJ, Narayanan S, Mourad YA, Forrest DM, Song KW, Nantel SH, Leach S, Krasnova AA, Wong SC, Hogge DE. Allogenic stem cell transplant in first complete remission improves outcome in acute myeloid leukaemia with the FLT-3 internal tandem duplication. 49th Annual Meeting of The American Society of Hematology. Atlanta GA, Dec 8-11, 2007. *Poster presentation by Power.*

15. Shooshtari PA, Bashashati A, Vulto I, Lansdorp PM, Gupta A, **Brinkman RR**. An automated method for measuring average telomere length using flow-FISH data. Genome BC Annual Genomics Forum. Vancouver BC, Apr 11, 2008. *Poster presentation by Shooshtari.*
16. Courtot M, The OBI Consortium, **Brinkman RR**. Flow cytometry ontology: use case with OBI. 24th Annual International Congress of the International Society for Analytical Cytology. Budapest Hungary, May 17-21, 2008. *Poster presentation by Courtot.*
17. Spidlen J, Courtot M, Goralczy E, Manion F, Qian Y, Scheuermann R, Tchuvatkina O, Wilkinson P, **Brinkman R**. Beyond list mode data files: revealing experimental details for intelligent machine processing. 24th Annual International Congress of the International Society for Analytical Cytology. Budapest Hungary, May 17-21, 2008. *Oral presentation by Spidlen.*
18. Shooshtari PA, Bashashati A, Vulto I, Lansdorp PM, Gupta A, **Brinkman RR**. An automated method for measuring average telomere length using flow-FISH Data. 24th Annual International Congress of the International Society for Analytical Cytology. Budapest Hungary, May 17-21, 2008. *Poster presentation by Shooshtari.*
19. Lo K, **Brinkman RR**, Gottardo R. Automated gating of flow cytometry data via robust model-based clustering. ISAC XXIV International Congress. Budapest Hungary, May 17-21, 2008. *Oral presentation by Lo.*
20. Lo K, **Brinkman RR**, Gottardo R. Flowclust: a clustering of software for automated gating of flow cytometry data. ISAC XXIV International Congress. Budapest Hungary, May 17-21, 2008. *Poster presentation by Lo.*
21. Courtot M, Malone J on behalf of OBI Consortium. OBI: the ontology for biomedical investigations. 16th Annual International Conference Intelligent Systems for Molecular Biology. Toronto ON, Jul 19-23, 2008. *Oral presentation by Courtot.*
22. Rocca-Serra P on the behalf of the OBI Consortium. OBI: the ontology for biomedical investigations. 16th Annual International Conference Intelligent Systems for Molecular Biology. Toronto ON, Jul 19-23, 2008. *Oral presentation by Rocca-Serra.*
23. Bashashati A, **Brinkman R**. New flow cytometry standards and data analysis with Bioconductor. Danish Institute for External Validation and Danish Society for Flow Cytometry Annual Meeting. Odense Denmark, Aug 28, 2008. *Oral presentation by Bashashati.*
24. Shooshtari P, **Brinkman R**. Developing a software pipeline for assessing quality of flow cytometry data. Canadian Student Conference on Biomedical Computing (CSCBC). Vancouver BC, Mar 12-14, 2009. *Oral presentation by Shooshtari.*
25. Benz C, Kent D, Ma E, Mader H, Cortes A, **Brinkman R,** Eaves C. The prevalence of murine hematopoietic stem cell subtypes with different lineage competencies changes during ontogeny. International Society for Stem Cell Research Meeting. Barcelona Spain. Jul 8-11, 2009. *Oral presentation by Benz.*
26. Courtot M, Gibson F, Lister AL, Malone J, Schober D, **Brinkman RR**, Ruttenberg A. MIREOT: The Minimum Information to Reference an External Ontology Term, International Conference on Biomedical Ontologies (ICBO) 2011, July 25th 2009, Buffalo, USA. *Oral presentation by Courtot M.*
27. He Y, Cowell L, Diehl AD, Mobley H, Peters B, Ruttenberg A, Scheuermann RH, **Brinkman RR**, Courtot M, Mungall C, Xiang Z, Chen F, Todd T, Colby L, Rush H, Whetzel T, Musen MA, Athey BD, Omenn GS, Smith B. VO: vaccine ontology. International Conference on Biomedical Ontologies (ICBO), Buffalo NY, Jul 24-26, 2009. *Oral presentation by He.*

28. Courtot M, Gibson F, Lister AL, Malone J, Schober D, **Brinkman RR**, Ruttenberg A. MIREOT Tool (Minimum Information to Reference External Ontology Terms), Neuroscience Information Framework Webinar, December 15th, 2009. *Oral presentation by Courtot M.*
29. O'Neill K, Dalal B, **Brinkman R**. Automated class prediction of leukemia subsets from flow cytometry data. UBC Bioinformatics Retreat. Vancouver BC, Mar 19, 2010. *Oral presentation by O'Neill*
30. O'Neill K, Aghaeepour N, Jalali A, Hogge D, Karsan A, Dalal B, **Brinkman RR**. Automated prediction of clinically relevant AML genotypes from bone marrow immunophenotype, Vancouver Bioinformatics User Group, April 2010. *Oral presentation by O'Neill.*
31. Shooshtari P, Gupta A; **Brinkman RR**. Spectral-based ensemble method for improving flow cytometry data clustering. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by Shooshtari.*
32. Bashashati A, Khodabakhashi AH, Lo K, Johnson N, Gascoyne R, Gottardo R, Weng A, **Brinkman RR**. Identifying a group of diffuse large B-cell lymphoma patients with inferior survival using automated analysis of flow cytometry data. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by Bashashati.*
33. Khodabakhashi A, Hahne F, Bashashati A, Chao-Jen W, Gascoyne R, Weng A, Seifert-Margolis V, Bourcier K, Asare A, Lumley T, Gentleman R, **Brinkman R**. Per-channel basis normalization methods for flow cytometry data. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by Khodabakhashi.*
34. Quinn J, Schoenfeld J, Franks T, Hart A, **Brinkman R**, Triester A. FlowDX automated classification tools for flow cytometric data. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Poster presentation by Quinn.*
35. Aghaeepour N, Khodabakhshi A, Finak G, Schoenfeld J, Gottardo R, Scheuermann R, **Brinkman R**. flowCAP: in search of the best automated gating algorithm. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by Aghaeepour.*
36. O'Neill K, Dalal B, Coupland R, **Brinkman R**. Automated prediction of clinically relevant acute myeloid leukaemia genotypes from flow cytometry data. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by O'Neill.*
37. Spidlen J, Barsky A, Angermann B, Wilkins P, **Brinkman R**. GenePattern flow cytometry suite. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by Spidlen.*
38. Kotecha N, Zimmerman N, Haaland P, Dunne J, **Brinkman R**. Flow informatics. XXV Congress of the International Society for Advancement of Cytometry. Seattle WA, May 8-12, 2010. *Oral presentation by Kotecha.*
39. He Y, Xiang Z, Todd T, Courtot M, **Brinkman RR**, Zheng J, Stoeckert CJ Jr., Malone J, Rocca-Serra P, Sansone SA, et al. Ontology representation and ANOVA analysis of vaccine protection investigation. Bio-Ontologies 2010: Semantic Applications in Life Sciences. 18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston MA, Aug 11-13, 2010. *Oral presentation by He.*
40. Zare H, Bashashati A, Weng A, Gascoyne R, Gupta A, **Brinkman R**. Lymphoma diagnosis based on automated analysis of flow cytometry data. Cancer Bioinformatics Workshop at Cambridge Research Institute. Cambridge UK, Sept 2-4, 2010. *Oral presentation by Zare.*

41. **Brinkman R.** FlowCAP: Flow Cytometry: critical assessment of population identification methods. 20th Cytometry Development Workshop: Technologies for Cell Analysis. Pacific Grove CA, Oct 20-24, 2010. *Poster presentation by self.*
42. Rowe K, Benz C, Copley M, Kent D, Cortes A, Brinkman R, Eaves CJ. Rapid expansion of the hematopoietic stem cell population in mice between E18.5 and 3-weeks after birth is accompanied by a selective accumulation of a subset that has defective lymphopoietic differentiation potential. Stem Cell Network's 10th Annual Scientific Meeting. Vancouver BC, Nov 22-24, 2010. *Oral presentation by Rowe.*
43. **Brinkman R.** FlowCAP, FlowSuite, FlowSite, FICCS. Fred Hutchinson Cancer Research Center. Seattle WA, Nov 30, 2010. *Poster presentation by self.*
44. Courtot M, and **Brinkman R**. Automated classification using ontology-based annotation. PCIRN (Public Health Agency of Canada / Canadian Institutes of Health Research Influenza Research Network), Infectious Disease Ontology workshop, December 9th 2010, Baltimore, USA. *Oral presentation by Courtot.*
45. Aghaeepour N, Chattopadhyay PK, O'Neill K , Ganesan A, Zare H, Brodie TM, Mascola JR, Hoos HH, Michael N, **Brinkman RR**, Roederer M. Early markers of HIV progression can be identified from complex multivariate flow cytometry datasets using bioinformatics tools. HIV Evolution, Genomics, Pathogenesis. Whistler BC, Mar 20-25, 2011. **Oral presentation by Aghaeepour.*
46. Courtot M, and **Brinkman R**. Automated classification using ontology-based annotation. PCIRN (Public Health Agency of Canada / Canadian Institutes of Health Research Influenza Research Network) Annual general meeting, April 20th 2011, Ottawa, Canada. *Oral presentation by Courtot.*
47. **Brinkman R**. Computational analysis of flow cytometry data with R/BioConductor. XXVI Congress of the International Society for the Advancement of Cytometry. Baltimore MD, May 20-25, 2011. *Poster presented by self.*
48. Mertens S, Khettabi F, Bushnell T, Perfetto S, Moore WA**, Brinkman RR**, Triester A. Automated cross-platform calculation of instrument sensitivity using K-means clustering. CYTO 2011 XXVI Congress of the International Society for the Advancement of Cytometry, Baltimore MD, May 20-25, 2011. *Poster presented by Mertens.*
49. Courtot M, and **Brinkman R**. "Towards an Adverse Event Reporting Ontology" Bioinformatics and Oncology Retreat (BTP/IOP) May 27 2011, Vancouver, Canada. *Oral presentation by Courtot M.*
50. **Brinkman R**. Early markers of HIV progression can be identified from complex multivariate flow cytometry datasets using automated gating and data analysis. 11th Annual Meeting of the Federation of Clinical Immunology Societies (FOCIS 2011). Baltimore MD, Jun 23-26, 2011. *Poster presented by self.*
51. **Brinkman R**. Flow Cytometry: critical assessment of population identification methods, FlowCAP. 11th Annual Meeting of the Federation of Clinical Immunology Societies (FOCIS 2011). Baltimore MD, Jun 23-26, 2011. *****Won Poster of Merit Award*** *Poster presented by self.*
52. Courtot M, **Brinkman R**. Building the OBO Foundry - one policy at a time, International Conference on Biomedical Ontologies (ICBO) 2011, July 25-30, 2011, Buffalo, USA. *Oral presentation by Courtot.*
53. Courtot M, and **Brinkman R**. "Towards an Adverse Event Reporting Ontology" International Conference on Biomedical Ontologies (ICBO) July 25-30, 2011 Buffalo, USA. *Oral presentation by Courtot.*

54. Droumeva R, Aubert G, Brinkman R, Lansdorp P, Mah P, Shooshtari P. Calculating telomere length using automated analyis of flow cytometry. BC Cancer Agency Annual Conference, Vancouver, BC, Dec 1-3, 2011. *Poster presentation by Droumeva.*
55. O'Neill K, Aghaeepour N, **Brinkman RR**. Improved preprocessing and feature extraction for automated analysis of AML immunophenotypes. BC Cancer Agency Annual Conference, Vancouver, BC, Dec 1-3, 2011. *Poster presentation by O'Neill.*
56. Spidlen S, Breuer K, Rosenberg C, Kotecha N, Nolan G, **Brinkman R**. FLOWREPOSITORY – a public store for FCS data associated with publications. BC Cancer Agency Annual Conference, Vancouver, BC, Dec 1-3, 2011. *Poster presentation by Spidlen.*
57. Courtot M, **Brinkman R**. Towards an adverse event reporting ontology. BC Cancer Agency Annual Conference, Vancouver, BC, Dec 1-3, 2011. *Poster presentation by Courtot.*
58. Benz C, Copley MR, Kent DG, Wohrer S, Mader H, Rowe K, Day C, Cortes A, Aghaeepour N, **Brinkman R**, Eaves CJ. Differential regulation of a novel subset of hematopoietic stem cells by the bone marrow microenvironment. BC Cancer Agency Annual Conference, Vancouver, BC, Dec 1-3, 2011. *Poster presentation by Benz.*
59. Bashashati A, Johnson NA, Khodabakhshi AH, Gascoyne RD, Weng AP, **Brinkman RR**. B-cells with high side scatter parameter by flow cytometry correlate with inferior survival in diffuse large B cell lymphoma. BC Cancer Agency Annual Conference, Vancouver, BC, Dec 1-3, 2011. *Poster presentation by Bashashati.*
60. Courtot M, **Brinkman R**. Adverse events following immunization: standardization, automatic case classification and signal detection, Conference on Semantics in Healthcare and Life Sciences (CSHALS) 2012, February 24th 2012, Boston, USA. *Oral presentation by Courtot.*
61. Courtot M, **Brinkman RR**, and Ruttenberg A. "Adverse events following immunization: standardization, automatic case classification and signal detection" Bioinformatics Program retreat March 15, 2012 Vancouver, Canada. *Oral presentation by Courtot***.**
62. Courtot M, **Brinkman RR**, Adverse events following immunization: standardization, automatic case classification and signal detection, Thursday Trainee Seminar Series, BC Cancer Research Centre, March 29th 2012, Vancouver, Canada. *Oral presentation by Courtot.*
63. Courtot M, **Brinkman RR**, and Ruttenberg A. "Adverse events following immunization: standardization, automatic case classification and signal detection" PHAC/CIHR Influenza Research Network annual general meeting April 11-12 2012, Ottawa, Canada. *Oral presentation by Courtot.*
64. Jalali Khooshahr A, **Brinkman R**. RchyOptimyx: Cellular hierarchy optimization for flow cytometry. The 3rd Annual Scientific Meeting of the Terry Fox Research Institute, Victoria, BC, May 10-12, 2012. *Poster presentation by Jalali.*
65. Courtot M, **Brinkman RR**, Flow cytometry and ontologies, immunology Ontologies and their application in processing clinical data workshop, June 12th 2012, Buffalo, USA. *Oral presentation by Courtot.*
66. Courtot M, **Brinkman RR**, and Ruttenberg A. "Adverse events following immunization: standardization, automatic case classification and signal detection" International Conference on Biomedical Ontology July 2012, Graz, Austria. *Oral presentation by Courtot.*
67. Aghaeepour N, Chattopadhyay P, Ganesan A, O'Neill K, Zare H, Jalali A, Hoos H, Roederer M, **Brinkman R**. Early immunologic correlates of HIV protection can be identified from computational

analysis of complex multivariate T-cell flow cytometry assays. ISAC XXVII International Congress Conference, Leipzig, Germany, June 23-27, 2012. *Oral presentation by Aghaeepour.*

68. Aghaeepour N, Finak G, Mosmann T, Gottardo R, **Brinkman R**, Scheuermann R. Critical assessment of cell population identification techniques for flow cytometry data: results of FlowCAP. ISAC XXVII International Congress Conference, Leipzig, Germany, June 23-27, 2012. *Oral presentation by Aghaeepour.*
69. Spidlen J, Breuer K, Rosenberg C, Kotecha N, **Brinkman R**. Flowrepository – building a resource of annotated flow cytometry experiments associated with peer-reviewed publications. ISAC XXVII International Congress Conference, Leipzig, Germany, June 23-27, 2012. *Oral presentation by Spidlen.*
70. **Brinkman R**, Spidlen J, Tarnok A. Publishing MIFlowCyt compliant data to ISAC's FlowRepository.org for Cytometry A and other journals. ISAC XXVII International Congress Conference, Leipzig, Germany, June 23-27, 2012. *Oral presentation by Spidlen.*
71. Aghaeepour N, Jalali A, O'Neill K, Hoos H, **Brinkman R**. RchyOptimyx: Gating Hierarchy Optimization for Flow Cytometry. ISAC XXVII International Congress Conference, Leipzig, Germany, June 23-27, 2012. *Oral presentation by Aghaeepour.*
72. O'Neill K, Aghaeepour N, **Brinkman R**. flowBin: a complete pipeline for immunophenotype extraction and classification of multi-tube flow cytometry data. ISAC XXVII International Congress Conference, Leipzig, Germany, June 23-27, 2012. *Oral presentation by O'Neill.*
73. Courtot M, **Brinkman R**, Ruttenberg A. Adverse Event Reporting Ontology (AERO), Vaccine and Drug Ontology in the Study of Mechanism and Effect (VDOSME 2012) workshop, July 21st 2012, Graz, Austria**.** *Oral presentation by Courtot.*
74. O'Neill K, Aghaeepour N, Jalali A, Hogge D, Karsan A, Dalal B, **Brinkman RR**., Deep phenotyping of multitube flow cytometry data reveals new cell types associated with NPM1 mutation in AML, Vancouver Bioinformatics User Group, September 2012**.** *Oral presentation by O'Neill.*
75. Knapp DJHF, Bendall SC, Miller PH, Cheung AMS, Imren S, Humphries RK, **Brinkman RR**, Oostendorp RAJ, Nolan GP, Eaves CJ. Short term signalling responses of the most primitive subsets of human hematopoietic cells stimulated *in vitro c*orrelate with their subsequent self-renewal behaviour. 54th Annual ASH conference, Atlanta GA, Dec 8-11, 2012. *Poster presentation by Knapp.*
76. Courtot M, **Brinkman RR**, and Ruttenberg A. "Adverse events following immunization: standardization, automatic case classification and signal detection" E-poster, 10th Canadian Immunization Conference December 4th 2012, Vancouver, Canada. *Oral presentation by Courtot.*
77. Knapp DJHF, Bendall SC, Miller PH, Cheung AMS, Imren S, Humphries RK, **Brinkman RR**, Oostendorp RAJ, Nolan GP, Eaves CJ. Short term signaling responses of the most primitive subsets of human hematopoietic cells stimulated *in vitro c*orrelate with their subsequent self-renewal behaviour. TFRI Node-BC Cancer Agency annual conference, Vancouver BC, Nov 29-Dec 1, 2012. *Poster presentation by Knapp.*
78. O'Neill K, Aghaeepour N, Jalali A, Hogge D, Karsan A, Dalal B, **Brinkman RR**. Deep Phenotyping of Multitube Flow Cytometry Data Reveals New Cell Types Associated with NPM1 Mutation in AML. 11th Asia Pacific Bioinformatics Conference (APBC2013) Vancouver BC, Jan 21-23, 2013. *Poster presentation by O'Neill.*
79. Courtot M, **Brinkman R**, Ruttenberg A. Enabling faster analysis of vaccine adverse event reports with ontology support, Knowledge Translation Seminar, March 2013, Vancouver, Canada. *Oral presentation by Courtot.*

80. Courtot M, **Brinkman R**, Ruttenberg A. Diagnostic criteria and clinical guidelines standardization to automate case classification, International Conference on Biomedical Ontologies (ICBO) 2013, July 2013, Montreal, Canada. *Oral presentation by Courtot.*
81. Courtot M, **Brinkman R**, Ruttenberg A. Enabling faster, more accurate analysis of vaccine adverse event reports with ontology support, September 4th 2013, Stanford, USA. *Oral presentation by Courtot.*
82. Courtot M, **Brinkman R**, Ruttenberg A. The logic of surveillance guidelines: An application of OWL ontology to analysis of vaccine adverse event reports, VanBUG meeting, October 10th 2013, Vancouver, Canada. *Oral presentation by Courtot.*
83. Johnstone J, Parsons R, Botelho F, Millar J, McNeil S, Fulop T, McElhaney J, Andrew M, Walter S, Devereaux PJ, **Brinkman R**, Malekesmaeili M, Mahony J, Bramson J, Loeb M. Immune Biomarkers Predictive of Respiratory Viral Infection in Elderly Nursing Home Residents. Association of Medical Microbiology and Infectious Diseases of Canada Annual Meeting, Victoria, BC, April 2-5 2014. *Poster presentation by Johnstone.*
84. Courtot M, Ruttenberg A, Hsiao WWL, Brinkman FSL, and **Brinkman RR**. "Effective automated classification using ontology-based annotation: experience with analysis of adverse event reports" Seventh International Biocuration Conference (ISB2014), April 7, 2014, Toronto, Canada. *Oral presentation by Courtot.*
85. Courtot M, **Brinkman R**. Effective automated classification using ontology-based annotation: experience with analysis of adverse event reports PCIRN (Public Health Agency of Canada/Canadian Institutes of Health Research Influenza Research Network) Annual general meeting, May 6-7, 2014, Toronto, Canada. *Oral presentation by Courtot.*
86. Wood J, Bigos M, **Brinkman R**, Chase E, Chen Y, Condello E, Hoffman RA, El Khettabi F, Moore WA, Nolan JP, Parks DR, Perfetto SP, Redelman D, Treister A, Van Dyke J, Wang L and Yan M. Evaluation of Statistical Photoelectron Scales Using Quadratic Fitting of LED Series Data and of Multilevel Bead Set Data to Facilitate Comparisons of Instrument Sensitivity. CYTO2014, Ft. Lauderdale, USA, May 17-21, 2014. *Oral presentation by Wood.*
87. Parks D, Bigos M, **Brinkman R**, Chase E, Chen Y, Condello DP, Hoffman RA, El Khettabi F, Moore WA, Nolan JP, Perfetto SP, Redelman D, Treister A, Van Dyke J, Wang L, Wood J and Yan M. Comparison of Instrument Sensitivity (Q) and Background (B) for 10 Dyes of Interest across an Array of Different Flow Cytometers. CYTO2014, Ft. Lauderdale, USA, May 17-21, 2014. *Oral presentation by Parks.*
88. Finak G, Langweiler M, Malekesmaeili M, Stanton R, Ramey J, Jaimes M, Nussenblatt RB, Qian Y, Scheuermann R, **Brinkman R**, Maecker HT, McCoy JP and Gottardo R. Standardizing Flow Cytometry Immunophenotyping: Automated Gating Recapitulates Central Manual Analysis with Low Variability CYTO2014, Ft. Lauderdale, USA, May 17-21, 2014. *Oral presentation by Finak.*
89. Spidlen J, Moore WP and **Brinkman R**. ISAC's Gating-ML 2.0 Is Analysis Exchange between Software Tools Finally Becoming a Reality? CYTO2014, Ft. Lauderdale, USA, May 17-21, 2014. *Oral presentation by Spidlen.*
90. Mosmann T, Aghaeepour N, **Brinkman R**, Finak G, Scheuermann R and Gottardo R. Flow Cytometry: Critical Assessment of Population Identification Methods (FlowCAP) IV: Results from Community Evaluation of Automated Analysis of Standardized Flow Cytometry Data CYTO2014, Ft. Lauderdale, USA, May 17-21, 2014. *Oral presentation by Mosmann.*

91. Rothe K, Lin H, Lin KBL, Leung A, Wang HM, Malekesmaeili M, **Brinkman RR**, Forrest DL, Gorski SM, Jiang X. The core autophagy protein ATG4B is critical to the survival of leukemic stem/progenitor cells and predicts clinical outcomes of CML patients treated with imatinib therapy ISSCR (International Society for Stem Cell Research), Vancouver, BC, June 18, 2014. *Poster presentation by Rothe.*
92. Malek M, Meskas J, Luche, H, Liang A, Abeler-Dorner L, **Brinkman R**. Automated supervised and unsupervised analysis of big flowcytometry data: Results from the International Mouse Phenotyping Consortium. Cyto Conference 2015. Glasgow, Scotland, June 28, 2015. *Oral presentation by Malek.*
93. Spidlen J, **Brinkman R.** Sneak Peek at New Features in Flow Repository. CYTO 2015 Conference. Glasgow, Scotland. UK. June 28, 2015. *Oral presentation by Spidlen.*
94. O'Donahue M, Lux M, Spidlen J, Panopoulos A, Quinn J, Wilson L, Chauve C, Golden M, Almarode J, Stadnisky M, **Brinkman R**. Fast Is Fine, But Accuracy Is Everything: Validation of Manual and Customized Automated QC and Automated Gating Pipelines for Clinical and Research Flow Cytometry. Cyto Conference 2017. Boston, MA, USA, June 10-15, 2017. *Oral presentation by O'Donahue.*
95. Conrad V, Malek M, Miller W, **Brinkman R**, Dubay C, Koguchi Y, Redmond W. Profling T Cell Subsets in Cancer Immunotherapy Using Flowdensity as Part of a Semi-Automated Analysis Pipeline. Cyto Conference 2017. Boston, MA, USA, June 10-15, 2017. *Oral presentation by Conrad.*
96. Rahim A, Lorenc A, Laing A, Saran N, White J, Dörner L, Hayday A, **Brinkman R**. Complete Assay of the Mammalian Immune Function. Cyto Conference 2017. Boston, MA, USA, June 10-15, 2017. *Oral presentation by Rahim.*
97. Grinek S, Chauve C, Mostafavi S, **Brinknkman RR**. Improving unsupervised clustering results in mass cytometry using subspace outlier detection. NIPS Workshop 2017. Long Beach, CA, USA. December 04-09, 2017. *Poster presentation by Grinek.*
98. Meskas J, **Brinkman R**. FlowCut. CYTO2017, Boston, MA, June 10-15, 2017.
99. **Brinkman R**. Designing Customized, High Throughput Flow Cytometry Data Analysis Pipelines Based on Free, Open Source Software. CYTO2017, Boston, MA, June 10-15, 2017.
100. Malek M, Laing A, Lorenc A, Abeler-Dörner L, and **Brinkman RR**. flowTypeFilter: Semi-Supervised Biomarker Discovery for High-Dimensional Analysis of Flow Cytometry Data. CYTO2018, Prague, Czech Republic. April 28 – May 02, 2018. *Poster presentation by Malek.*
101. Meskas J, Wang S, and **Brinkman R**. flowCut: Precise and Accurate Automated Removal of Outlier Events and Flagging of Files Based on Time versus Fluorescence Analysis. CYTO2018, Prague, Czech Republic. April 28 – May 02, 2018. *Poster presentation by Meskas*.
102. Meskas J, O'Donahue M, Lux M, Velazquezs-Palafox M, Spidlen J, Halpert R, Stadnisky M and **Brinkman R**. Customized Automated Analysis of Clinical FCM: A Knowledge- and Data-Driven QC and Analysis Pipeline in FlowJo. Cyto Conference 2018. Prague, Czech Republic. April 28 – May 02, 2018.
103. Wu A, Lin H, Rothe K, Chen M, Ruschmann J, Petriv O, O'Neill K, Maetzig T, Knapp D, Nakamichi N, **Brinkman R**, Birol I, Forrest DL, Hansen C, Humphries RK, Eaves CJ & Jiang X. Global transcriptome profiling identifies a key Mir-185-PAK6 axis that promotes survival of leukemic stem cells and drug-insensitive blasts in BCR-ABL+ human leukemia. 61st ASH Annual Meeting & Exposition, Dec 1 – 4, Blood 2018.

104. Meskas J, Wang S, and **Brinkman R**. f flowCut --- An R package for precise and accurate automated removal of outlier events and flagging of files based on time versus fluorescence analysis. BIG 19 - Bioinformatics Interdisciplinary Oncology Genome Science Research Day, Vancouver, BC. March 14, 2019. *Poster presentation by Wang.*

105. Rahim A, Meskas J, Drissler S, Yue A, Lorenc A, Laing A, Saran N, White J, Dörner L-A, Hayday A, **Brinkman RR**. Automated "Big Data" Analysis Methods for Population Identification. BIG 19 - Bioinformatics Interdisciplinary Oncology Genome Science Research Day, Vancouver, BC. March 14, 2019. *Poster presentation by Rahim.*

106. Wu A, Lin H, Rothe A, Chen M, Ruschmann J, Petriv O, O'Neill K, Maetzig T, Knapp D, Nakamichi N, **Brinkman R**, Birol I, Forrest D, Hansen C, Humphries K, Eaves C and Jiang X. Global transcriptome profiling identifies a key miR-185-PAK6 axis that promotes survival of leukemic stem cells and drug-insensitive blasts in BCR-ABL+ human leukemia. BIG 19 - Bioinformatics Interdisciplinary Oncology Genome Science Research Day, Vancouver, BC. March 14, 2019. *Poster presentation by Wu.*

107. Rahim A, Nutter L, **Brinkman RR**. Big Flow Cytometry Data Analysis Methods and Applications. International Symposium on Technical Innovations in Laboratory Hematology (ISLH) 2019, Vancouver, BC. May 9 – 11, 2019. ** ***Awarded Young Investigator Award,*** *Oral presentation by Rahim.*

108. Rahim A, Gaudilliere B, Aghaeepour N, **Brinkman R**. Automated Flow Cytometry Data Analysis and Its Application to the Analysis of the Immune Clock of Human Pregnancy. CYTO2019, Vancouver, BC. June 22-26, 2019. *Poster presentation by Rahim.*

109. Rahim A, McIlwain D, Gaudilliere B, Aghaeepour N, **Brinkman R**. Flow Cytometry: Critical Assessment of Population Identification Methods (FlowCAP-V). CYTO2019, Vancouver, BC. June 22-26, 2019. *Poster presentation by Rahim.*

110. Hidalgo RA, Eshghi S, **Brinkman R**, Drissler S, Yokosawa D, Green C, Mathews W. Implementation of Automated Gating Strategies for Quality Control and Analysis of Checkpoint Marker, PD-L1, in Hematologic Malignancies. *Poster presentation by Hidalgo Robert (Genentech Inc).*

111. Cossarizza A. Better together, with an avatar from the future. TEDxModena (Italy). https://www.youtube.com/watch?v=yj-KqlRxfG4

112. Cossarizza A. Cossarizza avatar in a video game: on Eve he teaches how to beat Covid. *TV Interview (Italy).* https://www.modenaindiretta.it/avatar-cossarizza-un-videogioco-eve-insegna-battere-covid-video/

113. Yue A, Chauve C, Libbrecht M, Brinkman R.Gating flow cytometry samples using few-shot image segmentation. Machine Learning in Computational Biology 2021. November 22-23, 2021. *Oral presentation by Yue.*

114. Yue A, Chauve C, Libbrecht M, Brinkman R.Gating flow cytometry samples using few-shot image segmentation. Machine Learning in Computational Biology 2021. November 22-23, 2021. *Spotlight video by Yue.*

115. Yue A, Chauve C, Libbrecht M, Brinkman R.Gating flow cytometry samples using few-shot image segmentation. Machine Learning in Computational Biology 2021. November 22-23, 2021. *Poster by Yue.*

(h) Other Scholarship of Education Activities

1. Mentor, S.U.C.C.E.S.S. Job Mentoring Program Coordinator, Career mentorship connections, 2007.
2. Mentor, SFU undergraduate Bioinformatics Students Club, 2008.

(i) Media Interviews and Coverage

***UVPM** - unique visitors per month; This is the number of unduplicated visitors to a website over the course of a specified time period.Tracking this number monthly is an industry standard for understanding if a site's audience is increasing, decreasing or staying even.*

1. **Online news article.** EVE Online players can help scientists understand the coronavirus. PC Gamer. June 15, 2020. UVPM: 14,248,598

   "EVE Online's Project Discovery initiative is back, and after helping scientists study how human cells are built and identify exoplanets it's now tasking players with analysing data to assist coronavirus research. "

2. **Online news article**. Fight COVID-19 By Playing EVE Online A new phase of Citizen Science initiative Project Discovery. MMORPG. June 15, 2020. UVPM: 779,803

   "Players in EVE Online can help with Project Discovery through a mini-game in which they use a tracing tool to mark groups of cells. Project Discovery's results will help to understand the immune system's response to COVID-19, in collaboration with scientists from McGill University, BC Cancer, and front-line COVID-19 clinicians. Players who participate in the mini-game will see rewards in the form of in-game content. There is a detailed in-game tutorial for Project Discovery available when players log into EVE Online."

3. **Online news article.** EVE Online's Project Discovery initiative tasks players with helping research COVID-19. Massively Overpowered. June 15, 2020. UVPM: 580,093

   "Project Discovery is working with McGill University, Dr Andrea Cossarizza, a Professor of Immunology at the University of Modena, and the Reggio Emilia School of Medicine in Italy in order to analyze data. Players can log in and help out with this data via a minigame involving a tracing tool to mark groups of cell populations present in blood, thereby helping scientists understand how different cell populations and types are altered through infection. Those who take part will not only help scientists battle COVID-19 but also get some rewards for doing so."

4. **Online news article.** EVE Online Project Discovery Lets You Fight COVID-19. Tech Raptor. June 15, 2020. UVPM: 528,610

   "CCP has launched the third phase of Project Discovery together with Massively Multiplayer Online Science (MMOS), which is both a citizen science project and mini-game that can be found within EVE Online."

5. **Online news article.** CCP's Project Discovery Offers EVE Players A Way To Help With COVID-19 Research. MMOBomb. June 15, 2020. UVPM: 265,678

   "Once again, CCP is activating EVE Online's Project Discovery. This program offers players of the space MMO a way to help with scientific research by engaging with data through the game. Previously, players assisted with mapping out the Human Protein Atlas and searching for exoplanets. Now, they'll be assisting scientists in understanding how the human immune system responds to the coronavirus."

6. **Media Feature.** Project Discovery: the video game to fight the coronavirus. Vogue (Italy), Maria Santoro. June 18, 2020.

7. **Online news article.** An EVE Online mini-game is helping researchers better analyze COVID-19 data. Gamasutra. June 15, 2020. UVPM: 734,189

   "This time around, CCP has brought Project Discovery back online to help scientists better understand how COVID-19 impacts human immune systems during a pandemic that has weighed on much of the world's population."

8. **Online news article.** FIGHT COVID-19 BY PLAYING EVE ONLINE IN “PROJECT DISCOVERY”. GamingLyfe. June 15, 2020. UVPM: 39,296
9. **Online news article.** Fight Covid-19 With EVE Online’s Citizen Science Initiative Project. MMOsWorld. June 15, 2020. UVPM: 5,172
10. **Online news article**. Eve Online - Project Discovery: Players versus COVID. VPESports. June 16, 2020. UVPM: 139,980

    "Across all game genres, we can find Player versus Environment or Player versus Player mechanics. Those who play Eve now have the option to Player versus COVID for a better future."
11. **Online news article.** EVE Online' Fight COVID-19 In New Phase of Citizen Science Initiative Project Discovery. WorthPlaying. June 15, 2020. UVPM: 67,903
12. **Online news article.** Fight COVID-19 by playing EVE Online in new phase of Citizen Science initiative Project Discovery. HGUnified. June 15, 2020. UVPM: 5,898
13. **Online news article.** EVE Online Mini-Game Lets Players Help In The Fight Against Covid-19. Kotaku. June 15, 2020. UVPM: 4,515,418

    “Project Discovery remains one of the most innovative ways for gamers to give back to the world at large while playing the games they love. As long as players remain inquisitive and engaged in the scientific process, there will always be more data for them to quantify and analyze.”
14. **Online news article.** EVE Online Players Are Helping Scientists Fight The Coronavirus. GameRant. June 16, 2020. UVPM: 4,652,202

    "Efforts like this show how video games can be used to make a better world, as EVE Online players have played a significant part in the fight against the Coronavirus pandemic, even if individual contributions may not be that much."
15. **News feature, Podcast, Interview.** Project Discovery: Could computer games help find a cure for COVID-19? BBC Science Focus Podcast. July 13, 2020. UVPM: 1,200,000

    "This week we speak to scientists Ryan Brinkman and Jerome Waldispuhl, and Project Discovery’s creator Atilla Szantner about why they intend to turn gamers into citizen scientists to help find a cure for COVID-19."
16. **News feature.** Space pilots fighting against Corona virus - How gamers support scientists. Tagesspiegel. July 14, 2020. UVPM: 100,000

    "Project Discovery is a prime example of 'Citizen Science'."; "Both preceding projects have been very successful, hundreds of thousands players took part. The third project, the Corona-research has started off well. After one week only, 34.000 players already analysed 3,8 million scans."
17. **Online news article.** CCP Games Calls on EVE Online Players to Level Up within Landmark COVID-19 Citizen Science Project. HGUnified. September 22, 2020.

    Today CCP Games, in conjunction with Massively Multiplayer Online Science (MMOS), are calling on EVE players to re-engage with the third phase of Project Discovery, the groundbreaking citizen science project and mini-game found within EVE Online, CCP’s deep and uniquely player-driven spacefaring MMO.
18. **Online News Article.** EVE Online players submitted over 41M classifications to fight COVID for CCP’s latest Project Discovery initiative. Massively Overpowered. September 22, 2020. UVPM: 721,581

    What’s better than a science MMO story or a feel-good MMO story? One that’s both. And this one is both, as EVE Online and CCP Games have officially announced the next phase of Project Discovery, the citizen science campaign it’s been waging to reward EVE players for helping in actual, real-world science projects.

19. **Online News Article.** EVE Online Players Helped Provide Nearly 150 Years Worth of COVID-19 Research. MMORPG. September 22, 2020. UVPM: 757,560

    In some much-needed good news, it seems like EVE Online players have submitted millions of data classifications towards COVID-19 research.

20. **Online News Article.** EVE Online' Players Contribute Over 40 Million Data Classifications for COVID-19 Research. WorthPlaying. September 22, 2020. UVMP: 56,750

    Set tens of thousands of years in the future, EVE Online is a breathtaking journey to the stars, to an immersive experience filled with adventure, riches, danger and glory. With nearly a quarter of a million subscribers worldwide inhabiting the same virtual universe, EVE features a vast player-run economy where your greatest asset is the starship, designed to accommodate your specific needs, skills and ambitions.

21. **Online News Article.** EVE Online Has Been Helpsing Scientists Learn More About COVID-19 With Project Discovery. MMOS. September 22, 2020. UVPM: 147,721

    The campaign has been such a huge success that CCP Games is planning to launch another phase with more complex mini-games.

22. **Online News Article.** CCP Games Calls on EVE Online Players to Level Up within Landmark COVID-19 Citizen Science Project. GamingLyfe. September 22, 2020. UVPM: 22,551

    Today, CCP is pleased to announce that it has already received an astounding 41.4 million submissions, with over 466,000 already verified and now able to be used in scientific research – a quantity and accuracy of data that would not exist without the efforts of EVE's dedicated players around the world.

23. **Online News Article.** EVE Online: Project Discovery - Milestone project of citizen research on COVID-19: Phase 3 started. games.ch. September 23, 2020. UVPM: 577,008

24. **Online News Article.** EVE Online: Project Discovery - Milestone project of citizen research on COVID-19: Phase 3 started. game7.de. September 23, 2020. UVPM: 10,896

25. **Online News Article.** EVE Online Players Help Fight COVID-19 In Citizen Science Project. Screen Rant. September 22, 2020. UVPM: 34,874,892

    COVID-19 continues to ravage hundreds of thousands of people across the globe, with over 200,000 deaths in the United States alone, and the Eve Online community is undoubtedly generating work that could create a major breakthrough in understanding such a new and deadly disease. Eve Online is currently free to play and download, so anyone is free to sign up, get their spaceship together, and play a video game to help save the human race (in real life).

26. **Online News Article.** Eve Online Players Analyze Over 40 Million Data Sets For COVID-19 Research. MMO Bomb. September 22, 2020. UVPM: 265,678

    Eve Online players being, well, Eve Online players, have been doing their best to help analyze data studying how COVID-19 impacts the human immune system. Since they started Project Discovery in June, 157K players have been doing research tasks in game, managing to work through more than 40 million data classifications, marking cell populations on graphs for researchers to analyze, and effectively doing over 32 years worth of work.

27. **Online News Article.** Leveling up citizen science. Nature. September 24, 2020. UVPM: 14,089,186

    Eve Online is a very special game. The player base is more mature and attuned to science than other player communities. The game is also slower paced and more complex, making it an almost too perfect match for citizen-science activities.

28. **Online News Article.** Borderlands 3 is using its millions of gamers to help map the human gut microbiome. Mobi Health News. October 16, 2020. UVPM: 179,551

    Szantner and MMOS's prior take on a citizen science research videogame was Project Discovery, which aimed to classify a large body of fluorescence microscopy images. Unlike other programs, Project Discovery was not released as a standalone game, but deployed within the sci-fi massive multiplayer online role-playing game Eve Online.

29. **Online News Feature.** EVE Online Developers, Scientists Talk Coronavirus Impact. Game Rant. October 27, 2020. UVPM: 4,969,708

    Between developer-driven conflicts involving alien invasions and player-driven conflicts building on years of bad blood, it seems there would be no time to participate in COVID-19 research - yet players have clearly put their differences aside and stepped up to the plate.

30. **Interview.** EVE Online Interview: Scientists Outline Coronavirus Research. Game Rant.October 29, 2020. UVPM: 4,969,708

    But of course, this is just a video game, so that animosity and drive on behalf of players is more indicative of how attached people are to the game. The developer has elected to use that passion for positive aims, partnering with the European Union-funded group Massively Multiplayer Online Science (MMOS) to take on a number of projects meant to advance humanitarian aims.

31. **Online News Article.** EVE Online: How the Popular MMORPG Is Tackling COVID-19. Comic Book Resources. November 11, 2020. UVPM: 16,856,725

    Scientists around the world are working around the clock to understand COVID-19 and create a vaccine. And they're getting some help from an unexpected source, an MMO game. That's right, EVE Online is conducting a citizen science project to assist with actual problems around the world.

32. **Online News Article.** EVE Online players have completed 47 million tasks to help researchers gather coronavirus data. PC Gamer. November 11, 2020. UVPM: 12,862,802

    Back in June, scientists at McGill University's School of Computer Science announced the return of Project Discovery, a minigame that helps them with data gathering. This time around, Project Discovery sheds some light on data about the coronavirus, simply by mapping groups of cell populations in-game.

33. **Online News Mention.** The next Unreal Engine hit is a real-life truck. PC Gamer. November 11, 2020. UVPM: 12,862,802

    It's interesting to see processes and tools from video games used somewhere else, just like in data gathering on the coronavirus in EVE Online—it's all good as long as car manufacturers don't take video games as inspiration for their self-driving modes.

34. **Online News Article.** Over 171,000 EVE Online players have contributed to Covid-19 research. TechSpot. Novembver 9, 2020. UVPM: 5,138,953

    So far, the 171,000 gamers mentioned before have completed more than 47 million tasks, equating to about 36 years of categorizing cells. Those are some astounding results, and it goes to show that gamers are willing to band together for the common good when given the opportunity to do so.

35. **Online News Article.** Eve Online: Players save 36 years of work for Corona research. GameStar. November 10, 2020. UVPM: 13,510,476

    More than 171,000 players have played Project Discovery and completed a considerable amount of work on behalf of research: they have solved and submitted 47 million tasks, which, according to the BBC video, corresponds to 36 years of work categorising cells.

36. **News Feature.** Eve Online video game helps scientists understand Covid-19. BBC News. November 9, 2020. UVPM: 603,400,000

    Players in the multi-player sci-fi game Eve Online can complete a mini game designed to help researchers understand the coronavirus. By marking out different cell populations researchers can then analyse how the virus affects the immune system. More than 171,000 gamers have completed 47 million mini game tasks amounting to 36 years categorising cells.

37. **News Feature.** YouTube - BBC Click Segment. BBC News. November 10, 2020. UVPM: 6,835

And we see one of the world's first trials of an artificial intelligence algorithm to help doctors quickly distinguish between Covid-19 and cancer treatment toxicity on scans. These decisions could be a matter of life and death and are challenging for the human eye to detect.

38. **Online News Article.** MMORPG EVE Online helps scientists study the coronavirus . Mein-MMO. November 10, 2020. UVPM: 2,429,154

    Players have so far been able to solve around 47 million of these mini-game tasks, which has given the scientists around 36 years of categorising cells. In other words, it would have taken scientists 36 years to collect this data using a conventional method.

39. **Online News Article.** "Eve Online" players save Corona researchers years of work. Web.de. November 10, 2020. UVPM: 22,000,000

    The 171,000 players participating in Project Discovery and the 47 million tasks they completed saved virus research 36 years of work in just four months, as would be the case, for example, with the categorisation of cells.

40. **Online News Article.** EVE Online players have completed 47 million tasks to help researchers gather coronavirus data. PC Gamer. November 09, 2020. UVPM: 22,200,000

    EVE Online players have since really stepped up to help, with more than 171,000 gamers completing a staggering 47 million tasks, according to BBC News. This number reveals the strength of citizen science—the number of minigames completed amounts to 36 years of categorising cells, something that would have been simply impossible for the team at McGill to do on their own.

41. **Online News Article.** Computer game "Eve-Online" helps fight against Covid-19. SWR (Radio). November 12, 2020. UVPM: 7,00,000

    "EVE Online" has been around for 17 years. A game with its own economy, its own stock exchange and a community of around 300,000 gamers. In an integrated mini-game, the gamers are now helping to research the coronavirus, very real.

42. **Feature.** BBC Click - Project Discovery BBC News. November 7, 2020. UVPM: 665,000,000

    And we see one of the world's first trials of an artificial intelligence algorithm to help doctors quickly distinguish between Covid-19 and cancer treatment toxicity on scans. These decisions could be a matter of life and death and are challenging for the human eye to detect.

43. **Invited Interview.** Project Discovery, RBK Games (Russian media outlet). June 2020.
44. **Invited Interview.** EVE Online against coronavirus. How gamers are helping fight COVID-19. Unian.net (Russian media outlet). September 03, 2020.
45. **Invited Interview.** Science and Entertainment Fusion: How EVE Online Helped Fight COVID-19. Regnum (Russian media outlet) August 12, 2020.
46. **Invited Interview.** Project Discovery, Kanobu (Russian media outlet). August 2020.
47. **Online News Article.** EVE Online: How the Popular MMORPG Is Tackling COVID-19. CRB.com. November 09, 2020.
48. **Interview.** EVE Online: gamers analyse COVID data The Naked Scientists Podcast (based at The University of Cambridge). November 11, 2020.
49. **Radio mention.** **"**Eve Online": Record battles, history books and more. Tobias Nowak, aka "Kollege Gamer" on SoundCloud. November 12, 2020. (German)
50. **Radio Feature.** "Eve Online" Supports COVID Research. Tobias Nowak, aka "Kollege Gamer" on SoundCloud. November 12, 2020. (German)

51. **Radio Feature.** Compter game “Eve-Online” Helps Fight COVID-19. SWR2. November 12, 2020. (German)
52. **Radio Feature.** The EVE Online game and reality. WDR radio station. November 12, 2020. (German)
53. **Interview**. Project Discovery. TVN Television. November 13, 2020. (Polish)
54. **Feature**. Gaming for Science - "EVE Online" helps with Covid-19 research. SWR. November 16, 2020. UVPMs: 6,799.013
55. **Online News Article**. The Computer Game Helping Scientists Beat Covid-19. Huffington Post. November 18, 2020. UVPMs: 5,300,000
56. **Online News Article**. EVE Online's COVID-19 Project Discovery Research Has Over 200,000 Participants. GameRant. November 29, 2020. UVMs: 6,799,013
57. **Online News Artcile**. "Eve Online": Gaming for research and against the coronavirus. Deutschlandfunk Nova. November 30, 2020. UVPMs: 310,590
58. **Online News Article**. Fight the corona virus with games. WDR Blog. December 02, 2020. UVPMs: 6,413,621
59. **Invited Interview.** Project Discovery and Borderlands Science. Devcom podcast, Twitch covering Project Discovery and Borderlands Science. December 17, 2020.
60. BCC Radio 4 – World at One. November 18, 2020.
61. **Online News Article.** How EVE Online and Borderlands 3 merge citizen science and gaming. PC Gamer. February 24, 2021.
62. **Online News Article.** So, It's Been A Year, Huh, Kotaku. March 18, 2021.
63. **Online News Article.** How EVE Online Players Saved Real-World Scientists 330 Years of Research on COVID-19. **IGN.** May 4, 2021. IGN UVPMs: 38,441,972
64. **Online News Article.** EVE Online Players Contributed 330 Years Of Work To COVID-19 Research. **Screen Rant.** May 5, 2021. Screen Rant UVPMs: 66,272,107
65. **News Feature.** Video games helping scientists study COVID-19 impacts. Northwest Florida Daily News. May 6, 2021.
66. **News Feature.** Coronavirus Briefing: What Happened Today. New York Times. May 6, 2021. UVPMs: 126,706,156
67. **Online News Article.** EVE ONLINE IS SAVING REAL-WORLD SCIENTISTS HUNDREDS OF YEARS IN COVID-19 RESEARCH. GCM. May 5, 2021.
68. **Online News Article.** EVE Online Saved Scientists 330 Years of Research. Game Pressure. May 6, 2021.
69. **Online News Mention.** Majority of life sciences investment for coming year going to emerging tech, says conference survey. **R&D World**. May 6, 2021.
70. **Online News Article.** CITIZEN SCIENCE GAMES MIX DESIGN WITH DISCOVERY. Science Connected Magazine. May 14, 2021.
71. **Online News Article.** EVE Online's Project Discovery Wins Webby Award For Its Citizen Science Initiative. MMORPG. May 18, 2021.

72. **Online News Article.** EVE Online' Wins Webby Award For Project Discovery. Worthplaying. May 18, 2021.
73. **Online News Article.** EVE Online's "Project Discovery" Wins Webby People's Voice Award for Public Service, Activism, and Social Impact. HGUnified. May 19, 2021.
74. **Online News Artcile (Mention).** Rainbow Six Pro Next1 Has Died at Age 24 Game Rant USA. May 24, 2021. UVPMS: 10,564,453
75. **News Features – Interview.** Interview Canadian scientists win Webby award for enlisting online gamers to identify COVID-19 in blood data. The Globe and Mail CA. May 25, 2021. UVPMs: 6,709,389
76. **Online News Article.** This COVID-19 Research and Analysis was Made Possible by 'EVE Online' Players — How? **Tech Times** USA. May 25, 2021. UVPMs: 1,099,657
77. **Interview.** Interview with Professor Jérôme Waldispühl on video games to help biologists. Radio Canada CA. June 2, 2021.
78. **Feature.** BC Cancer researcher brings science fiction into science. BC Cancer – News & Stories. July 20, 2021.
79. **Interview.** MMOS – Massive Multiplayer Online Science. Red Bull USA November 22, 2021. UVPMs: 6,395,862
80. **Interview & News Feature.** How gamers are helping in the COVID-19 fight. GlobalTV**.** February 12, 2022.
81. **Online News Artcile**. Quand les jeux vidéo s'attaquent à la COVID-19. Quebec Science. February 07, 2022.

(j) *Other Professional Contributions*

N/A

10. SERVICE TO THE UNIVERSITY

(a) *Areas of special interest and accomplishments*

N/A

(b) *Memberships on committees, including offices held and dates*

1. Graduate Student Representative, Medical Genetics Department, Faculty of Medicine, UBC (1997-98)
2. Graduate Student Representative, The Student Information Technology Access Committee (SITAC), UBC, 1998
3. Representative, CMMT Computer Oversight Group, 1998-2000
4. Member, Program Advisory Committee, Bioinformatics Training Program for Health Research, British Columbia. Graduate program offered jointly by SFU and UBC, 2000

5. Poster Judge, UBC Bioinformatics/Genetics Annual Retreat Genetics Graduate Program Retreat Poster Session , 2006
6. Mentor, UBC Faculty of Science, Life Sciences Tri-Mentoring Program, 2007
7. Poster Judge, UBC Bioinformatics/Genetics Annual Retreat, 2007
8. Medical Genetics Graduate Program Advisory Committee, 2008-2010
9. Poster Judge, UBC Bioinformatics/Genetics Annual Retreat, 2010
10. Medical Genetics Graduate Admissions Committee, 2008-2013
11. Committee member, Bioinformatics Training Program Review, Jan 2011

(c) *Faculty mentoring*

Name	**Affiliation**	**Start**	**Finish**	**Role**
Dr. Zargham Sepehrizadeh*	Tehran University of Medical Sciences, Iran	05/2015	08/2016	Visiting Research scientist

*Dr. Sepehrizadeh (academic staff in the Tehran University of Medical Sciences, the top ranked Iranian University, and a permanent Canadian resident) selected to do a sabbatical in the Brinkman lab.

(d) *Other service, including dates*

1. *Qualifying Exam Committee,* Benjamin Good, April 4, 2006
2. *Examination Chair,* Xingxing Cheng, Graduate Program: Doctor of Philosophy in Chemical and Biological Engineering [Supervisor: Professor Xiaotao Bi (Chemical and Biological Engineering)] Modeling and Simulation of a Novel i-CFB Reactor for Catalytic NOx Reduction, October 11, 2013
3. *Examination Chair,* Veronique Lecault, Chemical and Biological Engineering - Doctor of Philosophy, Microfluidic cell culture arrays for clonal expansion and characterization of mammalian cells on Friday, November 23, 2012
4. *Adjudicator* for the 2014 Roman M. Babicki Fellowship in Medical Research competition at request of Associate Dean, Graduate & Postdoctoral Education. September 2014
5. *Examination Committee,* Adriana Sedeno, October 9, 2014
6. *Examination Committee*, MSc, Samuel Hinshaw, October 4, 2018 [Supervisor: R.E.W. Hancock] Network-based integrative analysis of multi-omic data
7. *Examination Committee*, MSc, Uyen Nguyen, July 27, 2020 [Supervisor: M. Levings] The Immune Aspects Of Physical Exercise And Photopheresis To Ameliorate The Adverse Effects Of Stem Cell Transplantation
8. *Examination Committee*, PhD, Bioinformatics, Sohrab Salehi, January 25, 2021 [supervisor: A. Bouchard]
9. *Examination Committee*, MSc, Bioinformatics, Kristina Wright, August 5, 2021 [supervisor: I. Birol] Seasonal- and sex- dependent gene expression in emu (Dromaius novaehollandiae) fat tissues

10. *Examination Chair*, MSc, Bioinformatics, Qinkai Wu, September 23, 2021 [supervisor: P. Pavlidis]
11. *Examination Chair,* MSc, Bioinformatics, Eric Lee, December 01, 2021 [supervisor: A. Rothe]
12. Examination Chair, PhD Comprehensive, Bioinformatics, Sean Formby, April 5, 2022 [supervisor: G. Bakkeren]
13. Examination Chair, PhD Comprehensive, Bioinformatics, Aishwarya Sridhar, December 8, 2022 [supervisors: W. Hsiao, SFU & L.Hoang, BCCDC]

11. SERVICE TO THE HEALTH PROFESSIONS/HEALTH AUTHORITIES

(a) Areas of special interest and accomplishments

N/A

(b) Memberships on committees, including offices held and dates

1. Committee member, New approaches to clinical trials working group, Strategic Planning Committee, 2010
2. Member, Monday Noon Seminar Committee, September 2021 – present
3. Member, BC Cancer Studentship Committee, January 2022 - present

(c) Other service, including dates

1. Interview Panel for the Director of the Terry Fox Laboratory, 2018
2. Interview Panel for Research IT position, 2018, BC Cancer
3. Chair, Interview Panel for Director, Research Information Systems (BCCRC), 2022

12. SERVICE TO THE COMMUNITY

(b) Areas of special interest and accomplishments

1. Co-founder and member of organizing committee, Vancouver Bioinformatics User Group (http://vanbug.org/), 2002-2008
2. Founding Director, SOULCAP (Standardized Ontology for Unified Labeling of Cell Annotation in Populations), 2022–present. Founded and led this initiative from concept (first presented at Dotmatics Boston talk, 2022) to registered 501(c)(3) non-profit organization with tax-exempt status and board governance (2025). SOULCAP addresses the fundamental need for standardized cell population annotation terminology to enable AI-based analysis of flow cytometry data. Board members include: Jessica Houston (ISAC President; Professor, New Mexico State University), Mario Roederer (former NIH/NIAID/VRC; #2 lifetime-cited scholar in Cytometry; co-founder of FlowJo), Goce Bogdanoski (Director, IVD Strategy & Operations, Amgen; formerly Director at BMS), Kelly Lundsten (Director, Strategic Product Innovation, FluoroFinder), and Kamila Czechowska-Kusio (Chief of Diagnostic Development, Metafora Biosystems). Network encompasses 344 contacts across 183 organizations in 15 countries, including 70% of top-10 global pharma companies (Pfizer, Takeda, Roche, AstraZeneca,

GSK, Merck, BMS) and 100% of major flow cytometry instrument manufacturers (BD, Cytek, Sony, Thermo Fisher, Beckman Coulter). Engagement with leadership across all five major cytometry societies (ISAC, ESCCA, ICCS, IUIS, FOCIS) representing 125,000+ scientists globally.

(c) Memberships on scholarly societies, including offices held and dates

1. Panel Participant, Canadian Bioinformatics Workshops White Paper on Bioinformatics Training in Canada, 2002.
2. Panel Particpant, Canadian Cytometry and Microscopy Association (CCMA), Cytometry SRL Perspectives. "Integrating multiparameter analysis into your facility- from instrumentation to analysis". January 19, 2022.
3. Career Panel Speaker, Vancouver Bioinformatics User group (VanBUG) Career Night. May 19th, 2022.

(c) Memberships on other societies, including offices held and dates

1. Member, International Society for Computational Biology 1998-present
2. Co-Founder, International Society for Computational Biology Regional (Vancouver) Affiliate, 2002-2008
3. Member, International Society for Advancement of Cytometry, 2004-present
4. Chair, Public Flow Cytometry Repository Task Force, International Society for Advancement of Cytometry, 2007-2008
5. Member, Data Standards Task Force, International Society for Advancement of Cytometry, 2004-present
6. Chair, Data Standards Task Force, International Society for Advancement of Cytometry, 2008-2020
7. Member, Institute of Electrical & Electronic Engineers (IEEE) and IEEE Standards Association, 2005-2008
8. Chair, Working Group for Bioinformatics Standards for Flow Cytometry (IEEE-SA PAR 1953.2), 2005-2008
9. Core Coordinating Committee, Ontology for Biomedical Investigations (OBI), 2005-present
10. Co-founder & Member of Organizing Committee, Flow Informatics & Computational Cytometry Society, 2006-present
11. Member, Standards Committee, International Society for Advancement of Cytometry, 2008-present
12. Member, Image Cytometry Metadata Standards Taskforce (ICMST), International Society for Advancement of Cytometry, 2009-present
13. Councilor, International Society for Advancement of Cytometry, 2010-June 2016
14. Member, Scholar Selection Committee, International Society for Advancement of Cytometry, 2010-2011
15. FOCIS Centers of Excellence Immunophenotyping Technical Meeting at NIH (FITMaN), Feb 2011
16. Investigation/Study/Assay (ISA) Steering Committee, 2011-2012
17. Member, Chair, Flow Repository Steering Committee, International Society for Advancement of Cytometry, 2011-present

18. Cytometry 2050 Task Force, International Society for the Advancement of Cytometry, 2013
19. Canadian Human Immunophenotying Consortium Steering Committee, 2015-present
20. International Mouse Phenotyping Consortium Immunology Working Group, 2016-present
21. Member, FlowGate U01 CTSA Program Collaboration Innovation Award Projects (CCIA External Advisory Board, 2019
22. Member, Terry Fox Marathon of Hope Technology Working Group, Immune-profiling sub-committee, November 2019
23. ISAC Liason to Wiley, FlowRepository 2.0 transition, September 2021 – March 2022
24. ISAC Representative, NIST Flow Cytometry Standards Consortium; led FCS 4.0 metadata standardization efforts, 2024–present.
25. Member/Contributor, CDISC SDTM working group outreach for flow cytometry data standard integration with SOULCAP, 2024–present.

(d) Memberships on scholarly committees, including offices held and dates

1. Program Advisory Committee, CIHR/MSFHR Bioinformatics Training Program for Health Research, BC, 2000

(e) Memberships on other committees, including offices held and dates

N/A

(f) Editorships (list journal and dates)

1. Advances in Bioinformatics special issue "Recent Bioinformatics Advances in the Analysis of High Throughput Flow Cytometry Data", 2009
2. Journal of Clinical Bioinformatics, 2010-present
3. Cytometry Part A, 2010-present
4. International Scholarly Research Network (ISRN) Bioinformatics, 2011- present
5. Informatics, 2012-present
6. Dataset Papers in Science, 2012-present
7. Lead Associate Editor for *Cytometry A* Special Issue “Computational Data Analysis of High Dimensional Cytometry Data”, 2015.
8. Senior Editor, Special Issue: “AI in Clinical Flow Cytometry,” *Cytometry Part B: Clinical Cytometry*, 2024 (two volumes).

(g) Reviewer (journal, agency, etc. including dates)

1. NIH: Biodata Management and Analysis Study Section (BDMA), 2006-2007,
2. Michael Smith Foundation for Health Research, Junior Graduate Scholarship Panel, 2006, 2007
3. NIH: Ad hoc reviewer, 2008, 2010

4. *Briefings in Functional Genomics and Proteomics,* 2008
5. *IEEE Transactions on Biomedical Engineering*, 2008
6. NIH: American Recovery and Reinvestment Act Challenge Grants, 2009
7. *Cell Stem Cell*, 2009
8. *Nature Methods*, 2010
9. NIH: Special flow cytometry reviewer for AIDS and AIDS Related Research (AARR) Integrated Review Group, 2011
10. *Bioinformatics*, 2012, 2015
11. *Source Code for Biology and Medicine,* 2012
12. *BMC Bioinformatics*, 2009, 2010, 2013, 2014
13. *Nature Biotechnology*, 2013
14. *Cancer Immunology, Immunotherapy*, 2014
15. *Biology*, 2014
16. *PLoS Computational Biology*, 2007, 2014
17. *Cytometry A*, 2008 – present
18. *Cytometry: Part B - Clinical Cytometry*, 2020
19. *Frontiers in Immunology*, 2025

(h) External examiner (indicate universities and dates)

1. PhD Thesis, Adrin Jalali, Universität des Saarlandes, Germany. July 07, 2020.

(i) Consultant (indicate organization and dates)

Cytapex Bioinformatics Inc., March 2020-present

(j) Other service to the community

1. WestGrid Resource Allocation Committee, 2009
2. CIHR Institute of Infection and Immunity (III) consultation workshop (Human Immunology) Workshop, November 25th-26th, Toronto Ontario, 2014.
3. CIHR-III, is planning a strategic funding research initiative on human immunology. This consultation workshop aims to bring together the research community from the many diverse areas of human immunology, including immunotherapy, inflammatory disease, autoimmunity and vaccine to assist in planning this initiative, 2014.
4. Grant Reviewer, NIH/ NIAID Special Emphasis Panel (PAR-13-242: NIAID Resource-Related Research Projects (R24), 2015.
5. NIH Big Data to Knowledge (BD2K) sponsored meeting: Workshop on Community-Based Data and Metadata Standards. Bethesda, MD, February 25-26, 2015.

The goals of the workshop are to address the following: 1) Specific gap areas in data and metadata standards with greatest potential impact for NIH relevant research; 2) Common pain points in data and metadata standards development life cycle; 3) Possible NIH assistance mechanisms that could address pain points and accelerate and improve the quality of community-based data standards development efforts; and 4) Best practices for managing community based data standards development and evaluating near and longer term success.

13. AWARDS AND DISTINCTIONS

(a) Awards for Teaching (indicate name of award, awarding organizations, date)

N/A

(b) Awards and Recognition for Scholarship (indicate name of award, awarding organizations, date)

1. CIHR Studentship Research Award, 1997-2001 ($80,000)
2. International Society for Analytical Cytology Scholar, 2006 ($1,000)
3. Michael Smith Foundation of Health Research, Scholar Award, 2007-2013 ($480,000)
4. Terry Fox Research Institute, New Investigator Award, 2010-2013 ($435,252)

   Faculty of Medicine, Department of Medical Genetics, UBC, Outstanding Academic Performance (OAP), 2019, 2020

   OAP is awarded annually to faculty members after a department peer-reviewed process, in recognition of academic achievements performed over the past year. Receipt of an OAP is a reflection of your significant productivity in relation to that of your fellow Department members.

5. ScholarGPS Highly Ranked Scholar™ — Lifetime, 2025. Top 0.02% of all scholars worldwide (32nd of 60,712 scholars in Cytometry specialty). Rankings: #2 global in Flow Cytometry (5-year period); #13 lifetime in Flow Cytometry; #15 lifetime in Cytometry. 130 publications; h-index 52. (ScholarGPS® ID: 28368438179604)
6. Bibliometric Network Analysis Recognition, 2025. Identified as one of the “most influential contributors” and “core network nodes” in flow cytometry in an analysis by Lucas Black of 283,000+ papers, 500,000+ authors, and 11 million co-author connections. Recognized alongside Virginia Litwin, Andrea Cossarizza, and J. Paul Robinson.

(d) Awards for Service (indicate name of award, awarding organizations, date)

1. International Society for Advancement of Cytometry, Distinguished Service award, 2018

   The Distinguished Service Award was established to honor those individuals who served the Society in a major role, provided major support to the Society and its members, or made a significant contribution to the success of the Society.

(e) Other Awards

1. Best Poster. Likelihood of being affected with Huntington Disease by a particular age for a specific CAG size. UBC Genetics Program Annual Retreat, 1997, ($300 travel award)
2. Poster of Merit: Flow Cytometry: Critical Assessment of Population Identification Methods (FlowCAP), Federation of Clinical Immunology Societies (FOCIS) annual meeting, Baltimore MD, Jun 23-26, 2011. ($100 award)
3. Best Original Paper published in Clinical Cytometry for 2012-2013. This annual award is given for the manuscript published under the Origfinal Article category that is judged of the highest scientific quality, originality and impact by the Editors and Associate Editors of Clinical Cytometry. For "The phenotypic distribution and functional profile of Tuberculin-specific CD4 T-cells characterizes different stages of TB infections"
4. Webby Award | Honoring the Best of the Internet. 2021 People’s Voice Award – Public Service, Activisism and Social Impact. EVE Online – Project Discovery.

14. **<u>OTHER RELEVANT INFORMATION</u> (Maximum One Page)**

N/A

THE UNIVERSITY OF BRITISH COLUMBIA
Publications Record

SURNAME: Brinkman
FIRST NAME: Ryan
MIDDLE NAME(S): Remy
Initials: RRB
Date: 3/24/2026

1. REFEREED PUBLICATIONS

Notes: Supervised trainees are <u>underlined</u>.

Synopsis: **128 refereed publications**

- **h-index: 52**
- **10,785 citations**
- **Papers published by year:**

(a) Journals

Key to my contribution:

FA - First Author - typically performed the majority of the experiments in the manuscript, wrote the first draft
CA - Contributing Author – typically helped with experimental design, completed some experiments,
SA - Senior Author – typically conceived the experimental approach, supervised the writing of the manuscript, corresponding author for the paper
<u>Underline</u> – directly supervised trainees

1. Johnston M, Andrews S, **Brinkman R**, Cooper J, Ding H, Dover J, Du Z, Favello A, Fulton L, Gattung SC, Giesel C, Kirsten J, Kacuba T, Hillier L, Jier M, Johnston L, Langston Y, Latreille P, Louis EJ, Macri C, Mardis E, Menezes S, Mouser L, Nhan M, Rifkin L, Riles L, St.Peter H, Trevaskis E, Vaughan K, Vignati D, Wilcox L, Wohldman P, Waterston R, Wilson R & Vaudin M. Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII. *Science* 265: 2077-2082, 1994. **CA (IF 30.0; Citations 249)**
   As a member of the bioinformatics team that was part of this large effort I developed software tools to manage the finishing of genomic sequence data. I was also responsible for finishing a significant portion of the genomics sequence.
2. Vaudin M, Roopra A, Hillier L, **Brinkman RR**, Sulston J, Wilson RK & Waterston RH. The construction and analysis of M13 libraries prepared from YAC DNA. *Nucleic Acids Res* 23: 670-674, 1995. **CA (IF 7.6; Citations 20)**
   I was responsible for all statistical analysis of the data.
3. **Brinkman RR**, Mezei MM, Theilmann J, Almqvist E & Hayden MR. The likelihood of being affected with Huntington disease by a particular age, for a specific CAG size. *Am J Hum Genet* 60: 1202-1210, 1997. **FA (IF 12.6; Citations 191)**
   I conceived developed and led this research effort and wrote the manuscript detailing a major and impactful part of my graduate studies.

4. Chissoe SL, Marra MA, Hillier L, **Brinkman R**, Wilson RK & Waterston RH. Representation of cloned genomic sequences in two sequencing vectors: correlation of DNA sequence and subclone distribution. *Nucleic Acids Res* 25: 2960-2966, 1997. **CA (IF 7.6; Citations 12)**

   I was responsible for statistical analysis for the manuscript.

5. Wellington CL, **Brinkman RR**, O'Kusky JR & Hayden MR. Toward understanding the molecular pathology of Huntington's disease. *Brain Pathol* 7: 979-1002, 1997. **CA (IF 4.0; Citations 51)**
   I was responsible for statistical analysis for the manuscript under the direction of Dr. Wellington, as well as some novel analysis of my own design.

6. **The C. elegans Sequencing Consortium**. Genome sequence of the nematode *C. elegans*: a platform for investigating biology. *Science* 282: 2012-2018, 1998. **CA (IF 30.9; Citations 462)**

   This was a major international study involving many authors. However, my role at the Genome Sequencing Center in St. Louis was still important. I developed bioinformatics tools to aid in the analysis of the DNA sequence. I was also responsible for some of the “finishing” of sequence.

7. Almqvist EW, Crauford D, **Brinkman R** & Hayden MR. A worldwide assessment of the frequency of suicide, suicide attempts, or psychiatric hospitalization after predictive testing for Huntington disease. *Am J Hum Genet* 64: 1293-1304, 1999. **CA (IF 12.6; Citations 118)**

   I worked very closely with the lead author of the manuscript and this study was a chapter in my thesis. I was responsible for all statistical analysis of the data. I also helped in the design of research questions and in drafting the manuscript. I also was responsible for selecting the patient cohort based on the clinical database I developed for my prediction of onset in HD study.

8. Hadano S, Nichol K, **Brinkman RR**, Nasir J, Martindale D, Koop BF, Nicholson DW, Scherer SW, Ikeda JE & Hayden MR. A yeast artificial chromosome-based physical map of the jevenile amyotropic lateral sclerosis (ALS2) critical region on human chromosome 2q33-q34. *Genomics* 55: 106-112, 1999. **CA (IF 3.2; Citations 18)**

   I performed the bioinformatics analysis for this manuscript.

9. Falush D, Almqvist EW, **Brinkman RR**, Iwasa Y & Hayden MR. Measurement of mutational flow implies both a high new-mutation rate for Huntington disease and substantial underascertainment of late-onset cases. *Am J Hum Genet* 68: 373-385, 2001. **CA (IF 12.6; Citations 17)**

   I was responsible for statistical analysis of the data, related to the projected number of late-onset cases. I also was responsible for selecting the patient cohort based on the clinical database I developed for my prediction of onset in HD study.

10. Paulsen JS, Zhao H, Stout JC, **Brinkman RR**, Guttman M, Ross CA, Como P, Manning C, Hadyden MR & Shoulson I. Clinical markers of early disease in persons near onset of Huntington's disease. *Neurology* 57: 658-662, 2001. **CA (IF 4.9; Citations 166)**

    My methodology for predicting the likelihood of age of onset of was used to select patients included in the study.

11. Rosenblatt A, **Brinkman RR**, Liang KY, Almqvist EW, Margolis RL, Huang CY, Sherr M, Franz ML, Abbott MH, Hayden MR & Ross CA. Familial influence on age of onset among siblings with Huntington disease. *Am J Med Genet* 105: 399-403, 2001. **CA (IF 4.5; Citations 77)**

I was responsible for some of the statistical analysis of the data. I also was responsible for selecting the patient cohort based on the clinical database I developed for my original prediction of onset in HD study.

12. Almqvist EW, **Brinkman RR**, Wiggins S & Hayden MR. Psychological consequences and predictors of adverse events in the first 5 years after predictive testing for Huntington's disease. *Clin Genet* 64: 300-309, 2003. **CA (IF 2.9; Citations 98)**

    I helped develop the research questions, performed all of the statistical analysis and helped write and review the first and subsequent drafts of the manuscript. This manuscript formed a chapter of my thesis.

13. Djousse L, Knowlton B, Hayden M, Almqvist EW, **Brinkman RR**, Ross C, Margolis R, Rosenblatt A, Durr A, Dode C, Morrison PJ, Novelletto A, Frontali M, Trent RJ, McCusker E, Gomez-Tortosa E, Mayo D, Jones R, Zanko A, Nance M, Abramson R, Suchowersky O, Paulsen J, Harrison M, Yang Q, Cupples LA, Gusella JF, MacDonald ME & Myers RH. Interaction of normal and expanded CAG repeat sizes influences age at onset of Huntington disease. *Am J Med Genet* 119A: 279-282, 2003. **CA (IF 2.5; Citations 47)**

    In the first month of my PhD studies I realized that the combination of the clinical and research databases in Dr. Hayden's clinical practice and research group would generate a large patient cohort that could empower many clinical studies. I spent the next several moth's joining these two electronic resources, and as a result our together the largest cohort of HD patients data in the world. This cohort particular study I was responsible for identifying patients in the cohort that were applicable to the study in question.

14. Li JL, Hayden MR, Almqvist EW, **Brinkman RR**, Durr A, Dode C, Morrison PJ, Suchowersky O, Ross CA, Margolis RL, Rosenblatt A, Gomez-Tortosa E, Cabrero DM, Novelletto A, Frontali M, Nance M, Trent RJ, McCusker E, Jones R, Paulsen JS, Harrison M, Zanko A, Abramson RK, Russ AL, Knowlton B, Djousse L, Mysore JS, Tariot S, Gusella MF, Wheeler VC, Atwood LD, Cupples LA, Saint-Hilaire M, Cha JH, Hersch SM, Koroshetz WJ, Gusella JF, MacDonald ME & Myers RH. A genome scan for modifiers of age at onset in Huntington disease: The HD MAPS study. *Am J Hum Genet* 73: 682-687, 2003. **CA (IF 11.7; Citations 110)**

    For this large international study, I was responsible for patient selection and analysis based on information from the database I developed in the Hayden lab while developing the methodology to predict age of onset.

15. Djousse L, Knowlton B, Hayden MR, Almqvist EW, **Brinkman RR**, Ross CA, Margolis RL, Rosenblatt A, Durr A, Dode C, Morrison PJ, Novelletto A, Frontali M, Trent RJ, McCusker E, Gomez-Tortosa E, Mayo Cabrero D, Jones R, Zanko A, Nance M, Abramson RK, Suchowersky O, Paulsen JS, Harrison MB, Yang Q, Cupples LA, Mysore J, Gusella JF, MacDonald ME & Myers RH. Evidence for a modifier of onset age in Huntington disease linked to the HD gene in 4p16. *Neurogenetics* 5: 109-114, 2004. **CA (IF 3.5; Citations 60)**

    For this large international study, I was responsible for patient selection and analysis based on information from the database I developed in the Hayden lab while developing the methodology to predict age of onset.

16. Lafreniere RG, MacDonald ML, Dube MP, MacFarlane J, O'Driscoll M, Brais B, Meilleur S, **Brinkman RR**, Davidas O, Pape T, Platon C, Radomski C, Risler J, Thompson J, Guerra-Escobio AM, Davar G, Breakefield XO, Pimstone SN, Green R, Pryse-Phillips W, Goldberg YP, Younghusband HB, Hayden MR, Sherrington R, Rouleau G & Samuels ME. Identification of a novel gene (HSN2) causing

hereditary sensory and autonomic neuropathy type II through the Study of Canadian Genetic Isolates. *Am J Hum Genet* 74: 1064-1073, 2004. **CA (IF 11.7; Citations 96)**

Unlike other significant discoveries I was a part of while at Xenon, (that became part of the IP of the company and remain published), this study was instead one that was selected as suitable for publication. I led the bioinformatics group that developed the automated SNP discovery platform used by Xenon Genetics to identify candidate genes.

17. Langbehn DR, **Brinkman RR**, Falush D, Paulsen JS & Hayden MR. A new model for prediction of the age of onset and penetrance for Huntington's disease based on CAG length. *Clin Genet* 65: 267-277, 2004. **CA (IF 2.9; Citations 340)**

    I conceived, developed and led this research effort and wrote the first draft of the manuscript. I also solicited the participation of over 40 HD clinics worldwide to provide patient data to allow me to extend the prediction of onset model I had published earlier. I also made the fundamental discovery that a combination of parametric relationships would allow the combined analysis of the entire cohort. Dr. Lanbehn's expertise was the computer simulations that provided the numeric constants for the final equation. The manuscript was resubmitted to another journal without significant changes once I left the Hayden group upon completing my graduate studies, with Dr. Langbehn as first author.

18. **Brinkman RR**, Dubé M-P, Rouleau GA, Orr AC & Samuels ME. Human monogenic disorders - a source of novel drug targets. *Nat Rev Genet* 7: 249-260, 2006. **FA (IF 32.8; Citations 51)**

    While this was published in Nature Review Genetics, this article also contains extensive novel bioinformatics analysis I developed for the article involved in identifying the potential number of novel drug targets. This article represents part of the research I conducted while at Xenon Genetics Inc. and was published after I left the company to partially address the restrictions on publishing I incurred while at the company. I performed the analysis and co-wrote the manuscript with Dr. Samuels (my direct report while I was at Xenon).

19. Spidlen J, Gentleman RC, Haaland PD, Langille M, Le Meur N, Ochs MF, Schmitt C, Smith CA, Treister AS & **Brinkman RR**. Data standards for flow cytometry. *OMICS* 10: 209-214, 2006. **SA (IF 1.9; Citations 23)**

    I conceived of the research, directed the work and co-wrote the manuscript. This project was funded entirely by my NIH R01 (EB 50034)

20. Stoeckert C, Ball C, Brazma A, **Brinkman R**, Causton H, Fan L, Fostel J, Fragoso G, Heiskanen M, Holstege F, Morrison N, Parkinson H, Quackenbush E, Rocca-Serra P, Sansone SA, Sarkans U, Sherlock G, Stevens R, Taylor C, Taylor R, Whetzel P & White J. Wrestling with SUMO and bio-ontologies. *Nat Biotechnol* 24: 21-22, 2006. **CA (IF 31.1; Citations 5)**

    I wrote the first draft of the article and made a significant contribution to future revisions.

21. Whetzel PL, **Brinkman RR**, Causton HC, Fan L, Field D, Fostel J, Fragoso G, Gray T, Heiskanen M, Hernandez-Boussard T, Morrison N, Parkinson H, Rocca-Serra P, Sansone SA, Schober D, Smith B, Stevens R, Stoeckert CJ, Jr., Taylor C, White J & Wood A. Development of FuGO: an ontology for functional genomics investigations. *OMICS* 10: 199-204, 2006. **CA (IF 1.944; Citations 59)**

    As a member of the OBI coordinating committee I led the inclusion of flow cytometry-specific terms in the ontology, help direct the overall development of the ontology and helped write the manuscript. This research effort was funded in part by my NIH R01 (EB 50034).

22. **Brinkman RR**, Gasparetto M, Lee SJ, Ribickas AJ, Perkins J, Janssen W, Smiley R & Smith C. High-content flow cytometry and temporal data analysis for defining a cellular signature of graft-versus-host disease. *Biol Blood Marrow Transplant* 13: 691-700, 2007. **FA (IF 3.275; Citations 31)**

    I conceived of the approach to the analysis, directed the analysis and co-wrote the manuscript. This research effort was funded entirely from my start up funds.

23. Dykstra B, Kent D, Bowie M, McCaffrey L, Hamilton M, Lyons K, Lee S, **Brinkman R** & Eaves C. Long-term propagation of distinct hematopoietic differentiation programs in vivo. *Cell Stem Cell* 1: 218-229, 2007. **CA (IF 25.943; Citations 217)**

    I directed the graduate student who was responsible for the bioinformatics analysis requested by reviewers to validate the methodology in the initial version of the manuscript, leading to the eventual acceptance of the manuscript by the journal. This research effort was funded in part from my start up funds.

24. Le Meur N, Rossini A, Gasparetto M, Smith C & **Brinkman RR**. Data quality assessment of ungated flow cytometry data in high throughput experiments. *Cytometry A* 71: 393-403, 2007. **CA (IF 3.753; Citations 26)**

    The development of the data quality assessment methods took place in Dr. Gentleman's group, however, I helped guide the research effort and the writing of the manuscript. This research effort was funded entirely by my NIH R01 (EB 50034).

25. Smith B, the **OBI Consortium** et al. The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. *Nature Biotechnology* 25: 1251-1255, 2007. **CA (IF 31.090; Citations 547)**

    As a coordinator of the OBI Consortium I contributed to important guidelines for the OBO Foundry

26. Lee JA, Spidlen J, Boyce K, Cai J, Crosbie N, Dalphin D, Furlong J, Gasparetto M, Goldberg M, Goralczyk EM, Hyun B, Jansen K, Kollmann T, Kong M, Leif R, McWeeney S, Moloshok TD, Moore W, Nolan G, Nolan J, Nikolich-Zugich J, Parrish D, Purcell B, Qian Y, Selvaraj B, Smith C, Tchuvatkina O, Wertheimer A, Wilkinson P, Wilson C, Wood J, Zigon R, International Society for Advancement of Cytometry Data Standards Task Force, Scheuermann RH, **Brinkman RR.** MIFlowCyt: The Minimum Information about a Flow Cytometry experiment. *Cytometry A* 73: 926-930, 2008. **SA (IF 3.753; Citations 109)**

    I conceived, was equally responsible for the development and writing of the manuscript with the first authors, and led this international effort that laid the foundation for my group's flow cytometry data standards efforts. I pulled together a large collaborative group of leaders in the flow cytometry field to undertake this effort. Part way through our effort I became aware of a parallel effort from Richard Scheuermann's group so I initiated a collaboration to pool our efforts, and we have been collaborators ever since sharing several publications and more in the pipeline. His student was co-first author with my post doctoral fellow. This majority of this research effort was funded by my NIH R01 (EB 0050034). The first MIFlowCyt-compliant article was published in Cytometry A in February 2010. Now almost every article follows this recommendation. MIFlowCyt is also recommended by Mature Publishing Group. This effort set the foundation for my later development of the only public repository for flow cytometry data (FlowRepository.org; #59, #60, below).

This paper was 7th of the 10 most-accessed articles in **Cytometry Part A** from July through September 2011 2013. The data comes from the Wiley Online Library usage statistics of downloads. "http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1552-4930/homepage/MostAccessed.html"

27. Taylor CF, Field D, Sansone SA, Aerts J, Apweiler R, Ashburner M, Ball CA, Binz PA, Bogue M, Booth T, Brazma A, **Brinkman RR**, Michael Clark A, Deutsch EW, Fiehn O, Fostel J, Ghazal P, Gibson F, Gray T, Grimes G, Hancock JM, Hardy NW, Hermjakob H, Julian RK Jr, Kane M, Kettner C, Kinsinger C, Kolker E, Kuiper M, Le Novere N, Leebens-Mack J, Lewis SE, Lord P, Mallon AM, Marthandan N, Masuya H, McNally R, Mehrle A, Morrison N, Orchard S, Quackenbush J, Reecy JM, Robertson DG, Rocca-Serra P, Rodriguez H, Rosenfelder H, Santoyo-Lopez J, Scheuermann RH, Schober D, Smith B, Snape J, Stoeckert CJ Jr, Tipton K, Sterk P, Untergasser A, Vandesompele J, Wiemann S. Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. *Nat Biotechnol* 26: 889-896, 2008. **CA (IF 31.090; Citations 317)** This manuscript is the result a large international collaboration of leaders of various data standards efforts. I led the flow cytometry component of this work. This project was funded in part by my NIH R01 (EB 50034).

28. <u>Lo K</u>, **Brinkman RR** & Gottardo R. Automated gating of flow cytometry data via robust model-based clustering. *Cytometry A* 73: 321-332, 2008. **CA (IF 3.753; Citations 110)**

    I supervised the first author for four months while he embedded in my group as a graduate student developing this approach. I co-wrote the grant that funded his efforts as well as the manuscript. This project was funded in part by my NIH R01 (EB 50034) and by the MITACS grant I was a collaborator on. This article was the first of article of a renaissance of methods developed for the automated analysis of flow cytometry data, and paved the groundwork that was built upon by several other approaches. It was the first robust automated approach and set the bar for all future efforts.

29. Ramadan KM, Connors JM, Al Tourah AJ, Song KW, Gascoyne RD, Barnett MJ, Nevill TJ, Shepherd JD, Nantel SH, Sutherland HJ, Forrest DL, Hogge DE, Lavoie JC, Abou-Mourad YR, Chhanabhai M, Voss NJ, **Brinkman RR**, Smith CA & Toze CL. Allogeneic SCT for relapsed composite and transformed lymphoma using related and unrelated donors: long-term results. *Bone Marrow Transplant* 42: 601-608, 2008. **CA (IF 3.660; Citations 6)**

    I led the statistical analysis of the data presented in this manuscript.

30. <u>Spidlen J</u>, Leif RC, Moore W, Roederer M, International Society for Analytical Cytology Data Standards Task Force, **Brinkman RR**. Gating-ML: XML-based gating descriptions in flow cytometry. *Cytometry A* 73A: 1151-1157, 2008. **SA (IF 3.753; Citations 25)**

    I conceived and led this research effort and co-wrote the manuscript with my post-doctoral student who undertook the overwhelming majority of this effort under my supervision. This research effort was funded entirely by my NIH R01 (EB 50034).

31. <u>Bashashati A</u> & **Brinkman RR**. A survey of flow cytometry data analysis methods. *Adv Bioinformatics* 2009: 584603, 2009. **SA (IF n/a; Citations 34)**

    I conceived and co-wrote the manuscript with my post-doctoral student who undertook the overwhelming majority of this effort under my supervision. This research effort was funded entirely by my NIH R01 (EB 50034).

32. Bashashati A, Lo K, Gottardo R, Gascoyne RD, Weng A, & **Brinkman R.** A pipeline for automated analysis of flow cytometry data: preliminary results on lymphoma sub-type diagnosis. *Conf Proc IEE Eng Med Biol Soc* 2009: 4945-8, 2009. **(IF 0.9; Citations)**

33. Finak G, Bashashati A, **Brinkman R** & Gottardo R. Merging mixture components for cell population identification in flow cytometry. *Adv Bioinformatics* 2009: 1-12, 2009. **CA (IF n/a; Citations 32)**

    I initiated the research program that laid the foundation for this project through the co-development of the BioConductor packages upon which this effort was built. I provided scientific direction, with the work carried out in the group of a co-applicant of my NIH proposal, which funded this effort in part by NIH R01 (EB 50034) as did my CIHR bridge funding (the lymphoma dataset was the use case that drove this effort within my group).

34. Forrest DL, Trainor S, **Brinkman RR**, Barnett MJ, Hogge DE, Nevill TJ, Shepherd JD, Nantel SH, Toze CL, Sutherland HJ, Song KW, Lavoie JC, Power MM, Abou-Mourad Y & Smith CA. Cytogenetic and molecular responses to standard-dose imatinib in chronic myeloid leukemia are correlated with Sokal risk scores and duration of therapy but not trough imatinib plasma levels. *Leuk Res* 33: 271-275, 2009. **CA (IF 2.555; Citations 58)**

    I led the statistical analysis of the data presented in this manuscript.

35. Hahne F, LeMeur N, **Brinkman RR**, Ellis B, Haaland PD, Sarkar D, Spidlen J, Strain E & Gentleman R. flowCore: a bioConductor package for high throughput flow cytometry. *BMC Bioinformatics* 10: 106, 2009. **CA (IF 3.029; Citations 72)**

    The development of the computational infrastructure for the analysis of flow cytometry data analysis was the result of an ongoing collaboration between Dr. Gentleman's group and my own, funded entirely by my (as PI) NIH R01 (EB 50034). This work has been foundational for the field of high throughput flow cytometry data analysis and has enabled a large community of disparate developers to coalesce around a stable, high performance platform for automated flow cytometry data analysis, now supporting 33 different tools that have been widely used across the community. Most importantly personally was how this framework bootstrapped the efforts of my group in the area of flow cytometry informatics algorithms.

36. Johnson NA, Boyle M, Bashashati A, Leach S, Brooks-Wilson A, Sehn LH, Chhanabhai M, **Brinkman RR**, Connors JM, Weng AP & Gascoyne RD. Diffuse large B-cell lymphoma: reduced CD20 expression is associated with an inferior survival. *Blood* 113: 3773-80, 2009. **CA (IF 10.558; Citations 69)**

    Our group led the statistical analysis of the data presented in this manuscript

37. Lo K, Hahne F, **Brinkman RR** & Gottardo R. flowClust: a Bioconductor package for automated gating of flow cytometry data. *BMC Bioinformatics* 10: 145 2009. **CA (IF 3.029; Citations 52)**

    The development of software implementation of the first robust automated clustering infrastructure for the analysis of flow cytometry data analysis was the result of the ongoing collaboration between Dr. Gottardo's group and my own, funded in part by my NIH R01 (EB 50034). The first author performed some of the research while embedded in my research group for four months.

38. Qian Y*, Tchuvatkina O*, Spidlen J, Wilkinson P, Gasparetto M, Jones AR, Manion FJ, Scheuermann RH, Sekaly R-P, **Brinkman RR.** FuGEFlow: data model and markup language for flow cytometry. *BMC Bioinformatics* 10:184, 2009. **CA (IF 3.029; Citations 10)**

    *These two persons were noted to have contributed equally to the publication.

I conceived and led this research effort, in collaboration with several groups. This research effort was funded entirely by my NIH R01 (EB 50034)

39. Strain E, Hahne F, **Brinkman RR** & Haaland P. Analysis of high throughput flow cytometry data using plateCore. *Adv Bioinformatics* 2009: 1-10, 2009. **CA (IF n/a; Citations 7)**
    I initiated the research program that laid the foundation for this project through the co-development of the BioConductor packages upon which this effort was built. I provided scientific direction to its direction, with the work carried out in the group of a co-applicant of my NIH proposal, which funded this effort entirely (NIH R01 EB 50034).

40. Vercauteren SM, Bashashati A, Wu D, **Brinkman RR**, Eaves C, Eaves A & Karsan A. Reduction in multilineage and erythroid progenitors distinguishes myelodysplastic syndromes from non-malignant cytopenias. *Leuk Res* 33: 1636-1642, 2009. **CA (IF 2.555; Citation 1)**

    Our group led the statistical analysis of the data presented in this manuscript. This effort was a significant contribution to having this manuscript published as it had languished for 2 years awaiting appropriate analytical methodologies to be applied.

41. Blimkie D, Fortuno ES III, Thommai F, Xu L, Fernandes E, Crabtree J, Rein-Weston A, Jansen K, **Brinkman RR*** & Kollmann TR*. Identification of B cells through negative gating-An example of the MIFlowCyt standard applied. *Cytometry A* 77: 546-551, 2010. **CA (IF 3.753; Citations 11)**

    I co-conceived of this research effort with Dr. Kollmann and co-led the research effort.
    *Co-senior authors

42. **Brinkman RR**, Courtot M, Derom D, Fostel JM, He Y, Lord P, Malone J, Parkinson H, Peters B, Rocca-Serra P, Ruttenberg A, Sansone SA, Soldatova LN, Stoeckert CJ, Jr., Turner JA, Zheng J & OBI Consortium. Modeling biomedical experimental processes with OBI. *J Biomed Semantics* 1: S7 2010. **CA (IF 2.346; Citations 131)**

    Melanie Courtot was a core developer for OBI for one year and played a key role in its early development.

    Although listed first, authorship was collaborative through a consortium with no over-all leader.

43. Hahne F*, Khodabakhshi AH*, Bashashati A, Wong CJ, Gascoyne RD, Weng AP, Seyfert-Margolis S, Bourcier K, Asare A, Lumley T, Gentleman R & **Brinkman RR**. Per-channel basis normalization methods for flow cytometry data. *Cytometry A* 77: 121-131, 2010. **SA (IF 3.753; Citations 18)**

    *These two persons were noted to have contributed equally to the publication.
    Dr. Gentleman and I separately conceived of this project and subsequently pooled our efforts. I led this research effort and co-wrote the manuscript with my post-doctoral student who undertook the effort under my supervision. This research effort was funded entirely by my NIH R01 (EB 50034).

44. Jiang X, Forrest D, Nicolini F, Turhan A, Guilhot J, Yip C, Holyoake T, Jorgensen H, Lambie K, Saw KM, Pang E, Vukovic R, Lehn P, Ringrose A, Yu M, **Brinkman RR**, Smith C, Eaves A & Eaves C. Properties of CD34$^+$ CML stem/progenitor cells that correlate with different clinical responses to imatinib mesylate. *Blood* 116: 2112-2121, 2010. **CA (IF 10.558; Citations 26)**

45. Shooshtari P, Fortuno ES III, Blimkie D, Yu M, Gupta A, Kollmann TR & **Brinkman RR**. Correlation analysis of intracellular and secreted cytokines via the generalized integrated mean fluorescence intensity. *Cytometry A* 77: 873-880, 2010. **SA (IF 3.753; Citations 13)**

My group conceived of the methodology and the analysis was led by my graduate student. This effort was funded entirely by my NIH R01 (EB 50034).

46. Spidlen J, Moore W, Parks D, Goldberg M, Bray C, Bierre P, Gorombey P, Hyun B, Hubbard M, Lange S, Lefebvre R, Leif R, Novo D, Ostruszka L, Triester A, Wood J, Murphy RF, Roederer M, Sudar D, Zigon R & **Brinkman RR**. Data file standard for flow cytometry, version FCS 3.1. *Cytometry A* 77: 97-100, 2010. **SA (IF 3.753; Citations 21)**

    I conceived and led this research effort, in collaboration with a large international collaborative team. My post doc was instrumental in its success. This research effort was funded entirely by my NIH R01 (EB 50034).

47. Xiang Z, Courtot M, **Brinkman RR**, Ruttenberg A & He Y. OntoFox: web-based support for ontology reuse. *BMC Res Notes* 3: 175, 2010. **CA (IF 3.729 Citations 48)**

    Melanie Courtot co-developed this research.

48. Zare H, Shooshtari P, Gupta A & **Brinkman RR**. Data reduction for spectral clustering to analyze high throughput flow cytometry data. *BMC Bioinformatics* 11: 403, 2010. **SA (IF 3.029*; Citations 85)**

    *This article received "Highly accessed" designation at the journal (29 days after being published, the paper was accessed 1004 times).

    This work was co-led by two graduate students in my group who shared first-author status. I led and supervised the work. This work was funded by the R01 I am a co-I on, led by Drs Robert Gentleman and now by Raphael Gottardo. This was the best performing supervised method in the FlowCAP evaluation.

49. Aghaeepour N, Nikolic R, Hoos HH & **Brinkman RR**. Rapid cell population identification in flow cytometry data. *Cytometry A* 79: 6-13, 2011. **SA (IF 3.729; Citations 82)** (top 10 accessed article for 2011 within journal)
    Nima is the graduate student in my group who led this work funded by an NIH R01 I am a co-I on, led initially by Dr. Robert Gentleman and now by Raphael Gottardo. Radina did her MSc thesis in my group and this project was a major component of her work. This work was specially highlighted in the issue with a one page review/discussion focused on this work by an invited expert. It also was the best performing method in the FlowCAP competition in terms of time/accuracy for unsupervised analysis.

    This paper was among the top 10 most-accessed articles in Cytometry Part A from January through March 2011 2013. The data comes from the Wiley Online Library usage statistics of downloads. "http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1552-4930/homepage/MostAccessed.html"

50. Courtot M, Gibson F, Lister AL, Malone J, Schober D, **Brinkman RR** & Ruttenberg A. MIREOT: The minimum information to reference an external ontology term. *Appl Ontol* 6: 23-33, 2011. **CA (IF 1.08; Citations 65)**

    MIREOT has great potential to facilitate ontology development, and is now being actively sued in several projects.

51. Rocca-Serra P, Ruttenberg A, O'Connor M, Greenbaum J, Courtot M, Sansone SA, Scheuermann R, The OBI Consortium and Peters B. Overcoming the ontology enrichment bottleneck with Quick Term Templates. *Applied Ontology* 6: 13-22, 2011.**CA (IF 1.08; Citations 16)**

52. Spidlen J, Shooshtari P, Kollmann TR & **Brinkman RR**. Flow cytometry data standards. *BMC Res Notes* 4: 50, 2011. **SA (IF 3.729 Citations 3)**

This is a review paper of the current state of the art of flow cytometry data standards.

53. Zare H, Bashashati A, Kridel R, Aghaeepour N, Haffari G, Connors JM, Gascoyne RD, Gupta A, ***Brinkman RR**, *Weng AP. Automated analysis of multidimensional flow cytometry data improves diagnostic accuracy between mantle cell lymphoma and small lymphocytic lymphoma. *American Journal of Clinical Pathology* 137: 75-85, 2012. **SA (IF 2.504; Citations 19)**

    This paper is the start of the application of my group's automated flow cytometry algorithms to the clinical flow cytometry data. I directed this research by a graduate student in my group.

    *Co-senior authors

54. Bashashati A, Johnson, NA, Khodabakhshi AH, Whiteside MD, Scott DW, Lo K, Gottardo R, Brinkman FSL, Connors JM, Slack GW, Gascoyne RD, Weng AP*, **Brinkman RR***. B-cells with high side scatter parameter by flow cytometry correlate with inferior survival in diffuse large B cell lymphoma. *Am J Clin Pathol* 137:805-814, 2012**. SA (IF 2.504; Citations 2)**

    *Co-senior authors

    This paper is the start of the application of my group's automated flow cytometry algorithms to the clinical flow cytometry data. I directed this research by a graduate student in my group.

55. Aghaeepour N, Chattopadhyay PK, Gansesan A, O'Neill K, Zare H, Jalali A, Hoos HH, Roederer M & **Brinkman RR**. Early immunologic correlates of HIV protection can be identified from computational analysis of complex multivariate T-cell flow cytometry assays. *Bioinformatics* 28: 1009-1016, 2012. **SA (IF 4.877; Citations 45)**

    I directed the graduate student in my group who led this effort to develop a new comprehensive data analysis approach. This is a landmark paper in terms of the amount and complexity of data analyzed and the significant improvement over what had been done on a previous manual analysis of the same dataset.

56. Aghaeepour N, Jalali A, O'Neill K, Chattopadhyay PK, Roederer M, Hoos HH & **Brinkman RR**. RchyOptimyx: cellular hierarchy optimization for flow cytometry. *Cytometry A* 81: 1022-1030, 2012. **SA (IF 3.729 ; Citations 35)**

    I directed the three graduate students in my group who led this effort to extend the high-dimensional data analysis approach for flow cytomery biomarker discovery. Many different groups have successfully applied this approach in collaboration with my group, with two manuscripts already published (#65, #70), and several others in progress. We have continued to develop this approach, leading to a second publication (#71).

    This paper was 3rd of the 10 most-accessed articles in **Cytometry Part A** from January through March 2013. The data comes from the Wiley Online Library usage statistics of downloads. "http://onlinelibrary.wiley.com/journal/10.1002/(ISSN)1552-4930/homepage/MostAccessed.html"

57. Benz C, Copley MR, Kent DG, Wohrer S, Cortes A, Aghaeepour N, Ma E, Mader H, Rowe K, Day C, Treloar D, **Brinkman RR** & Eaves CJ. Hematopoietic stem cell subtypes expand differentially during development and display distinct lymphopoietic programs. *Cell Stem Cell* 10: 273-283, 2012. **CA (IF 25.943; Citations 121)**

    My team led the statistical analysis of the data included in the paper.

58. Bray C, Spidlen J & **Brinkman RR**. FCS 3.1 Implementation guidance. *Cytometry A* 81: 523-526, 2012. **(group 80%) SA (IF 3.729; Citations 1)**

I led this effort as Chair of ISAC's data standards task force, technical work completed by a research associate in my group.

59. Cheung AM, Leung D, Rostamirad S, Dhillon K, Miller PH, Droumeva R, **Brinkman RR**, Hogge D, Roy DC & Eaves CJ. Distinct but phenotypically heterogeneous human cell populations produce rapid recovery of platelets and neutrophils after transplantation. *Blood* 119: 3431-3439, 2012. **CA (IF 10.558; Citations 13)**

My team led the statistical analysis of the data included in the paper.

60. Spidlen J, Breuer K, Rosenburg C, Kotecha N & **Brinkman RR**. FlowRepository: a resource of annotated flow cytometry datasets associated with peer-reviewed publications. *Cytometry A* 81: 727-731, 2012. **SA (IF 3.729; Citations 33)**

I conceived of the project and led the development team who built flowRepository, which we published this step-by-step instruction guide on its use as well as the academic article immediately following.

61. Streitz M, Fuhrmann S, Thomas D, Cheek E, Nomura L, Maecker H, Martus P, Aghaeepour N, **Brinkman RR**, Volk HD & Kern F. The phenotypic distribution and functional profile of tuberculin-specific CD4 T-cells characterizes different stages of TB infection. *Cytometry B Clin Cytom* 82: 360-368, 2012. **CA (IF 2.525; Citations 5)**

Best Original Paper published in Clinical Cytometry for 2012-2013. This annual award is given for the manuscript published under the Original Article category that is judged of the highest scientific quality, originality and impact by the Editors and Associate Editors of Clinical Cytometry. The Award was presented at the 2013 ESCCA meeting in Luxembourg, November 12- 14, 2013. My graduate student contributed to the computational analysis of the dataset described in this paper. We are currently working on a follow-up manuscript.

62. Aghaeepour N, Finak G, FlowCAP Consortium, DREAM Consortium, Hoos H, Mosmann TR, **Brinkman R***, Gottardo R* & Scheuermann RH*. Critical assessment of automated flow cytometry data analysis techniques. *Nat Methods* 10: 228-238, 2013. **SA (IF 25.953 Citations 243)**

*Indicates equal contribution from these authors

I conceived of this project, brought together the coordinating group involving two different consortia (98 co-authors) that co-led the effort. Due to the large size of the effort senior authorship was shared among three PIs, listed alphabetically. My graduate student was the first author, led the analysis components of the manuscript and the first version was drafted in my group. This paper set the benchmark for the evaluation of automated data analysis methods for flow cytometry data involving every group active in the field in an open evaluation of the state of the art. I also secured funding for a meeting at the NIH involving all the groups to present and discuss the results to the consortia and to lay the ground work for further efforts in the field, leading to now a total of four Challenges being completed (the latest is now being analyzed). One of the algorithms developed in my group (flowType) was identified as having the best performance (combination of time to analyze samples and accuracy).

64. Hills M, O'Neill K, Falconer E, **Brinkman R** & Lansdorp PM. BAIT: Organizing genomes and mapping rearrangements in single cells. *Genome Med* 5: 82 2013. **CA (IF 3.91; Citations 12)**

My graduate student conceived the algorithm in collaboration with the lead author that is the foundation of all the results and developed and implemented the approach and analyzed the data.

65. Kannan N, Huda N, Tu L, Droumeva R, Aubert G, Chavez E, **Brinkman RR**, Lansdorp P, Emerman J, Abe S, Eaves C & Gilley D. The luminal progenitor compartment of the normal human mammary gland constitutes a unique site of telomere dysfunction. *Stem Cell Reports* 1: 28-37, 2013. **CA (IF 3.766; Citations 30)**

    My group performed all the statistical analysis for this manuscript.

66. O'Neill K, Aghaeepour N, Spidlen J & **Brinkman R**. Flow cytometry bioinformatics. *PLoS Comput Biol* 9: e1003365 2013. **SA (IF 4.867; Citations 36)**

    This work was entirely conducted by my group under my direction.

67. Spidlen J, Barsky A, Breuer K, Carr P, Nazaire MD, Hill BA, Qian Y, Liefeld T, Reich M, Mesirov JP, Wilkinson P, Scheuermann RH, Sekaly RP & **Brinkman RR**. GenePattern flow cytometry suite. *Source Code Biol Med* 8: 14 2013. **SA (IF 1.33; Citations 2)**

    I conceived, directed and led this effort, with all the effort conducted by my group.

68. Villanova F, Di Meglio P, Inokuma M, Aghaeepour N, Perucha E, Mollon J, Nomura L, Hernandez-Fuentes M, Cope A, Prevost AT, Heck S, Maino V, Lord G, **Brinkman RR** & Nestle FO. Integration of lyoplate based flow cytometry and computational analysis for standardized immunological biomarker discovery. *PLoS One* 8: e65485 2013. **CA (IF 5.534; Citations 8)**

    We performed the computational analysis component of the research, later validated by manual analysis.

69. Zare H, Haffari G, Gupta A & **Brinkman RR**. Scoring relevancy of features based on combinatorial analysis of Lasso with application to lymphoma diagnosis. *BMC Genomics* 14: doi: 10.1186/1471-2164-14-S1-S14 2013. **SA (IF 4.07; Citation 15)**

    I directed the graduate student in my group who developed this new approach to feature analysis, which we applied to have a best-performing method in FlowCAP evaluation.

70. Courtot M, **Brinkman RR** & Ruttenberg A. The logic of surveillance guidelines: an analysis of vaccine adverse event reports from an ontological perspective. *PLoS One* 9: e92632 2014. **SA (IF 3.534; Citation 6)**
    My graduate student performed all the analysis and work and this was the final chapter in her thesis. I directed all her work in collaboration with Dr. Ruttenberg, who was placed as senior author as Melanie was first.

71. Craig FE, **Brinkman R**, Ten Eyck S & Aghaeepour N. Computational analysis optimizes the flow cytometric evaluation for lymphoma. *Cytometry B Clin Cytom* 86: 18-24, 2014. **CA (IF 2.231; Citations 4)**

    Dr. Craig and I put Nima (my graduate student) as last author for his leadership role in this project under my supervision, and we used her data and research question. My graduate student (as senior author) in collaboration with the first author (Collaborating PI) used the algorithmic approach we published separately to analyze the data, make interpret the results and draft the manuscript.

72. Johnstone J, Parsons R, Botelho F, Millar J, McNeil S, Fulop T, McElhaney J, Andrew MK, Walter SD, Devereaux PJ, Malekesmaeili M, **Brinkman RR**, Mahony J, Bramson J & Loeb M. Immune biomarkers predictive of respiratory viral infection in elderly nursing home residents. *PLoS One* 9: e108481, 2014. **CA (IF 5.534; Citations 14)**

73. O'Neill K, Jalali A, Aghaeepour N, Hoos H & **Brinkman RR**. Enhanced flowType/RchyOptimyx: A BioConductor pipeline for discovery in high-dimensional cytometry data. *Bioinformatics* 30: 1329-1330, 2014. **SA (IF 5.323; Citations 16)**

    This paper is a full re-implementaion and extension of our previously published approach and the effort was conducted by 3 graduate students in my group. Dr. Hoos provided feedback on the algorithmic approach and made suggestions for improvements.

74. Rothe K, Lin H, Lin KB, Leung A, Wang HM, Malekesmaeili M, **Brinkman RR**, Forrest DL, Gorski SM & Jiang X. The core autophagy protein ATG4B is a potential biomarker and therapeutic target in CML stem/progenitor cells. *Blood.* 123: 3622-3634, 2014. **CA (IF 9.060; Citations 69)**

    We performed all the statistical analysis for the manuscript.

75. Von Rossum A, Enns W, Shi YP, MacEwan GE, Malekesmaeili M, **Brinkman R** & Choy JC. Bim regulates alloimmune-mediated vascular injury through effects on T-cell activation and death. *Arterioscler Thromb Vasc Biol* 34: 1290-1297, 2014. **CA (IF 6.338; Citations 2)**

    We performed all the automated analysis that was required to get this paper accepted after initial rejection, using our existing approaches to provide more robust results requested by reviewers.

76. Spidlen J, Bray C, ISAC Data Standards Task Force & **Brinkman RR**. ISAC's classification results file format. *Cytometry A* 87: 86-88, 2015. **(IF 3.07; Citations 3)**

77. Malek M, Taghiyar MJ, Chong L, Finak G, Gottardo R & **Brinkman RR**. flowDensity: reproducing manual gating of flow cytometry data by automated density-based cell population identification. *Bioinformatics* 31: 606-7, 2015. **(IF 5.766; Citations 33)**

78. Courtot M, Meskas J, Diehl AD, Droumeva R, Gottardo R, Jalali A, Taghiyar MJ, Maecker HT, McCoy JP, Ruttenberg A, Scheuermann RH & **Brinkman RR**. flowCL: ontology-based cell population labeling in flow cytometry. *Bioinformatics* 31:1337-9, 2015. **(IF 4.98; Citations 10)**

79. Kvistborg P, Gouttefangeas C, Aghaeepour N, Cazaly A, Chattopadhyay PK, Eckl J, Ferrari G, Finak G, Hadrup SR, Maecker HT, Maurer D, Mosman, T, Qiu P, Scheuermann RH, Marij JPM, **Brinkman RR*** & Britten CM*. Thinking outside the gate: single-cell assessments in multiple dimensions. *Immunity* 42:591-2, 2015. **(IF 24.082 ; Citations 34)** *Indicates equal contribution from these authors

80. O'Neill K, Aghaeepour N, Hogge D, Karsan A, Dalal B & **Brinkman R**. Deep profiling of multitube flow cytometry data. *Bioinformatics* 31:1623-31, 2015. **(IF 4.98; Citations 1)**

81. Spidlen J, Moore W, ISAC Data Standards Task Force & **Brinkman RR**. ISAC's Gating-ML 2.0 data exchange standard for gating description. *Cytometry A* 87(7):683-7, 2015. **(IF 3.07 ; Citations 8)**

82. Aghaeepour N, Chattopadhyay P, Chikina M, Dhaene T,Van Gassen S, Kursa M, Lambrecht BN, Malek M, Qian Y, Qiu P, Saeys Y, Stanton S, Tong D, Vens C, Walkowiak S, Wang S, Finak G, Gottardo R, Mosmann T, Nolan G, Scheuermann RH & **Brinkman RR**. A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. *Cytometry A* 89 (1): 16-21, 2016. **(IF 3.222; Citations 21)**

83. Finak G, Langweiller M, Jaimes M, Malek M, Taghiyar J, Korin Y, Raddassi K, Devine L, Obermoser G, Pekalski ML, Pontikos N, Diaz A, Heck S, Villanova F, Terrazzini N, Kern F, Qian Y, Stanton R, Wang K, Brandes A, Ramey J, Aghaeepour N, Mosmann T, Scheuermann RH, Reed E, Palucka K, Pascual V, Blomberg BB, Nestle F, Nussenblatt RB, **Brinkman RR**, Gottardo R, Maecker H & McCoy JP. Standardizing Flow Cytometry Immunophenotyping Analysis from the Human ImmunoPhenotyping Consortium. *Sci Rep* 10;6:20686, 2016. **(IF 5.23; Citations 63)**

84. **Brinkman RR**, Aghaeepour N, Finak G, Gottardo R, Mosmann T & Scheuermann RH. Automated analysis of flow cytometry data comes of age. *Cytometry A* 89(1):13-5, 2016. **(IF 3.18; Citations 8)**

85. O'Neill K & **Brinkman RR**. Publishing code is essential for reproducible flow cytometry bioinformatics. *Cytometry A* 89(1): 10-1, 2016. **(IF 3.18; Citations 6)**

86. Fletez-Brant K, Spidlen J, **Brinkman RR**, Roederer M & Chattopadhyay PK. flowClean: Automated identification and removal of fluorescence anomalies in flow cytometry data. *Cytometry A* 89(5):461-71, 2016. **(IF 3.18; Citations 8)**

87. Bandrowski A, **Brinkman R**, Brochhausen M, Brush MH, Bug B, Chibucos MC, Clancy K, Courtot M, Derom D, Dumontier M, Fan L, Fostel J,Fragoso G, Gibson F, Gonzalez-Beltran A, Haendel MA, He Y, Heiskanen M, Hernandez-Boussard T, Jensen M, Lin Y, Lister AL, Lord P, Malone J, Manduchi E, McGee M, Morrison N, Overton JA, Parkinson H, Peters B, Rocca-Serra P, Ruttenberg A, Sansone SA, Scheuermann RH, Schober D, Smith B, Soldatova LN, Stoeckert CJ Jr, Taylor CF, Torniai C, Turner JA, Vita R, Whetzel PL & Zheng J. The Ontology for Biomedical Investigations. *PLos One* 1(4):e0154556, 2016. **(IF 3.54; Citations 49)**

88. Johnstone J, Parsons R, Botelho F, Millar J, McNeil S, Fulop T, McElhaney J, Andrew MK, Walter SD, Devereaux PJ, Malek M, **Brinkman RR**, Bramson J & Loeb M. T-cell Phenotypes Predictive of Frailty and Mortality in Elderly Nursing Home Residents. *J Am Geriatr Soc* 65(1):153-59, 2017. **(IF 3.84; Citations 7)**

89. Parks DR, El Khettabi F, Chase E, Hoffman RA, Perfetto SP, Spidlen J, Wood JC, Moore WA & **Brinkman RR**. Evaluating flow cytometer performance with weighted quadratic least squares analysis of LED and multi-level bead data. *Cytometry A* 91(3):232-249, 2017. **(IF 3.22; Citations 4)**

90. Cossarizza A, Chang HD, Radbruch A, Andra I, Annunziato F, Bacher P, Barnaba V, Battistini L, Bauer WM, Baumgart S, Becher B, Beisker W, Berek C, Blanco A, Borsellino G, Boulais PE, **Brinkman RR**, Buscher M, Busch DH, Bushnell TP, Cao X, Cavani A, Chattopadhyay PK, Cheng Q, Chow S, Clerici M, Cooke A, Cosma A, Cosmi L, Cumano A, Dang VD, Davies D, De Biasi S, Del Zotto G, Della Bella S, Dellabona P, Deniz G, Dessing M, Diefenbach A, Di Santo J, Dieli F, Dolf A, Donnenberg VS, Dorner T, Ehrhardt GRA, Endl E, Engel P, Engelhardt B, Esser C, Everts B, Falk CS, Fehniger TA, Filby A, Fillatreau S, Follo M, Forster I, Foster J, Foulds GA, Frenette PS, Galbraith D, Garbi N, Garcia-Godoy MD, Ghoreschi K, Gibellini L, Goettlinger C, Goodyear CS, Gori A, Grogan J, Gross M, Grutzkau A, Grummitt D, Hahn J, Hammer Q, Hauser AE, Haviland DL, Hedley D, Herrera G, Herrmann M, Hiepe F, Holland T, Hombrink P, Houston JP, Hoyer BF, Huang B, Hunter CA, Iannone A, Jack HM, Javega B, Jonjic S, Juelke K, Jung S, Kaiser T, Kalina T, Keller B, Khan S, Kienhofer D, Kroneis T, Kunkel D, Kurts C, Kvistborg P, Lannigan J, Lantz O, Larbi A, LeibundGut-Landmann S, Leipold MD, Levings MK, Litwin V, Liu Y, Lohoff M, Lombardi G, Lopez L, Lovett-Racke A, Lubberts E, Ludewig B, Lugli E, Maecker HT, Martrus G, Matarese G, Maueroder C, McGrath M, McInnes I, Mei HE, Melchers F, Melzer S, Mielenz D, Mills K, Mjosberg J, Moore J, Moran B, Moretta A, Moretta L, Mosmann TR, Muller S, Muller W, Munz C, Multhoff G, Munoz LE, Murphy KM,

Nakayama T, Nasi M, Neudorfl C, Nolan J, Nourshargh S, O'Connor JE, Ouyang W, Oxenius A, Palankar R, Panse I, Peterson P, Peth C, Petriz J, Philips D, Pickl W, Piconese S, Pinti M, Pockley AG, Podolska MJ, Pucillo C, Quataert SA, Radstake T, Rajwa B, Rebhahn JA, Recktenwald D, Remmerswaal EBM, Rezvani K, Rico LG, Robinson JP, Romagnani C, Rubartelli A, Ruland J, Sakaguchi S, Sala-de-Oyanguren F, Samstag Y, Sanderson S, Sawitzki B, Scheffold A, Schiemann M, Schildberg F, Schimisky E, Schmid SA, Schmitt S, Schober K, Schuler T, Schulz AR, Schumacher T, Scotta C, Shankey TV, Shemer A, Simon AK, Spidlen J, Stall AM, Stark R, Stehle C, Stein M, Steinmetz T, Stockinger H, Takahama Y, Tarnok A, Tian Z, Toldi G, Tornack J, Traggiai E, Trotter J, Ulrich H, van der Braber M, van Lier RAW, Veldhoen M, Vento-Asturias S, Vieira P, Voehringer D, Volk HD, von Volkmann K, Waisman A, Walker R, Ward MD, Warnatz K, Warth S, Watson JV, Watzl C, Wegener L, Wiedemann A, Wienands J, Willimsky G, Wing J, Wurst P, Yu L, Yue A, Zhang Q, Zhao Y, Ziegler S & Zimmermann J. Guidelines for the use of flow cytometry and cell sorting in immunological studies. *Eur J Immunol* 47:1584-1797, 2017. **(IF 4.25; Citations 131)**

As of May/June 2019, this highly cited paper received enough citations to place it in the top 1% of the academic field of Immunology based on a highly cited threshold for the field and publication year. (Web of Science).

91. Spidlen J & **Brinkman RR**. Use FlowRepository to share your clinical data upon study publication. *Cytometry B Clinical Cytometry* 94(1):196-98, 2018. (**IF 2.82; Citations 1)**
92. Rahim A, Meskas J, Drissler S, Yue A, Lorenc A, Laing A, Saran N, White J, Abeler-Dorner L, Hayday A & **Brinkman RR**. High Throughput Automated Analysis of Big Flow Cytometry Data. *Methods* 134-135:164-76, 2018. (**IF 3.80; Citations 1)**
93. Lux M, **Brinkman RR**, Chauve C, Laing A, Lorenc A, Abeler-Dorner L & Hammer B. flowLearn: Fast and precise identification and quality checking of cell populations in flow cytometry. *Bioinformatics* 34:2245-53, 2018. **(IF 5.48; Citations 4)**
94. Brink BG, Meskas J, **Brinkman RR**. ddPCRclust - An R package and Shiny app for automated analysis of multiplexed ddPCR data. *Bioinformatics* 34:2687-89, 2018. **(IF 5.48; Citations)**
95. Parks D, Moore W, **Brinkman RR**, Chen Y, Condello D, El Khettabi F, Molan JP, Perfetto SP, Redelman D, Spidlen J, Van Dyke J, Wang L & Wood JCS. Methodology for evaluating and comparing fluorescence measurement capabilities: Multi-site study of 23 flow cytometers. *Cytometry A* 93A:1087-1091, 2018. **(IF 3.260; Citations)**
96. Ivison S, Malek M, Garcia RV, Broady R, Halpin A, Richaud M, Brant R, Wang S-I, Goupil M, Guan Q, Ashton P, Warren J, Rajab A, Urschel S, Kumar D, Streitz M, Sawitzki B, Schlickeiser S, Bijl J, Wall DA, Delisle J-S, West LJ, **Brinkman RR** and Levings MK. A standardized immune phenotyping and automated data analysis platform for multicenter biomarker studies. *The Journal of Clinical Investigation Insight* 3:e121867, 2018.
97. Conrad VK, Dubay CJ, Malek M, **Brinkman RR**, Koguchi Y & Redmond WL. Implementation and Validation of an Automated Flow Cytometry Analysis Pipeline for Human Immune Profiling. *Cytometry Part A* 95:183-191, 2019. **(IF 3.260; Citations 1)**
98. Lee AH§, Shannon C§, Amenyogbe N§, Bennike TB§, Diray-Arce J§, Idoko O, Gill EE, Ben-Othman R*, Pomat WS, van Haren S, Lê Cao K-A, Cox M, Darboe A, Falsafi R, Ferrari D, Harbeson D, He D, Bing C, Hinshaw SH, Ndure J, Njie-Jobe J, Pettengill MA, Richmond PC, Ford R, Saleu G, Masiria G, Matlam JP, Kirarock W, Roberts E, Malek M, Sanchez-Schmitz G, Singh A, Angelidou A, Smolen KK, the EPIC Consortium, **Brinkman RR**, Ozonoff A, Hancock R, van den Biggelaar AHJ, Steen H*,

Tebbutt SJ*, Kampmann B*, Levy O* & Kollmann TR*. Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. *Nature Comm* 10:1092, 2019. **(IF 12.353; Citations)**

§ Co-first authors; *Co-senior authors

99. Montante S, Brinkman RR. Flow cytometry data analysis: Recent tools and algorithms. *International Journal of Laboratory Hematology* 41: 56-62, 2019. **SA**

100. Tighe RM, Redente EF, Yu YR, Herold S, Sperling AI, Curtis JL, Duggan R, Swaminathan S, Nakano H, Zacharias WJ, Janssen WJ, Freeman CM, **Brinkman RR**, Singer BD, Jakubzick CV & Misharin AV. Improving the Quality and Reproducibility of Flow Cytometry in the Lung. An Official American Thoracic Society Workshop Report. *Am J Respir Cell Mol Biol* 61:150-161, 2019. **CA**

101. Czechowska K, Lannigan J, Wang L, Arcidiacono J, Ashhurst TM, Barnard RM, Bauer S, Bispo C, Bonilla DL, **Brinkman RR**, Cabanski M, Chang H-D, Chakrabarti L, Chojnowski G, Cotleur B, Degheidy H, Dela Cruz GV, Eck S, Elliott J, Errington R, Filby A, Gagnon D, Gardner R, Green C, Gregory M, Groves CJ, Hall C, Hammes F, Hedrick M, Hoffman R, Icha J, Ivaska J, Jenner DC, Jones D, Kerckhof F-M, Kukat C, Lanham D, Leavesley S, Lee M, Lin-Gibson S, Litwin V, Liu Y, Molloy J, Moore JS, Müller S, Nedbal J, Niesner R, Nitta N, Ohlsson-Wilhelm B, Paul NE, Perfetto S, Portat Z, Props R, Radtke S, Rayanki R, Rieger A, Rogers S, Rubbens P, Salomon R, Schiemann M, Sharpe J, Sonder SU, Stewart JJ, Sun Y, Ulrich H, Van Isterdael G, Vitaliti A, van Vreden C, Weber M, Zimmermann J, Vacca G, Wallace P & Tárnok A. Cyt-Geist: Current and Future Challenges in Cytometry: Reports of the CYTO 2018 Conference Workshops. *Cytometry A* 95:598-644, 2019. **CA**

102. **Brinkman RR**. Improving the Rigor and Reproducibility of Flow Cytometry-Based Clinical Research and Trials Through Automated Data Analysis. *Cytometry A* 97:107-112, 2019. **FA**

103. Cossarizza A, Chang HD, Radbruch A, Acs A, Adam D, Adam-Klages S, Agace WW, Aghaeepour N, Akdis M, Allez M, Almeida LN, Alvisi G, Anderson G, Andrä I, Annunziato F, Anselmo A, Bacher P, Baldari CT, Bari S, Barnaba V, Barros-Martins J, Battistini L, Bauer W, Baumgart S, Baumgarth N, Baumjohann D, Baying B, Bebawy M, Becher B, Beisker W, Benes V, Beyaert R, Blanco A, Boardman DA, Bogdan C, Borger JG, Borsellino G, Boulais PE, Bradford JA, Brenner D, **Brinkman RR**, Brooks AES, Busch DH, Büscher M, Bushnell TP, Calzetti F, Cameron G, Cammarata I, Cao X, Cardell SL, Casola S, Cassatella MA, Cavani A, Celada A, Chatenoud L, Chattopadhyay PK, Chow S, Christakou E, Čičin-Šain L, Clerici M, Colombo FS, Cook L, Cooke A, Cooper AM, Corbett AJ, Cosma A, Cosmi L, Coulie PG, Cumano A, Cvetkovic L, Dang VD, Dang-Heine C, Davey MS, Davies D, De Biasi S, Del Zotto G, Dela Cruz GV, Delacher M, Della Bella S, Dellabona P, Deniz G, Dessing M, Di Santo JP, Diefenbach A, Dieli F, Dolf A, Dörner T, Dress RJ, Dudziak D, Dustin M, Dutertre CA, Ebner F, Eckle SBG, Edinger M, Eede P, Ehrhardt GRA, Eich M, Engel P, Engelhardt B, Erdei A, Esser C, Everts B, Evrard M, Falk CS, Fehniger TA, Felipo-Benavent M, Ferry H, Feuerer M, Filby A, Filkor K, Fillatreau S, Follo M, Förster I, Foster J, Foulds GA, Frehse B, Frenette PS, Frischbutter S, Fritzsche W, Galbraith DW, Gangaev A, Garbi N, Gaudilliere B, Gazzinelli RT, Geginat J, Gerner W, Gherardin NA, Ghoreschi K, Gibellini L, Ginhoux F, Goda K, Godfrey DI, Goettlinger C, González-Navajas JM, Goodyear CS, Gori A, Grogan JL, Grummitt D, Grützkau A, Haftmann C, Hahn J, Hammad H, Hämmerling G, Hansmann L, Hansson G, Harpur CM, Hartmann S, Hauser A, Hauser AE, Haviland DL, Hedley D, Hernández DC, Herrera G, Herrmann M, Hess C, Höfer T, Hoffmann P, Hogquist K, Holland T, Höllt T, Holmdahl R, Hombrink P, Houston JP, Hoyer BF, Huang B, Huang FP, Huber JE, Huehn J, Hundemer M, Hunter CA, Hwang WYK, Iannone A, Ingelfinger F, Ivison SM, Jäck HM, Jani PK, Jávega B, Jonjic S, Kaiser T, Kalina T, Kamradt T, Kaufmann SHE, Keller B, Ketelaars SLC,

Khalilnezhad A, Khan S, Kisielow J, Klenerman P, Knopf J, Koay HF, Kobow K, Kolls JK, Kong WT, Kopf M, Korn T, Kriegsmann K, Kristyanto H, Kroneis T, Krueger A, Kühne J, Kukat C, Kunkel D, Kunze-Schumacher H, Kurosaki T, Kurts C, Kvistborg P, Kwok I, Landry J, Lantz O, Lanuti P, LaRosa F, Lehuen A, LeibundGut-Landmann S, Leipold MD, Leung LYT, Levings MK, Lino AC, Liotta F, Litwin V, Liu Y, Ljunggren HG, Lohoff M, Lombardi G, Lopez L, López-Botet M, Lovett-Racke AE, Lubberts E, Luche H, Ludewig B, Lugli E, Lunemann S, Maecker HT, Maggi L, Maguire O, Mair F, Mair KH, Mantovani A, Manz RA, Marshall AJ, Martínez-Romero A, Martrus G, Marventano I, Maslinski W, Matarese G, Mattioli AV, Maueröder C, Mazzoni A, McCluskey J, McGrath M, McGuire HM, McInnes IB, Mei HE, Melchers F, Melzer S, Mielenz D, Miller SD, Mills KHG, Minderman H, Mjösberg J, Moore J, Moran B, Moretta L, Mosmann TR, Müller S, Multhoff G, Muñoz LE, Münz C, Nakayama T, Nasi M, Neumann K, Ng LG, Niedobitek A, Nourshargh S, Núñez G, O'Connor JE, Ochel A, Oja A, Ordonez D, Orfao A, Orlowski-Oliver E, Ouyang W, Oxenius A, Palankar R, Panse I, Pattanapanyasat K, Paulsen M, Pavlinic D, Penter L, Peterson P, Peth C, Petriz J, Piancone F, Pickl WF, Piconese S, Pinti M, Pockley AG, Podolska MJ, Poon Z, Pracht K, Prinz I, Pucillo CEM, Quataert SA, Quatrini L, Quinn KM, Radbruch H, Radstake TRDJ, Rahmig S, Rahn HP, Rajwa B, Ravichandran G, Raz Y, Rebhahn JA, Recktenwald D, Reimer D, Reis E Sousa C, Remmerswaal EBM, Richter L, Rico LG, Riddell A, Rieger AM, Robinson JP, Romagnani C, Rubartelli A, Ruland J, Saalmüller A, Saeys Y, Saito T, Sakaguchi S, Sala-de-Oyanguren F, Samstag Y, Sanderson S, Sandrock I, Santoni A, Sanz RB, Saresella M, Sautes-Fridman C, Sawitzki B, Schadt L, Scheffold A, Scherer HU, Schiemann M, Schildberg FA, Schimisky E, Schlitzer A, Schlosser J, Schmid S, Schmitt S, Schober K, Schraivogel D, Schuh W, Schüler T, Schulte R, Schulz AR, Schulz SR, Scottá C, Scott-Algara D, Sester DP, Shankey TV, Silva-Santos B, Simon AK, Sitnik KM, Sozzani S, Speiser DE, Spidlen J, Stahlberg A, Stall AM, Stanley N, Stark R, Stehle C, Steinmetz T, Stockinger H, Takahama Y, Takeda K, Tan L, Tárnok A, Tiegs G, Toldi G, Tornack J, Traggiai E, Trebak M, Tree TIM, Trotter J, Trowsdale J, Tsoumakidou M, Ulrich H, Urbanczyk S, van de Veen W, van den Broek M, van der Pol E, Van Gassen S, Van Isterdael G, van Lier RAW, Veldhoen M, Vento-Asturias S, Vieira P, Voehringer D, Volk HD, von Borstel A, von Volkmann K, Waisman A, Walker RV, Wallace PK, Wang SA, Wang XM, Ward MD, Ward-Hartstonge KA, Warnatz K, Warnes G, Warth S, Waskow C, Watson JV, Watzl C, Wegener L, Weisenburger T, Wiedemann A, Wienands J, Wilharm A, Wilkinson RJ, Willimsky G, Wing JB, Winkelmann R, Winkler TH, Wirz OF, Wong A, Wurst P, Yang JHM, Yang J, Yazdanbakhsh M, Yu L, Yue A, Zhang H, Zhao Y, Ziegler SM, Zielinski C, Zimmermann J, Zychlinsky A. Guidelines for the use of flow cytometry and cell sorting in immunological studies (second edition). *Eur J Immunol* 49:1457-1973, 2019. **CA**

104. Czechowska K, Lannigan J, Aghaeepour N, Back JB, Begum J, Behbehani G, Bispo C, Bitoun D, Fernandez AB, Boova ST, **Brinkman RR**, Ciccolella CO, Cotleur B, Davies D, Dela Cruz GV, Del Rio-Guerra R, Des Lauriers-Cox AM, Douagi I, Dumrese C, Bonilla Escobar DL, Estevam J, Ewald C, Fossum A, Gaudilliere B, Green C, Groves C, Hall C, Haque Y, Hedrick MN, Hogg K, Hsieh EWY, Irish J, Lederer J, Leipold M, Lewis-Tuffin LJ, Litwin V, Lopez P, Nasdala I, Nedbal J, Ohlsson-Wilhelm BM, Price KM, Rahman AH, Rayanki R, Rieger AM, Robinson JP, Shapiro H, Sun YS, Tang VA, Tesfa L, Telford WG, Walker R, Welsh JA, Wheeler P & Tarnok A. Cyt-Geist: Current and Future Challenges in Cytometry: Reports of the CYTO 2019 Conference Workshops. *Cytometry A* 95:1236-1274, 2019. **CA**
105. Yue A, Chauve C, Libbrecht M & **Brinkman R**. Identifying differential cell populations in flow cytometry data accounting for marker frequency. *bioRxiv* 837765, 2019.

106. Nissen MD, Kusakabe M, Wang X, Simkin G, Gracias D, Tyshchenko K, Hill A, Meskas J, Hung S, Chavez EA, Ennishi D, Aoki T, Sarkozy C, Connors JM, Farinha P, Slack GW, Gascoyne RD, **Brinkman RR**, Scott DW, Steidl C & Weng AP. Single Cell Phenotypic Profiling of 27 DLBCL Cases Reveals Marked Intertumoral and Intratumoral Heterogeneity. *Cytometry A* 97:620-629, 2020. **CA**

107. Abeler-Dorner L, Laing AG, Lorenc A, Ushakov DS, Clare S, Speak AO, Duque-Correa MA, White JK, Ramirez-Solis R, Saran N, Bull KR, Moron B, Iwasaki J, Barton PR, Caetano S, Hng KI, Cambridge E, Forman S, Crockford TL, Griffiths M, Kane L, Harcourt K, Brandt C, Notley G, Babalola KO, Warren J, Mason JC, Meeniga A, Karp NA, Melvin D, Cawthorne E, Weinrick B, Rahim A, Drissler S, Meskas J, Yue A, Lux M, Song-Zhao GX, Chan A, Ballesteros Reviriego C, Abeler J, Wilson H, Przemska-Kosicka A, Edmans M, Strevens N, Pasztorek M, Meehan TF, Powrie F, **Brinkman R**, Dougan G, Jacobs W, Jr., Lloyd CM, Cornall RJ, Maloy KJ, Grencis RK, Griffiths GM, Adams DJ & Hayday AC. High-throughput phenotyping reveals expansive genetic and structural underpinnings of immune variation. *Nat Immunol* 21:86-100, 2020. **CA**

108. Lin H, Rothe K, Chen M, Wu A, Babaian A, Yen R, Zeng J, Ruschmann J, Petriv OI, O'Neill K, Maetzig T, Knapp D, Nakamichi N, **Brinkman R**, Birol I, Forrest DL, Hansen C, Humphries KK, Eaves CJ & Jiang X. The miR-185/PAK6 Axis Predicts Therapy Response and Regulates Survival of Drug-Resistant Leukemic Stem Cells in CML. *Blood* 136:596-609, 2020. **CA**

109. Idoko OT, Smolen KK, Wariri O, Imam A, Shannon CP, Dibassey T, Diray-Arce J, Darboe A, Strandmark J, Ben-Othman R, Odumade OA, McEnaney K, Amenyogbe N, Pomat WS, van Haren S, Sanchez-Schmitz G, **Brinkman RR**, Steen H, Hancock REW, Tebbutt SJ, Richmond PC, van den Biggelaar AHJ, Kollmann TR, Levy O, Ozonoff A & Kampmann B. Clinical Protocol for a Longitudinal Cohort Study Employing Systems Biology to Identify Markers of Vaccine Immunogenicity in Newborn Infants in The Gambia and Papua New Guinea. *Front Pediatr* 8:197, 2020. **CA**

110. Brook B, Harbeson DJ, Shannon CP, Cai B, He D, Ben-Othman R, Francis F, Huang J, Varankovich N, Liu A, Bao W, Bjerregaard-Andersen M, Schaltz-Buchholzer F, Sanca L, Golding CN, Larsen KL, Levy O, Kampmann B, **EPIC Consortium**, Tan R, Charles A, Wynn JL, Shann F, Aaby P, Benn CS, Tebbutt SJ, Kollmann TR & Amenyogbe N. BCG vaccination-induced emergency granulopoiesis provides rapid protection from neonatal sepsis. *Sci Transl Med* 12:2020. **CA**

111. Shannon CP, Blimkie TM, Ben-Othman R, Gladish N, Amenyogbe NA, Drissler S, Edgar RD, Chan Q, Krajden M, Foster LJ, Kobor MS, Mohn B, **Brinkman RR**, Le Cao K-A, Scheuermann RH, Tebbutt SJ, Hancock REW, Koff W, Kollmann T, Sadarangani M, Lee AH. Multi-omic data integration allows baseline immune signatures to predict hepatitis B vaccine response in a small cohort. *Frontiers in Immunology, Vaccines and Molecular Therapeutics*, 11:578801, 2020. **CA**

112. Ben-Othman R, Cai B, Liu A,Varankovicha N, He D, Blimkie TM, Lee A, Gill EE, Novotny M, Aevermann B, Drissler S, Shannon CP, McCann S, Marty K, Bjornson G, Edgar RD. Lin DTS. MacIsaac J, Amenyogbe N, Chan Q, Llibre A, Joyce C, Landais E, Le K, Reiss SM, Havenar-Daughton C, Heran M, Sangha B, Walt D, Krajden M, Crotty S, Sok D, Briney B, Burton D, Duffy D, Foster LJ, Mohn WW, Kobor MS, Tebbutt SJ, **Brinkman RR,** Scheuermann R, Hancock RE, Kollmann T, Sadarangani M. Systems Biology Methods Applied to Blood and Tissue for a Comprehensive Analysis of Immune Response to Hepatitis B Vaccine in Adults. *Frontiers in Immunology*, 11:580373, 2020. **CA**

113. Bennike TB, Fatou B, Angelidou A, Diray-Arce J, Falsafi R, Ford R, Gill EE, van Haren SD, Idoko OT, Lee AH, Ben-Othman R, Pomat WS, Shannon CP, Smolen KK, **on belalf of the EPIC Consortium,**

Tebbutt SJ, Ozonoff A, Richmond PC, Biggelaar AHJvd, Hancock REW, Kampmann B, Kollmann TR, Levy O & Steen H. Preparing for Life: Plasma Proteome Changes and Immune System Development During the First Week of Human Life. *Front Immunol* 11:578505, 2020. **CA**

114. Cuvelier GDE, Li A, Drissler S, Kariminia A, Abdossamadi S, Rozmus J, Chanoine JP, Ng B, Mostafavi S, **Brinkman RR**, Schultz KR. "Age Related Differences in the Biology of Chronic Graft-Versus-Host Disease After Hematopoietic Stem Cell Transplantation". *Front Immunol* 11:571884, 2020. **CA**
115. Spidlen J, Moore W, Parks D, Goldberg M, Blenman K, Cavenaugh JS, **Brinkman R**. Data File Standard for Flow Cytometry, Version FCS 3.2. *Cytometry Part A* 99:100-102, 2021. **SA**
116. Blenman KRM, Spidlen J, Parks DR, Moore W, Treister A, Leif R, Bray C, Goldberg M, Force IDST & **Brinkman R**. ISAC Probe Tag Dictionary: Standardized Nomenclature for Detection and Visualization Labels Used in Cytometry and Microscopy Imaging. *Cytometry Part A* 99:103-106, 2021. **SA**
117. Hill AJ, Zhang C, Kusakabe M, Gowing K, **Brinkman RR**, Wang X, Weng AP, Craig JW. Occurrence of T-cell and NK-cell subsets with less well-recognized phenotypes in peripheral blood submitted for routine flow cytometry analysis. *Cytometry B Clin Cytom* 100:235-239, 2021. **CA**
118. Yue A, Chauve C, Libbrecht M & **Brinkman RR**. Automated identification of maximal differential cell populations in flow cytometry data. *Cytometry A* 101:177-184, 2022. **SA**
119. Meskas J, Yokosawa D, Wang S, Segat GC & **Brinkman RR**. flowCut: An R package for automated removal of outlier events and flagging of files based on time versus fluorescence analysis. *Cytometry A* 103:71-81, 2023. (IF 3.3)**SA**
120. Wang X, Nissen M, Gracias D, Kusakabe M, Simkin G, Jiang A, Duns G, Sarkozy C, Hilton L, Chavez E, Segat G, Wong R, Kim J, Aoki T, Islam R, May C, Hung S, Tyshchenko K, **Brinkman R**, Hirst M, Karsan A, Freeman CL, Sehn LH, Morin RD, Roth AJ, Savage KJ, Craig JW, Shah SP, Steidl C, Scott DW, Weng AP. Single-cell profiling reveals a memory B cell-like subtype of follicular lymphoma with increased transformation risk. Nat Commun 13:6772, 2022. (IF 15.7)**CA**

121. Sebastiano Montante, Yixuan Chen, **Ryan R. Brinkman.** flowSim: Near duplicate detection for flow cytometry data. *Cytometry A* 103:483-489, 2024. CA (IF 3.3) PMID: 37530476
122. Ng DP, Simonson PD, Tarnok A, Lucas F, Kern W, Rolf N, Bogdanoski G, Green C, **Brinkman RR,** Czechowska K. Recommendations for using artificial intelligence in clinical flow cytometry. Cytometry B Clin Cytom 106:228-238, 2024. (IF 3.1)

123. Martino D, Kresoje N, Amenyogbe N, Ben-Othman R, Cai B, Lo M, Idoko O, Odumade OA, Falsafi R, Blimkie TM, An A, Shannon CP, Montante S, Dhillon BK, Diray-Arce J, Ozonoff A, Smolen KK, **Brinkman RR**, McEnaney K, Angelidou A, Richmond P, Tebbutt SJ; EPIC-HIPC consortium; Kampmann B, Levy O, Hancock REW, Lee AHY, Kollmann TR. DNA methylation signatures underpinning blood neutrophil to lymphocyte ratio during first week of human life. Nat Commun 15:8167, 2024. (IF 15.7)

124. An AY, Acton E, Idoko OT, Shannon CP, Blimkie TM, Falsafi R, Wariri O, Imam A, Dibbasey T, Bennike TB, Smolen KK, Diray-Arce J, Ben-Othman R, Montante S, Angelidou A, Odumade OA,

Martino D, Tebbutt SJ, Levy O, Steen H, Kollmann TR, Kampmann B, Hancock REW, Lee AH; EPIC Consortium. Predictive gene expression signature diagnoses neonatal sepsis before clinical presentation. EBioMedicine 110:105411, 2024. (IF 10.8)

EPIC Consortium: Nelly Amenyogbe, Asimenia Angelidou, Winnie Bao, Rym Ben-Othman, Tue Bennike, Travis Blimkie, Morten Bjerregaard-Andersen, **Ryan R. Brinkman,** Byron Brook, Kendyll Burnell, Bing Cai, Abhinav Checkervarty, Jing Chen, Virginia Chen, Mitchell Cooney, Momoudou Cox, Alansana Darboe, Bhavjinder K. Dhillon, Tida Dibassey, Joann Diray-Arce, Reza Falsafi, Benoit Fatou, Rebecca Ford, Freddy Francis, Christian N. Golding, Robert E.W. Hancock, Danny J. Harbeson, Daniel He, Samuel H. Hinshaw, Annmarie Hoch, Joe Huang, Olubukola T. Idoko, Abdulazeez Imam, Beate Kampmann, Wendy Kirarock, Tobias R. Kollmann, Meagan E. Karoly, Ken Kraft, Kristina Larsen, Jessica Lasky-Su, Amy H. Lee, Ofer Levy, Aaron Liu, A, Mark Liu, M, Mehrnoush Malek, Arnaud Marchant, Geraldine Masiria, David Jim Martino, John Paul Matlam, Kerry McEnaney, Caitlyn McLoughlin, Sebastiano Montante, Elena Morrocchi, Jorjoh Ndure, Athena Nguyen, Jainaba Njie-Jobe, Oludare A. Odumade, Al Ozonoff, Jensen Pak, Paolo Palma, Edward P.K. Parker, Matthew A. Pettengill, Alec Plotkin, William S. Pomat, Shun Rao, Peter C. Richmond, Elishia Roberts, Gerard Saleu, Lilica Sanca, Guzman Sanchez-Schmitz, Frederik Schaltz-Buchholzer, Casey P. Shannon, Amrit Singh, Maren Smith, Kinga K. Smolen, Hanno Steen, Julia Strandmark, Caitlin Syphurs, Scott J. Tebbutt, Anita H.J. van den Biggelaar, Simon D. van Haren, Natallia Varankovich, Sofia Vignolo, Diana Vo, and Oghenebrume Wariri

125. Wang Z, Amenyogbe N, Ben-Othman R, Cai B, Lo M, Idoko OT, Odumade OA, Falsafi R, Blimkie TM, An A, Shannon CP, Montante S, Dhillon BK, Diray-Arce J, Ozonoff A, Smolen KK, **Brinkman RR**, McEnaney K, Angelidou A, Richmond P, Tebbutt SJ, Kampmann B, Hancock REW, Lee AHY, Levy O, Kollmann TR, Martino D. Higher promoter methylation of the Ubiquitin Associated and SH3 domain containing A (UBASH3A) gene is associated with T-lymphocyte ontogeny and reduced susceptibility to early-onset sepsis. J Infect Dis 2025 Dec 17. [Online ahead of print]. CA
126. Yue A**, Brinkman R**R, Nash V, Junker F, Bogdanoski G, Divekar A, Tyznik A, Spidlen J, Kern W, Petriz J, Wloka K, Czechowska K. AI in flow cytometry: Current applications and future directions. Cytometry B Clin Cytom 108:404-420, 2025. (IF 3.1)
127. Wallace PK, Jellison ER, Thornton S, Kluepfel K, Back J, Beadnell TC, Bebes A, Behrends J, Belkina AC, Black M, Bogdanoski G, Bollati-Fogolín M, Bonte S, Van der Borght K, **Brinkman RR**, Brundage K, Bushnell T, Chiu DT, Chow N, Ciccolella CO, Cochran M, Czechowska K, Dagla K, Daniel B, de la Cruz G, Van Duyse J, Ferrer Font L, Fornas O, Garcia-Garcia S, Gardner R, Van Gassen S, Gimenes D, Grenfell R, Grider-Hayes MJ, Grose R, Hall C, Hally KE, Hameetman M, Hogg K, Houston J, Irish JM, Van Isterdael G, Jaimes M, Janetzki S, Kim C, Koladiya A, Lamote J, Lannigan J, Leconte J, Litwin V, Longhini A, Loof N, Lozano-Andrés E, Lundsten K, Mage P, Mair F, Gregório Martins C, McCausland M, McGuire HM, Meskas J, Murphy W, Nolan J, Oliveira B, Ordoñez-Rueda D, Orlowski-Oliver E, Christie Petersen C, Poulton NJ, Putri G, Quadrini KJ, Ramasz B, Ruhrmund D, Singh VV, Small SJ, Smith NJ, Spidlen J, Stegen C, Tak T, Thompson S, Thomson M, Vocelle D, Walker RV, Walsh RE, Wang L, Wang YF, Weglarz M, Winker M, Wood JCS, Woolard S, Yeh NY, Yuecel R, Rajwa B. Cyt-Geist: Current and Future Challenges in Cytometry: Reports of the CYTO 2025 Conference Workshops. Cytometry A 109:5-41, 2026. CA

128. Yue A, **Brinkman RR**, Nash V, Junker F, Bogdanoski G, Divekar A, Tyznik A, Spidlen J, Kern W, Petriz J, Wloka K, Czechowska K. Response to "Bridging the implementation gap in AI-assisted flow cytometry". Cytometry B Clin Cytom 2026 Jan 21. [Online ahead of print]. SA

(b) *<u>Conference Proceedings</u>*

1. Ramadan KM, Connors JM, Gascoyne RD, Song K, Barnett MJ, Nantel SH, Nevill TJ, Shepherd JD, Sutherland HJ, Lavoi J, Forrest DL, Hogge DE, Voss NJ, **Brinkman R**, Smith CA, Toze CL. Long term results of myeloablative allogeneic stem cell transplantation using related and unrelated donors in patients with relapsed composite low and intermediate grade (including transformed) lymphoma. *Blood* 108: 3139, 2006.
2. Ramadan KM, Connors JM, Al-Tourah AJ, Gascoyne RD, Song K, Barnett MJ, Nantel SH, Nevill TJ, Shepherd JD, Sutherland HJ, Lavoi J, Forrest DL, Hogge DE, Voss NJ, **Brinkman R**, Smith CA, Toze CL. Prior rituximab reduces relapse and improves survival following high dose chemotherapy and stem cell transplantation for relapsed composite low and intermediate grade (including transformed) lymphoma. *Blood* 108: 3662, 2006.
3. Irvine DA, Barnett MJ, **Brinkman R**, Forrest DL, Hogge DE, Lavoie J, <u>Lei L</u>, Nantel SH, Nevill TJ, Nitta J, Shepherd J, Song K, Toze C, Sutherland HJ. Induction therapy with high-dose Dex alone in newly diagnosed myeloma patients produces a 57% partial response and is predictive of progression free survival. *Blood* 108: 2098, 2006.
4. Irvine DA, Barnett MJ, **Brinkman R**, et al. Induction therapy with high-dose dexamethasone alone in newly diagnosed myeloma patients produces a high partial response rate which is predictive of progression free and overall survival. *British Journal of Haematology* 137: 38, 2007.
5. O'Leary HM, Savage KJ, Toze CL, Connors JM, Gascoyne RD, Abou Mourad Y, Barnett MJ, Forrest DL, Hogge DE, Lavoie J, Nantel SH, Nevill TJ, Shepherd JD, Smith C, Sutherland HJ, Voss N, **Brinkman R**, Song K. Allogeneic stem cell transplantation as treatment for relapsed and high-risk peripheral T-cell lymphoma. *Blood* 110:3040, 2007.
6. Power MM, Di Sauro G, Brooks-Wilson A, Nevill TJ, Lavoie JC, Smith CA, Shepherd JD, Toze CL, Sutherland HJ, Barnett MJ, Abou Mourad YA, Song KW, Forrest DL, Nantel SH, Wong SC, Krasnova AA, **Brinkman R,** Hogge DE. Allogeneic stem cell transplant in first complete remission overcomes the poor prognosis associated with the FLT-3 internal tandem duplication in acute myeloid leukemia. Blood 110:3491, 2012.
7. Leif RC, <u>Spidlen J</u>, **Brinkman RR.** Cytometry standards continuumin. Imaging, Manipulation and Analysis of Biomolecules, Cells, and Tissues VI. VD Farkas, RC Leif, and DV Nicolau (Eds), *SPIE Proc*. 6859, 2008.
8. <u>Courtot M</u>, Bug W, Gibson F, Lister AL, Malone J, Schober D, **Brinkman R**,Ruttenberg A. The OWL of biomedical investigations. The 5th OWLED Workshop on OWL: Experiences and Directions, ISWC, 2008.
9. Ramadan KM, Song KW, Connors JM, Al-Tourah A, Gascoyne RD, Barnett MJ, Nantel SH, Nevill TJ, Shepherd JD, Sutherland HJ, Lavoi J, Forrestt DL, Hogge DE, Voss N, **Brinkman R**, Abou Mourad

YR, Power MM, Narayanan S, Smith CA, Toze CL. Comparison of outcome between refractory/relapsed de novo diffuse large B-cell and transformed lymphoma using related and unrelated allogeneic hematopoietic SCT. *Blood* 112: 2173, 2008.

10. Ramadan KM, Connors JM, Al-Tourah A, Gascoyne RD, Song KW, Barnett MJ, Nantel SH, Nevill TJ, Shepherd JD, Sutherland HJ, Lavoi J, Forrestt DL, Hogge DE, Voss N, **Brinkman R**, Abou Mourad YR, Power MM, Narayanan S, Smith CA, Toze CL. Salvage therapy with allogeneic stem cell transplantation results in better outcome for patients with relapsed-refractory follicular lymphoma compared to those with transformed Non-Hodgkin lymphoma: A population-based comparative study. *Blood* 112: 975, 2008.
11. Ramadan KM, Connors JM, Al-Tourah A, Gascoyne RD, Song KW, Barnett MJ, Nantel SH, Nevill TJ, Shepherd JD, Sutherland HJ, Lavoi J, Forrestt DL, Hogge DE, Voss N, **Brinkman R**, Abou Mourad YR, Power MM, Narayanan S, Smith CA, Toze CL. Autologous stem cell transplantation is superior to myeloablative allogeneic SCT as a salvage therapy for patients with refractory/relapsed transformed lymphoma. *Blood* 112: 4459, 2008.
12. Toze CL, Sangara RN, Connors JM, Nevill TJ, Shepherd JD, Lavoie J, Barnett MJ, Nantel SH, Voss M, Hogge DE, Sitherland HJ, Forrest DL, Song KW, Abou Mourad Y, Power MM, Narayanan S, **Brinkman R**, Smith C. Impact of comorbidity index on outcome with allogeneic hematopoietic stem cell transplantation for chronic lymphocytic leukemia. *Blood* 112: 3305, 2008.
13. Bashashati A, Lo K, Gottardo R, Gascoyne R, Weng A, **Brinkman R,** A pipeline for automated analysis of flow cytometry data: preliminary results on lymphoma sub-type diagnosis. *Conf Proc IEE Eng Med Biol Soc* 2009: 4945-8, 2009.
14. The OBI consortium, **Brinkman R**, Bug B, Causton H, Clancy K, Cocos C, Courtot M, Derom D, Deutsch E, Fan L, Field D, Fostel J, Fragoso G, Gibson F, Gray T, Greenbaum J, Grenon P, Grethe J, He Y, Heiskanen H, Hernandez-Boussard T, Lord P, Lister A, Malone J, Manduchi E, Montecchi L, Morrison N, Mungall C, Parkinson H, Peters B, Pocock M, Rocca-Serra P, Rubin D, Ruttenberg A, Sansone SA, Scheuermann R, Schober D, Smith B, Soldatova LN, Stenzhorn H, Stoeckert C, Taylor C, Vita R, Westbrook J, White J, Whetzel PL, Wiemann S, ZhengJ. Modelling biomedical experimental processes with OBI. International Conference on Biomedical Ontologies (ICBO), 2009.
15. Leif RC, Spidlen J, **Brinkman RR**. A container for the advanced cytometry standard (ACS). Manipulation and Analysis of Biomolecules, Cells and Tissues. *SPIE Proc.* 7182, 2009.
16. Courtot M, Gibson F, Lister A, Malone J, Schober D, **Brinkman RR**, Ruttenberg A. MIREOT: the Minimum Information to Reference an External Ontology Term. *International Conference on Biomedical Ontologies (ICBO)*, 2009.
17. Rocca-Serra P, Ruttenberg A, Greenbaum J, Courtot M, Sansone SA, Scheuermann R, the **OBI Consortium,** Peters B. Overcoming the ontology enrichment bottleneck with Quick Term Templates. *International Conference on Biomedical Ontologies (ICBO)*, 2009.
18. Aghaeepour N, Khodabakhshi AH, **Brinkman RR**. Empricial study of cluster evaluation metrics. Clustering: Science or Art? Towards Principled Approaches. *NIPS Workshop*, 2009.
19. Jiang X, Forrest D, Nicolini F, Turhan A, Guilhot F, Yip C, Holyoake T, Jorgensen H, Lambie K, Saw KM, Pang E, Vukovic R, Lehn P, Ringrose A, Yu M, **Brinkman RR**, Smith C, Eaves A, Eaves C. Properties of CD34+ CML stem/progenitor cells that correlate with different clinical responses to imatinib mesylate. 38th Annual Scientific Meeting of the ISEH-Society-for-Hematology-and-Stem-Cells

Location: Athens, GREECE Date: SEP 09-12, 2009 Sponsor(s): ISEH Soc Hematol & Stem Cells: *Experimental Hematology* 37 (9): S41-S42 2009.

20. He Y, Xiang Z, Todd T, Courtot M, **Brinkman R**, Zheng J, Stoeckert Jr. CJ, Malone J, Rocca-Serra P, Sansone SA, Fostel J, Soldatova LN, Peters B, Ruttenberg A. Ontology representation and ANOVA analysis of vaccine protection investigation. *Bio-ontologies Special Interest Group*, 2010.
21. Courtot M, Mungall C, **Brinkman R**, Ruttenberg A. Building the OB Foundry – one policy at a time. WOMBO workshop, *ICBO*, 2011.
22. Benz C, Copley M, Kent D, Woehrer S, Rowe K, Day C, Cortes A, Aghaeepour N, **Brinkman R**, Eaves CJ. Lymphoid-deficient hematopoietic stem cells appear in mice before birth and expand rapidly and preferentially thereafter. *Exp Hematol* 38: S34, 2011.
23. **Brinkman, RR**, Zare H, Kridel R, Aghaeepour N, Haffari G, Connors JM, Gascoyne RD, Gupta A, Weng AP, Bashashati A. Bioinformatics to Bedside: An Automated and Generalizable Multidimensional Flow Cytometry Data Analysis Approach Improves Diagnostic Accuracy Between Mantle cell Lymphoma and Small Lymphocytic lymphoma. *Cytometry B Clin Cytom B* 80: 376-377, 2011.
24. Knapp DJHF, Bendall SC, Miller PH, Cheung AMS, Imren S, Humphries RK, **Brinkman RR**, Oostendorp RAJ, Nolan GP, Eaves CJ. Short term signalling responses of the most primitive subsets of human hematopoietic cells stimulated *in vitro c*orrelate with their subsequent self-renewal behavior. *Blood* 120: 2341, 2012.
25. Villanova F, Di Meglio P, Inokuma M, Heck S, Perucha E, **Brinkman R**, Fuentes MH, Lord G, Maino SV, Nestle FO. Biomarker discovery in psoriasis using a multiparameter flow cytometry platform. B*r J Dermatol* 16: e37-e37, 2012.
26. Scheuermann R, Finak G, Ramey J, Taghiyar J, Stanton R, Brandes A,De Jager P, Qiu P, McCoy J, Hafler D, Maecker H, Mosmann T, **Brinkman R**, and Gottardo R. FlowCAP: comparison of automated and manual gating of standardized lyoplate flow cytometry data J. *Immunology*, 190, 135.1: P3374, 2013.
27. Villanova F, Di Meglio P, Inokuma M, Aghaeepour N, Perucha E, Mollon J, Nomura L, Hernandez-Fuentes M, Cope A, Heck S, Maino V, Lord G, Brinkman RR and Nestle FO. Integration of lyoplate based flow cytometry and computational analysis for standardized biomarker discovery in inflammatory skin diseases. *Japanese Soc Investigat Dermatol* 133(1)**:** S23-S23, 2013.
28. Craig FE, **Brinkman R**, Ten Eyck SP, Aghaeepour N. Optimizing Manual Flow Cytometric Analysis for Lymphoma Using an Automated Computational Tool. *Laboratory Investigation* 93(1) : 326A-326A, 2013.
29. Ivison S, Janmohamed S, Malek M, Garcia R, Broady R, Halpin A, Richaud M, Brant R, Delisle J-S, West L, **Brinkman RR** & Levings M. Standardized Immunophenotyping in the Canadian National Transplant Research Program: pilot trial of post HSCT samples and development of automated gating pipelines. *Transplantation* 101:S62, 2017.
30. Li AM, Drissler S, Kariminia A, Subrt P, **Brinkman RR** & Schultz K. An Early Naïve T Cell Population Lacking PD1 Expression at Day 100 As A Prognostic Biomarker of Chronic GVHD. *Transplantation* 101:S40, 2017.

31. Rahim A, Nutter L, **Brinkman RR**. Big Flow Cytometry Data Analysis Methods and Applications. *International Society of Laboratory Hematology* 41 (Suppl. 2) : 146, 2019.

(c) Other

N/A

2. NON-REFEREED PUBLICATIONS

(a) Journals

1. Eirew P, Yu M, **Brinkman R**, Eaves CJ. Reassessing the human mammary stem cell concept by modelling limiting dilution transplantation assays. *Nature Medicine* 15: 604-605, 2009.
2. Gottardo R, **Brinkman RR**, Luta G, Wand MP. Recent bioinformatics advances in the analysis of high throughput flow cytometry data. High Throughput Flow Cytometry Data. *Advances in Bioinformatics* 2009: 461763, 2009.
3. **Brinkman RR**, Aghaeepour N, Finak G, Gottardo R, Mosmann T, Scheuermann RH. State-of-the-Art in the Computational Analysis of Cytometry Data. *Cytometry A*. 87:591-3, 2015.
4. Meskas J, Wang S, **Brinkman RR**. FlowCut — An R package for precise and accurate automated removal of outlier events and flagging of files based on time versus fluorescence analysis. *bioRxiv* 2020.04.23.058545; doi: https://doi.org/10.1101/2020.04.23.058545.
5. Yue A, Chauve C, Libbrecht M, **Brinkman R**. Identifying differential cell populations in flow cytometry data accounting for marker frequency. 2021. *bioRxiv* 837765; doi: https://doi.org/10.1101/837765

(b) Conference Proceedings

1. Peeling R, Pennie R, **Brinkman R**, Gautier M. Prevalence of Chlamydial infection in a post-secondary student population in Ottawa. Meeting of the Royal College of Physicians and Surgeons of Canada, Sept 1992.
2. Surh L, Hunter A, Kasaboski CA, **Brinkman R**, Damini J, Hastings V, Pluscauskas M, Wright P. Impact of molecular genetic services on a health care system. Meeting of the American Society of Human Genetics, Nov 1992.
3. Hillier L, Gish W, Green P, Dear S**, Brinkman R.** Cooper M, Chinwalla A, Ficenec D, Hodgson D, Holman M, Maffitt D, Marth G, Parsons J, Platt D, Wendl M, Waterston R and Genome Sequencing Consortium. Software for large-scale DNA sequencing projects. Genome Mapping and Sequencing Meeting. Cold Spring Harbor Laboratory CA, May 1996.
4. **Brinkman RR,** Paulsen J, *Hayden MR*. Design of clinical trials for Huntington Disease. Canadian Genetic Diseases Network 1998 Annual Scientific Meeting. Montreal QC, May 1998.

5. **Brinkman RR,** Paulsen JS, *Hayden MR*. Pharmocogenomic approaches to the design of clinical trials for polyglutamine expansion diseases: Huntington Disease as a prototype. American Society of Human Genetics. 48th Annual Meeting. Denver CO, Oct 1998.
6. Almqvist E, **Brinkman R**, *Hayden MR*. Successful introduction of a community-based predictive testing protocol for Huntington Disease in British Columbia. American Society of Human Genetics. 48th Annual Meeting. Denver CO, Oct 1998.
7. Whetzel PL, **Brinkman RR**, Causton HC, Fan L, Field D, Fostel J, Fragoso G, Gray T, Heiskanen M, Hernandez-Boussard T, Parkinson H, Rocca-Serra P, Sansone S-A, Schober D, Smith B, Stevens R, Stoeckert C, Taylor C, White J. Status of the development of the Functional Genomics Investigation Ontology (FuGO). Joint BioLINK and 9th Bio-Ontologies Meeting, Intelligent Systems for Molecular Biology. Foraleza, Brazil, Aug 6-10, 2006.
8. Whetzel PL, **Brinkman RR**, Causton HC, Fan L, Field D, Fostel J, Fragoso G, Gray T, Heiskanen M, Hernandez-Boussard T, Parkinson H, Rocca-Serra P, Sansone S-A, Schober D, Smith B, Stevens R, Stoeckert C, Taylor C, White J. Status of the development of the Functional Genomics Investigation Ontology (FuGO). 3rd International Workshop on Data Integration in the Life Sciences (DILS'06). Hinxton UK, Aug 20-22, 2006.
9. He Y, Cowell L, Diehl AD, Mobley HL, Peters B, Ruttenberg A, Scheuermann RH, Brinkman RR, Courtot M, Mungall C, Xiang Z, Chen F, Todd T, Colby LA, Rush H, Whetzel T, Musen MA, Athey BD, Omenn GS, Smith B. Proceedings of the 1st International Conference on Biomedical Ontology (ICBO 2009), Buffalo, NY, USA. VO: Vaccine Ontology. The 1st International Conference on Biomedical Ontology (ICBO 2009), Buffalo, NY, USA. Nature Precedings. 2009. http://precedings.nature.com/documents/3553/version/1.
10. Knapp DJHF, Bendall SC, Miller PH, Cheung AMS, Imren S, Humphries RK, **Brinkman RR**, Oostendorp RAJ, Nolan GP, Eaves CJ. Short term signalling responses of the most primitive subsets of human hematopoietic cells stimulated in vitro correlate with their subsequent self-renewal behaviour. TFRI Node-BC Cancer Agency annual conference, Vancouver BC, Nov 29-Dec 1, 2012.
11. O'Neill K, Aghaeepour N, Jalali A, Hogge D, Karsan A, Dalal B, **Brinkman RR**. Deep Phenotyping of Multitube Flow Cytometry Data Reveals New Cell Types Associated with NPM1 Mutation in AML. 11th Asia Pacific Bioinformatics Conference (APBC2013) Vancouver BC, Jan 21-23, 2013.
12. Wang X, Nissen M, Gracias D, Kusakabe M, Simkin G, Duns G, Sarkozy C, Chavez E, Segat GC, Kim J, Jiang A, Aoki T, Islam R, May C, Hung S, Tyshchenko K, Brinkman R, Hirst M, Karsan A, Freeman CL, Sehn LH, Savage KJ, Craig JW, Scott DW, Steidl C, Shah SP & Weng AP. Single-Cell Profiling Reveals Clinically Relevant Evolutionary Trajectories and Alternate Biologies in Human Follicular Lymphoma. Blood 138:450-450, 2021.

(c) Other

3. BOOKS

i. Authored

N/A

(b) Edited

N/A

(c) Chapters

1. Spidlen J, Breuer K, **Brinkman R**. Preparing a Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) compliant manuscript using the International Society for Advancement of Cytometry (ISAC) FCS file repository (flowrepository.org). *Current Protocols Cytometry* 10: 10.18, 2012. **SA (IF n/a Citations 5)**

   I conceived of the project and led the development team who built flowRepository, which we published this step-by-step instruction guide on its use as well as the academic article immediately following.
2. Spidlen J, Breuer K, **Brinkman R.** MIFlowCyt: Guidelines for Systems Biology in W. Dubitzky, O. Wolkenhauer, K. Cho & H. Yokota (eds.), Encyclopedia of Systems Biology, DOI 10.1007/978-1-4419-9863-7, Springer Science & Business Media, LLC 2013.
3. Aghaeepour N, **Brinkman R.** Computational analysis of high-dimensional flow cytometric data for diagnosis and discovery in Fienberg H and Nolan G (eds.). Current Topics in Microbiology and Immunology (CTMI) volume on "Novel techniques of multiparametric cytometry and large scale data analysis". 377:159-75, 2014.
4. Wang S, **Brinkman RR**. Data-Driven Flow Cytometry Analysis in McGuire H, PhD and Ashhurst T (eds.). Mass Cytometry: Methods and Protocols, Springer Science+Business Media, LLC, part of Springer Nature 1989:245-265 2019. DOI 10.1007/978-1-4939-9454-0_16.

4. PATENTS

1. Brownlie AJ, Tafuri SRAE, **Brinkman RR,** Chagnovich D, Chatterjee A, Donaldson GC, Dube M-P, Goldberg YP, Jerva LF, Lafrenier RG, Ludwig E, Samuels ME, Wu C, *Hayden MR*. Novel therapeutic target for treating vascular diseases, dyslipidemias and related disorders.
   Application number: WO 2004003159 WO2003US20410 20030627 Priority number: US20020391878P 20020627. Patent number: WO 2001/062954
2. Brownlie AJ, Tafuri SRAE, **Brinkman RR,** Chagnovich D, Chatterjee A, Donaldson GC, Dube M-P, Wu C. ORP9, A novel therapeuric target for increasing HDL levels.
   Application number: WO2004US16227 20040521 Priority number: US20030472341P 20030521. Patent number: PLT/US2004/016227

7. SPECIAL COPYRIGHTS

N/A

6. ARTISTIC WORKS, PERFORMANCES, DESIGNS

N/A

7. OTHER WORKS

(a) Co-presentations

1. Shaw C, **Brinkman RR**. Visual analytics and flow cytometry visualization using SFA. 6th Annual Rocky Mountain Bioinformatics Conference. Aspen/Snowmass CO, Dec 4-7, 2008.

8. WORK SUBMITTED

Sebastiano Montante, Daniel Yokosawa, Leon Li, Alexander Butyaev, Mehrnoush Malek, Razzi Movassaghi, Quentin Michalchuk, Chieh-Ting, Jimmy Hsu, David Shmil, Albina Rahim, Andrea Cossarizza, Julia Boira Esteban, Kornél Erhart, Bergur Finnbogason, George Kelion, Hjalti Leifsson, Josh Rivers, David Ecker, Attila Szantner, Jérôme Waldispühl, **Ryan R. Brinkman**. Citizen science gamers enable automated flow cytometry gating through machine learning. https://doi.org/10.1101/2025.10.07.679685 (Submitted Jan 15, 2026)