Oliver Hofmann

Personalia

date of birth	12. August 1972
place of birth	Cologne
nationality:	German

Education

2000–2004 **Doctor of Science**, *Department of Biochemistry, University of Cologne*, Cologne, Germany.
Determination of dependencies between enzymatic activities and disease related concepts by automatic evaluation of the scientific literature.

1993–1999 **Diploma Biology**, *University of Cologne*, Cologne, Germany.
Major subject: genetics, minor subjects: developmental biology, biochemistry

Experience

Academic

2022–Present **Professor**, *University of Melbourne*, Melbourne, Australia.

2016–2022 **Associate Professor**, *University of Melbourne*, Melbourne, Australia.

2016–Present **Head of Bioinformatics**, *Collaborative Centre for Genomic Cancer Medicine, University of Melburne Center for Cancer Research (formerly Centre for Cancer Research)*, Melbourne, Australia.

- Building a Genomics Platform Group to support clinically accredited sequencing with a focus on rapid whole genome/transcriptiome sequencing of cancer samples
- Develop national genomics infrastructure
- Co-leading Australian Genomics Data Working Group.
- Co-lead for the National Approach to Genomic Information Management implementation phase.
- Co-leading the Large Scale Genomnics working group for the Global Alliance for Genomics and Health.
- Co-lead for the Illumina-University of Melbourne Genomics Hub and the Advanced Genomics Collaboration, a public/private partnership to develop new genomic technologies, develop Victoria's workforce and drive clinical translation.
- Appointed to the Expert Advisory Committee for Genomics Australia by the Federal Department of Health and Ages Care

2015–2016 **Visiting Associate Professor**, *Department of Biostatistics, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

- Provide strategic support to the Harvard T.H. Chan Bioinformatics Core on research development.
- Designed and taught a "Massive Open Online Course" on re-sequencing study design and analysis through the edX platform.

2015–2016 **Reader**, *Institute of Cancer Sciences, University of Glasgow*, Glasgow, UK.

2015–2016 **Head of Bioinformatics**, *Wolfson-Wohl Cancer Research Center*, Glasgow, UK.

- Planned and deployed the computational infrastructure and software required to support a local Illumina X10 system maintained by Dr. Sean Grimmond.
- Provided guidance and bioinformatics support for new initiatives such as the Scottish Genome Partnership (in collaboration with University of Edinburgh and Genomics England) and the Cancer Research UK Big Data Initiative.
- Supported the NHS Scotland with the development of a clinical gene panel for patient diagnostics.
- Developed methods for improved interrogation of WGS data (structural variation, minority variant detection, prioritisation).

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2014–2015 **Director**, *Bioinformatics Core, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

- Raised funding from Harvard Medical School and the Harvard NeuroDiscovery Center, expanding our bioinformatics support to these communities.
- Engaged industry through funded collaborations. Research topics included shorter projects such as optimising NGS workflows on AWS (Intel), benchmarking research computing infrastructure for large scale WGS analysis (Dell), validating gene panels (Color Genomics) and porting our NGS workflow to the Azure Cloud Computing environment (Microsoft) as well as an ongoing, multi-year collaboration with AstraZeneca to improve methods for processing cancer genomics data (structural variation, subclonal structure).
- Initiated a bioinformatics training program, hiring two full time trainers to develop and teach one day and ten day workshops on best practices in data management, scientific computing, programming and NGS data analysis; the program had 200 students in the first year and has been renewed.

2012–2015 **Senior Research Scientist**, *Department of Biostatistics, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

2011–Present **Affiliated Faculty**, *Harvard Stem Cell Institute*, Cambridge, MA, US.

- Expanded the HSPH Bioinformatics Core to serve as the bioinformatics support unit for stem cell researchers in the Harvard Community.
- Helped to raise funding for the Harvard Stem Cell Commons, a data repository to support reproducible research and data dissemination.

2010–2012 **Research Scientist**, *Department of Biostatistics, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

2008–2014 **Associate Director**, *Bioinformatics Core, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

- Re-organized the Bioinformatics Core to focus on next-generation sequencing technology support.
- Increased the Core staff to a total of ten analysts, developers and research computing specialists.
- Achieved full self-sustainability for the Core through a recharge center model.
- Expanded bioinformatics support to the HIV community (funds raised from the Harvard Center for AIDS Research) and translational medicine (as the only bioinformatics group to receive funding from Harvard Catalyst).
- Supported >300 projects over six years, ranging from ChIP-Seq to large scale exome-sequencing, single-cell RNA-Seq and more customized technologie. Projects included large scale collaborative efforts to study predisposition to breast cancer (6000 patient exome-seq cohort) and early onset of Alzheimer's Disease (1500 WGS).

2008–2009 **Research Associate**, *Department of Biostatistics, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

- Started the T.H. Chan Bioinformatics Core, supporting the Director Dr. Winston Hide.
- Studied the expression patterns of Cancer Testis Antigens in public expression data in collaboration with the Ludwig Institute for Cancer Research.

2007–2008 **Research Fellow**, *Department of Biostatistics, Harvard T.H. Chan School of Public Health*, Boston, MA, US.

2005–2007 **Post-doctoral researcher**, *South African National Bioinformatics Institute (SANBI), University of the Western Cape*, Cape Town, South Africa.

- Developed and maintained the eVOC controlled vocabulary system.
- Analysed public EST data for splicing patterns and tissue specificity.
- Participated in FANTOM4 and FANTOM5, implementing new methods for CAGE sequence analysis.

2000–2004 **PhD student**, *Department of Biochemistry, University of Cologne*, Cologne, Germany.

- Adapted Natural Language Parsing (NLP) methods for data extraction from PubMed records.
- Participated in the design and taught courses for the Cologone Post-Graduate Bioinformatics Program.

Industry

2001–2002 **Research fellow**, *deCODE genetics*, Reykajvik, Iceland.

Expanded existing tools for pattern matching and gene clustering for use with internal human genome builds. Advised by Dr. Daniel Oskarson, Head of Bioinformatics.

Teaching

2015 **Introduction to Bioinformatics**, *Harvard Medical School*, Boston, MA, US.
Co-organized 80h, in-depth bioinformatics and NGS course

2015 **edX PH525: Case study: Variant Discovery and Genotyping**, *edX MOOC*, Cambridge, MA, US.
NGS using the command line in a MOOC environment

2012–2015 **NGS Workshops**, *Harvard T.H. Chan School of Public Health*, Boston, MA, US.
NGS in Galaxy (Exome-Seq, RNA-Seq, ChIP-Seq)

2011–2015 **Postgrad lectures**, *Harvard T.H. Chan School of Public Health*, Boston, MA, US.
Bio 517, Introduction to next-generation sequencing

2011 **Postgrad lectures**, *Cold Spring Harbor Laboratories*, Laurel Hollow, NY, US.
Programming for biology

2010 **Tutorial**, *ISMB Conference*, Boston, MA, US.
Large scale biological data mining for functional genomics and metagenomics

2005–2007 **Undergrad lectures**, *University of Cape Town and University of the Western Cape*, Cape Town/Bellville, South Africa.
Computational biology, information extration and data integration

2005 **Student advisor**, *South African National Bioinformatics Institute, University of the Western Cape*, Bellville, South Africa.
Supervisor of Honours' students Feziwe Mpondo and Thurayah Davids

2003–2004 **Post-grad lectures**, *CUBIC*, Cologne, Germany.
Pattern recognition, hidden markov models, suffix trees and natural language processing

2002 **Post-grad lectures**, *CUBIC*, Cologne, Germany.
Genome analysis (assembly, comparison, annotation) and text mining

2002–2004 **Curriculum development**, *CUBIC (Bioinformatics Competence Center Cologne)*, Cologne, Germany.
Course planning for a one-year post-graduate school in computational biology

2001–2002 **Student advisor**, *deCODE genetics*, Reykajvik, Iceland.
Co-supervision of Master's students Fionna Cunningham and Chrysi Kirtay

2000–2004 **Teaching assistant**, *Department of Biochemistry, University of Cologne*, Cologne, Germany.
Graduate courses in protein homology modelling

Professional Activities

Advisory Role

2010–2012 **Technical Advisory Committee**, *Harvard Institute for Quantitative Social Science.*

2012–2015 **Tools and Technology Committee**, *Harvard Medical School.*

2016 **Informatics Guidance Group**, *Scottish Genome Partnership.*

2016 **Big Data in Cancer Strategy Committee**, *Cancer Research UK.*

2016–2022 **Common Workflow Language Steering Group**, *Global Alliance for Genomics and Health.*

2016–2022 **Bioinformatics Commons Pathfinder Project Steering Committee**, *Bioplatforms Australia.*

2018 **Rare Disease Data Advisory Group**, *Genome Canada.*

2023–2025 **Expert Advisory Group on Genomics Australia**, *Australian Government Department of Health and Aged Care.*

2024–Present **Strategic Advisory Board**, *Global Alliance for Genomics and Health.*

2024–Present **Data Science Steering Committee**, *Garvan Institute of Medical Research.*

2024–Present **Infrastructure Advisory Board**, *European Genomics Data Infrastructure.*

Consortium Participation

2006–2012 **FANTOM 4-6**.
Functional Annotation of the Mammalian Genome.

2012–2016 **Genome in a Bottle Consortium**, *National Institute of Standards and Technology*.
Developing genomic reference standards for sequence analysis.

2013-2015 **The Human Heredity and Health in Africa (H3Africa) Initiative**.
Development of bioinformatics expertise in Africa.

2015–Present **Global Alliance for Genomics and Health (GA4GH)**.
Interoperable approaches to genomic data analysis and sharing.

Consortium Leadership

2016–2025 **Australian Genomic Health Alliance**.
Bioinformatics Program Co-lead, Building re-usable genomics infrastructure for Australia.

2017–Present **Global Alliance for Genomics and Health (GA4GH)**.
Workstream Co-lead, Large Scale Genomics; Member Steering Committee.

2019–Present **GA4GH National Initiatives Forum (NIF)**.
Steering Committee.

Funding

HSPH Bioinformatics Core.
Raised funding to move the Harvard T.H. Chan Bioinformatics Core from subsidies to a fully self-sustained recharge center. I was a named investigagtor (key personnel) on **more than 30 NIH grants** and secured funding to support bioinformatics infrastructure development from industry, including **Biogen**, **Color Genomics**, **Microsoft**, **Dell** and **Intel**. Notable other funding sources included:

- since 2008: Bioinformatics Core for the **Harvard NIEHS Center for Environmental Health**, $40,000/year
- since 2009: Bioinformatics Consulting for **Harvard Catalyst**, $50,000/year
- since 2011: Center for Stem Cell Bioinformatics, **Harvard Stem Cell Institute**, $150,000/year
- 2012: **Archon Genomics X-Prize** through EdgeBio to build a variant calling validation framework, $90,000
- since 2013: Bioinformatics Core for the **Harvard Center for AIDS Research**, $40,000/year
- 2013: **Cure Alzheimer's Fund** through Rudy Tanzi, Massachusetts General Hospital, $500,000 to process and analyze 1500 whole genome samples from families with a history of Alzheimer's Disease
- since 2014: Bioinformatics Support for the **Harvard NeuroDiscovery Center**, $200,000/year
- since 2014: Bioinformatics Support for **Harvard Medical School**, $400,000/year
- since 2014: Funding from **AstraZeneca** to develop novel methods for cancer genome analysis and RNA-Seq, $200,000/year.

Wolfson Wohl Cancer Research Center.
Co-Investigator and co-lead bioinformatics (with Colin Semple, IGMM, Edinburgh) for the **Scottish Genome Partnership**, total budget of 6,000,000 GBP.

University of Melbourne.
Co-investigator for **The Australian Pancreatic Cancer Organoid Biobank** (Avner Foundation, $916,000 AUD), **The Australian Genomics Health Alliance** (NHMRC, $300,000 AUD/year), Dissecting mutational landscapes and cellular ecosystems of pancreatic cancer (NHMRC, $884,000 AUD) and an ARC-LIEF Grant for Merit Allocation to the National Computational Infrastructure ($4,000,000 AUD). Co-lead of the **Illumina - University of Melbourne Genomics Hub** ($60,000,000 AUD) and **GUARDIANS** (NCRIS, National Genomics Infrastructure, $25,000,000 AUD. CI on the Breast Cancer Atlas project (DOD, 5,800,000 USD).)

Publications

E. DeBortoli, E. McGahan, T. Yanes, J. Berkman, L.G. Aoude, A.K. Smit, A. Gokoolparsadh, A. Hermes, L. Newett, M. Bourke, S. Hanson, H. Hughes, O. Hofmann, I. Goranitis, R. McWhirter, V. Milch, J. Steinberg, A. McInerney-Leo, *Utility of Germline, Somatic and ctDNA Testing in Adults With Cancer*, Cancer Medicine, (2025)

R.J. Rebello, A. Posner, R. Dong, O.W.J. Prall, T. Sivakumaran, C. B. Mitchell, A. Flynn, A. Caneborg, C. Mitchell, S. Kanwal, C. Fedele, S. Webb, K. Fisher, H-L. Wong, S. Balachander, W. Zhu, S. Nicolson, V. Dimitriadis, N. Wilcken, A. DeFazio, B. Gao, M. Singh, I.M. Collins, C. Steer, M. Warren, N. Karanth, H. Xu, A. Fellowes, R.J. Hicks, K.P. Stewart, C. Shale, P. Priestley, S-J. Dawson, J.H.A. Vissers, S.B. Fox, P. Schofield, D. Bowtell, O. Hofmann, S.M. Grimmond, L. Mileshkin, R.W. Tothill, *Whole genome sequencing improves tissue-of-origin diagnosis and treatment options for cancer of unknown primary*, Nature Comms, (2025)

Z. Stark, D. Glazer, O. Hofmann, A. Rendon, C.R. Marshall, G.S. Ginsburg, C. Lunt, N. Allen, M. Effingham, J. Hastings Ward, S.L. Hill, R. Ali, P. Goodhand, A. Page, H.L. Rehm, K.N. North, R.H. Scott, *A call to action to scale up research and clinical genomic data sharing*, Nature Review Genetics, (2024).

M. Vu, K. Degeling, G.L. Ryland, O. Hofmann, A.P. Ng, D. Westerman, M.J. IJzerman, *Economic Impact of Whole Genome Sequencing and Whole Transcriptome Sequencing Versus Routine Diagnostic Molecular Testing to Stratify Patients with B-Cell Acute Lymphoblastic Leukemia*, Journal of Molecular Diagnostics, (2024).

A. Wickramarachchi, B. Hosking, Y. Jain, J. Grimes, M.J. O'Brien, T. Wright, M. Burgess, V.S.K. Lin, F. Reisinger, O. Hofmann, M. Lawley, L.O.W. Wilson, N.A. Twine, D.C. Bauer, *Scalable genomic data exchange and analytics with sBeacon*, Nature Biotechnology, (2024).

A Matched Molecular and Clinical Analysis of the Epithelioid Haemangioendothelioma Cohort in the Stafford Fox Rare Cancer Program and Contextual Literature Review, *A. Abdelmogod, L. Papadopoulos, S. Riordan, M. Wong, M. Weltman, R. Lim, C. McEvoy, A. Fellowes, S. Fox, J. Bedo, J. Penington, K. Pham, O. Hofmann, J.H.A. Vissers, S. Grimmond, G. Ratnayake, M. Christie, C. Mitchell, W. Murray, K. McClymont, P. Luk, A.T. Papenfuss, D. Kee, C.L. Scott, D. Goldstein, H.E. Barker*, Cancers, (2023).

Targeting homologous recombination deficiency in uterine leiomyosarcoma, *I.M. Collins, G. Dall, C.J. Vandenberg, K. Nesic, G. Ratnayake, W. Zhu, J.H.A. Vissers, J. Bedo, J. Penington, M.J. Wakefield, D. Kee, A. Carmagnac, R. Lim, K. Shield-Artin, B. Milesi, A. Lobley, E.L. Kyran, E. O'Grady, J. Tram, W. Zhou, D. Nugawela, K.P. Stewart, R. Caldwell, L. Papadopoulos, A.P. Ng, H.E. Barker, A. Dobrovic, S.B. Fox, O. McNally, J. Power, T. Meniawy, T.H. Tan, O .Klein, S. Barnett, I. Olesen, A. Hamilton, O. Hofmann, S. Grimmond, A.T. Papenfuss, C.L. Scott*, J Exp Clin Cancer Res, (2023).

Z. Stark, T. Boughtwood, M. Haas, J. Braithwaite, C.L. Gaff, I. Goranitis, A.B. Spurdle, D.P. Hansen, O. Hofmann, N. Laing, S. Metcalfe, A.J. Newson, H.S. Scott, N. Thorne, R.L. Ward, M.E. Dinger, S. Best, J.C. Long, S.M. Grimmond, J. Pearson, N. Waddell, C.P. Barnett, M. Cook, M. Field, D. Fielding, S.B. Fox, J. Gecz, A. Jaffe, R.J. Leventer, P.J. Lockhart, S. Lunke, A.J. Mallett, J. McGaughran, L. Mileshkin, K. Nones, T. Roscioli, I.E. Scheffer, C. Semsarian, C. Simons, D.M. Thomas, D.R. Thorburn, R. Tothill, D. White, S. Dunwoodie, P.T. Simpson, P. Phillips, MJ Brion, K. Finlay, M.C.J. Quinn, T. Mattiske, E. Tudini, K. Boggs, S. Murray, K. Wells, J. Cannings, A.H. Sinclair, J. Christodoulou, K.N. North, *Australian Genomics: Outcomes of a 5-year national program to accelerate the integration of genomics in healthcare*, The American Journal of Human Genetics, (2023).

ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium, *Genomic and molecular analyses identify molecular subtypes of pancreatic cancer recurrence*, Gastroenterology, (2022).

A.D. Yates, J. Adams, S. Chaturvedi, R.M. Davies, M. Laird, R. Leinonen, R. Nag, N.C. Sheffield, O. Hofmann, T.M. Keane, *Refget: standardized access to reference sequences*, Bioinformatics, (2022).

G.L. Ryland, A. Bajel, M. Dickinson, P.G. Ekert, O. Hofmann, M. IJzerman, A.P. Ng, A. Oshlack, B. Schmidt, I.S. Tiong, M. Vu, D.A. Westerman, S. Grimmond, P. Blombery, *Diagnostic Utility of Multimodal Genomic Profiling for Molecular Classification and MRD Assessment in Adult B-Cell Acute Lymphoblastic Leukemia*, Blood, (2021).

The Global Alliance for Genomics and Health Consortium, *GA4GH: International policies and standards for data sharing across genomic research and healthcare*, Cell Genomics, (2021).

Z. Stark, R.E. Foulger, E. Williams, B.A. Thompson, C. Patel, S. Lunke, C. Snow, I. Leong, A. Puzriakova, L.C. Daugherty, S. Leigh, C. Boustred, O. Niblock, A. Rueda-Martin, O. Gerasimenko, K. Savage, W. Bellamy, V. San Kho Lin, R. Valls, L. Gordon, H.K. Brittain, E.R.A. Thomas, A.L.T. Tavares, M. McEntagart, S.M. White, T.Y. Tan, A. Yeung, L. Downie, I. Macciocca, E. Savva, C. Lee, A. Roesley, P. De Fazio, J. Deller, Z.C. Deans, S.L. Hill, M.J. Caulfield, K.N. North, R.H. Scott, A. Rendon, O Hofmann, E.M. McDonagh, *Scaling national and international improvement in virtual gene panel curation via a collaborative approach to discordance resolution*, The American Journal of Human Genetics, (2021).

A. Senf, R. Davies, F. Haziza, J. Marshall, J. Troncoso-Pastoriza, O. Hofmann, T.M. Keane, *Crypt4GH: a file format standard enabling native access to encrypted data*, Bioinformatics, (2021).

Z. Stark, R.E. Foulger, E. Williams, B. Thompson, C. Patel, I.U.S. Leong, L.C. Daugherty, S. Leigh, C. Snow, C. Boustred, O. Niblock, A. Rueda-Martin, O. Gerasimenko, E. Ivanov, K. Savage, W. Bellamy, V. San Kho Lin, R. Valls, L. Gordon, H. Brittain, R.H. Scott, E.R.A. Thomas, A. de Burca, A.L.T. Tavares, Z. Hyder, M. McEntagart, C. Turnbull, S.M. White, T.Y. Tan, A. Yeung, L. Downie, S. Lunke, J. Deller, Z.C. Deans, S.L. Hill, M.J. Caulfield, K.N. North, A. Rendon, O. Hofmann, E.M. McDonagh, *PanelApp: accelerating international consensus on virtual gene panels through collaboration on a federated open platform*, European Journal of Human Genetics, (2020).

D. Prokopenko, S.L. Morgan, K. Mullin, O. Hofmann, B. Chapman, R. Kirchner, S. Amberkar, I. Wohlers, C. Lange, W. Hide, L. Bertram, R.E. Tanzi, *Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development*, Alzheimer's and Dementia, (2020).

S. Nakken, V. Saveliev, O. Hofmann, P. Moller, O. Myklebost, E. Hovig, *Cancer Predisposition Sequencing Reporter (CPSR): a flexible variant report engine for germline screening in cancer*, International Journal of Cancer, (2020).

D. Prokopenko, J. Hecker, R. Kirchner, B.A. Chapman, O. Hofmann, K. Mullin, W. Hide, L. Bertram, N. Laird, D.L. DeMeo, C. Lange, R.E. Tanzi, *Identification of Novel Alzheimer's Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data*, Sci Rep, (2020).

L.K. Cuddy, D. Prokopenko, E.P. Cunningham, R. Brimberry, P. Song, R.RKirchner, B.A. Chapman, O. Hofmann, W. Hide, D. Procissi, T. Hanania, S.C. Leiser, R.E. Tanzi, R. Vassar, *Ab-accelerated neurodegeneration caused by Alzheimer's-associated ACE variant R1279Q is rescued by angiotensin system inhibition in mice*, Sci Transl Med, (2020).

G.L. Ryland, A. Barraclough, C.Y. Fong, S. Fleming, A. Bajel, O. Hofmann, D. Westerman, S. Grimmond, P. Blombery, *Inotuzumab ozogamicin resistance associated with a novel CD22 truncating mutation in a case of B-acute lymphoblastic leukaemia*, Br J Haematol, (2020).

O.W.J. Prall, V. Nastevski, H. Xu, C.R.E. McEvoy, J.H.A. Vissers, D.J. Byrne, E. Takano, S. Yerneni, S. Ellis, T. Green, C.A. Mitchell, W.K. Murray, C.L. Scott, S.M. Grimmond, O. Hofmann, A. Papenfuss, D. Kee, A. Fellowes, I.S. Brown, G. Miller, M.P. Kumarasinghe, A. Perren, C.B. Nahm, A. Mittal, J. Samra, M. Ahadi, S.B. Fox, A. Chou, A.J. Gill, *RAF1 rearrangements are common in pancreatic acinar cell carcinomas*, Mod Pathol, (2020).

ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium, *Pan-cancer analysis of whole genome*, Nature, (2020).

J. Dahlberg, J. Hermansson, S. Sturlaugsson, M. Lysenkova, P. Smeds, C. Ladenvall, R.V. Guimera, F. Reisinger, O. Hofmann, P. Larsson, *Arteria: An automation system for a sequencing core facility*, GigaScience, (2019).

D.P. Hansen, M.E. Dinger, O. Hofmann, N. Thorne, T.F. Boughtwood, *Preparing Australia for genomic medicine: data, computing and digital health*, Med J Aust (2019).

G. Macintyre, T.E. Goranova, D. De Silva, D. Ennis, A.M. Piskorz, M. Eldridge, D. Sie, L.A. Lewsley, A. Hanif, C. Wilson, S. Dowson, R.M. Glasspool, M. Lockley, E. Brockbank, A. Montes, A. Walther, S. Sundar, R. Edmondson, G.D. Hall, A. Clamp, C. Gourley, M. Hall, C. Fotopoulou, H. Gabra, J. Paul, A. Supernat, D. Millan, A. Hoyle, G. Bryson, C. Nourse, L. Mincarelli, L.N. Sanchez, B. Ylstra, M. Jimenez-Linan, L. Moore, O. Hofmann, F. Markowetz, I. McNeish, J.D. Brenton, *Copy number signatures and mutational processes in ovarian carcinoma*, Nat Genet, (2018).

A. Li, B. Hooli, K. Mullin, R.E. Tate, A. Bubnys, R. Kirchner, B. Chapman, O. Hofmann, W. Hide, R.E. Tanzi, *Silencing Of The Drosophila Ortholog Of Sox5 Leads To Abnormal Neuronal Development And Behavioral Impairment*, Hum Mol Genet, (2017).

J.L. Humphris, A.M. Patch, K. Nones, P.J. Bailey, A.L. Johns, S. McKay, D.K. Chang, D.K. Miller, M. Pajic, K.S. Kassahn, M.C. Quinn, T.J. Bruxner, A.N. Christ, I. Harliwong, S. Idrisoglu, S. Manning, C. Nourse, E. Nourbakhsh, A. Stone, P.J. Wilson, M. Anderson, J.L. Fink, O. Holmes, S. Kazakoff, C. Leonard, F. Newell, N. Waddell, S. Wood, R.S. Mead, Q. Xu, J. Wu, M. Pinese, M.J. Cowley, M.D. Jones, A.M. Nagrial, V.T. Chin, L.A. Chantrill, A. Mawson, A. Chou, C.J. Scarlett, A.V. Pinho, I. Rooman, M. Giry-Laterriere, J.S. Samra, J.G. Kench, N.D. Merrett, C.W. Toon, K. Epari, N.Q. Nguyen, A. Barbour, N. Zeps, N.B. Jamieson, C.J. McKay, C.R. Carter, E.J. Dickson, J.S. Graham, F. Duthie, K. Oien, J. Hair, J.P. Morton, O.J. Sansom, R. Gretzmann, R.H. Hruban, A. Maitra, C.A. Iacobuzio-Donahue, R.D. Schulick, C.L. Wolfgang, R.A. Morgan, R.T. Lawlor, B. Rusev, V. Corbo, R. Salvia, I. Cataldo, G. Tortora, M.A. Tempero; Australian Pancreatic Cancer Genome Initiative, O. Hofmann, J.R. Eshleman, C. Pilarsky, A. Scarpa, E.A. Musgrove, A.J. Gill, J.V. Pearson, S.M. Grimmond, N. Waddell, A.V. Biankin, *Hypermutation In Pancreatic Cancer*, Gastroenterology, (2017).

M.J. Ahdesmaki, B. Chapman, P.E. Cingolani, O. Hofmann, A. Sidoruk, Z. Lai, G. Zakharov, M. Rodichenko, M. Alperovich, D. Jenkins, T.H. Carr, D. Stetson, B. Dougherty, J.C. Barrett, J. Johnson, *Prioritisation of Structural Variant Calls in Cancer Genomes*, PeerJ, (2017).

S. Lindstrom, A. Ablorh, B. Chapman, A. Gusev, G. Chen, C. Turman, A.H. Eliassen, A.L. Price, B.E. Henderson, L. Le Marchand, O. Hofmann, C.A. Haiman, P. Kraft, *Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities*, Breast Cancer Res, (2016).

C. Grasso, M. Anaka, O. Hofmann, R. Sompallae, K. Broadley, W. Hide, M.V. Berridge, J. Cebon, A. Behren, M.J. McConnell, *Iterative sorting reveals CD133+ and CD133- melanoma cells as phenotypically distinct populations*, BMC Cancer, (2016).

L.D. Wang, S.B. Ficarro, J.N. Hutchinson, R. Csepanyi-Komi, P.T. Nguyen, E. Wisniewski, J. Sullivan, O. Hofmann, E. Ligeti, J.A. Marto, A.J. Wagers, *Phosphoproteomic profiling of mouse primary HSPCs reveals new regulators of HSPC mobilization*, Blood, (2016)

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