

JOHN-SEBASTIAN EDEN

PERSONAL INFORMATION

- Full name: John-Sebastian Eden
- Date of birth: 28th April 1985
- Nationality: Australian

CONTACT DETAILS

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APPOINTMENTS

Current

- 2018 – present: Research Scientist in Bioinformatics and Genomics, Centre for Virus Research, The Westmead Institute for Medical Research, Australia
- 2018 – present: Senior Research Fellow, Sydney Medical School, The University of Sydney, Australia

Previous

- 2014 – 2017: NHMRC Early Career Fellow with Professor Edward C. Holmes, School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, Australia
- 2013 – 2017: Affiliate, Centre for Virus Research, The Westmead Institute for Medical Research, Australia
- 2013 – 2014: Post-doctoral Research Fellow with Professor Edward C. Holmes, School of Biological Sciences, Faculty of Science, The University of Sydney, Australia
- 2012 – 2013: Research Associate with Professor Peter A. White, School of Biotechnology and Biomolecular Sciences, Faculty of Science, University of New South Wales, Australia

RESEARCH SUMMARY

Dr John-Sebastian Eden is a Research Scientist in Bioinformatics and Genomics at the Centre for Virus Research, Westmead Institute for Medical Research and Senior Research Fellow in the Sydney Medical School. Dr Eden joined the Institute in early 2018 from the University of Sydney where he was an NHMRC Early Career Fellow (2014-2017) in the School of Life and Environmental Sciences under the supervision of Prof Eddie Holmes. Before moving to the University of Sydney in 2013, he completed his PhD in Virology at the University of New South Wales with Prof Peter A. White (ASM referee). A major theme of his research has been to better define the link between virus genetics and infection outcomes with a particularly focus on (i) the evolution of virulence, (ii) the emergence of drug-resistance, (iii) pathogen evolution in immunocompromised hosts and (iv) pathogen discovery. His research uses high-throughput sequencing and comparative genomics to explore the patterns of genetic variation, evolution and molecular epidemiology of clinically important viruses such as norovirus, hepatitis C virus, and respiratory syncytial virus. This work has provided important insights into the sources and mechanisms of how viral pathogens emerge, spread and evolve in populations. Recent projects have included the development of novel assays

for sequencing individual HIV proviruses to explore the latent reservoir and the application of bulk RNA sequencing, referred to as “meta-transcriptomics” to pathogen discovery in both unknown cases of human disease and wildlife outbreaks.

ACADEMIC QUALIFICATIONS

- 2012: Doctor of Philosophy, Microbiology and Immunology specialisation), School of Biotechnology and Biomolecular Sciences, Faculty of Science, University of New South Wales, Australia; Thesis entitled ‘*The Evolutionary Dynamics of Norovirus*’ and supervised by Professor Peter A. White
- 2011: Graduate Certificate in Research Management and Commercialisation, University of New South Wales, Australia
- 2009: Diploma in Innovation Management, University of New South Wales, Australia
- 2007: Bachelor of Medical Science (Hons I) majoring in Medical Microbiology and Immunology, University of New South Wales, Australia including:
 - MICR2201 Fundamentals of Microbiology and Immunology
 - GENS6033 HIV and other unconquered infections
 - MICR2011 Microbiology 1
 - MICR3081 Bacteria and Disease
 - MICR3061 Viruses and Disease
 - MICR4033 Medical Microbiology and Immunology Honours FT

PROFESSIONAL SERVICE

- Member of *Australian Virology Society* (2009 – present)
- Associate member of *Australian Society for Microbiology* (2008 – present)
- Member of *American Society for Microbiology* (2011 – present)
- Member of *Australian Centre for Hepatitis Virology* (2012 – 2015)
- Member of *Marie Bashir Institute for Infectious Diseases and Biosecurity* (2014 – present)
- External grant reviewer: National Research Foundation (South Africa)
- Peer review for *Emerging Infectious Diseases*, *Eurosurveillance*, *Molecular Biology & Evolution*, *Plos One*, *BMC Genomics*, *BMC Public Health*, *Current Opinion in Virology*, *Virology*, *Virology Journal*, *Journal of Medical Virology*, *Journal of Clinical Virology*, *Infection*, *Genetics and Evolution*, *Scientific Reports*, *Virus Research*, *Journal of Virological Methods*, *Wellcome Open Research*.

TEACHING & MENTORSHIP

- 2014 – present: Hosted and presented a number of workshops including,
 - “*Viral sequence analysis using CLC Genomics*”, University of Sydney (2016 & 2017)
 - “*RNA-Seq using High Performance Computing*”, University of Sydney (2016)
 - “*Grant writing for NHMRC Early Career Fellowships*”, University of Sydney (2015)
 - “*Evolutionary Analysis using BEAST*”, Joint Academic Microbiology Seminars (2014)
- 2009 – present: Co-supervision of 4 honours, 1 masters and 3 PhD students (2 active).
- 2008 – present: Tutor, demonstrator and lecturer for undergraduate science and medical courses covering topics in Virology, Microbiology, Infectious Diseases and Bioinformatics at the University of Sydney, University of New South Wales and the University of Technology Sydney. Most recently lectures include “*Viral genomic sequencing and discovery*” (UTS in April 2017) and “*Biomedical research methods – Bioinformatics*” (USYD in November 2016).

CONFERENCES & SEMINARS (Last 5 years)

- 2018: Invited speaker, Wildlife Health Australia annual meeting, Sydney, NSW, Australia
- 2018: Invited speaker, COMBINE bioinformatics careers workshop, Garvan Institute for Medical Research, Sydney, NSW, Australia
- 2018: Invited seminar, Taishan Medical University, Taian, Shandong, China
- 2018: Invited speaker, Molecular Microbiology Meeting 2018, Sydney, NSW, Australia
- 2017: Invited seminar, Introduction to Pathogen Phylogenetic Analysis Workshop, University of Melbourne, VIC, Australia
- 2017: Invited speaker, Joint session on RSV, 12th Australian Influenza Symposium & Australian Respiratory Virology Meeting, Melbourne, VIC, Australia
- 2017: Invited speaker, Australasian HIV&AIDS Conference 2017 – Bioinformatics workshop, Canberra, ACT, Australia
- 2017: Oral presentation, Australasian Ornithological Congress 2017, Geelong, VIC, Australia
- 2017: Oral presentation, International Union of Microbiological Societies Congresses 2017
- 2017: Oral presentation, Transmission Conference 2017, Hong Kong
- 2017: Oral presentation, 5th ISIRV-AVG Conference, Shanghai, China (including Gilead Award for Best Oral Presentation)
- 2017: Invited seminar, Marie Bashir Institute for Infectious Diseases and Biosecurity Annual Colloquium, Sydney, NSW, Australia
- 2017: Attended, AdaptNSW Wildlife Disease Surveillance workshop, Sydney, NSW, Australia
- 2017: Invited speaker: Australian Society for Veterinary Pathology Conference, Sydney, NSW, Australia
- 2017: Invited seminar, Statistical Bioinformatics Seminar, University of Sydney, NSW, Australia
- 2017: Invited seminar, Illumina MiSeq workshop, Westmead, NSW, Australia
- 2017: Invited seminar, Virology Research Laboratory seminar series, Prince of Wales Hospital, Sydney, NSW, Australia
- 2017: Invited seminar, Westmead Hub Bioinformatics and Omics seminar series, Westmead, NSW, Australia
- 2016: Invited seminar, Next-Generation Sequencing Special Interest Group Meeting, Garvan Institute of Medical Research, Sydney NSW, Australia
- 2016: Invited seminar, CIDM Public Health Annual Colloquium, Sydney, NSW, Australia
- 2016: Invited seminar, Nam Khoa-Biotek Laboratory, Ho Chi Minh City, Vietnam
- 2015: Co-chair of 'Viral Epidemiology and Diagnostics' section, oral & poster presentation, 8th Australasian Virology Society Meeting, Hunter Valley, NSW, Australia
- 2015: Oral presentation, 10th Asia-Pacific Congress of Medical Virology, Taipei, Taiwan
- 2015: Invited seminar, Marie Bashir Institute for Infectious Diseases and Biosecurity Annual Colloquium, Sydney, NSW, Australia
- 2014: Attended, Microbiology & Infectious Diseases Asia Congress, Singapore
- 2014: Invited seminar, Bioinformatics Workshop hosted by Joint Academic Microbiology Seminars, Sydney, NSW, Australia
- 2014: Invited seminar, 4th Molecular Microbiology Meeting, Sydney, NSW, Australia
- 2013: Oral presentation, 7th Australasian Virology Society Meeting, Queenstown, New Zealand
- 2013: Invited seminar, Joint Academic Microbiology Seminars, Sydney, NSW, Australia
- 2013: Attended, 9th National Scientific Workshop of the Australian Centre for HIV and Hepatitis Virology Research, Katoomba, NSW, Australia

RESEARCH GRANTS

- 2019 – 2023: National Health and Medical Research Council, Program Grant, \$16,136,755, *Addressing the major challenges in HIV vaccine and cure research*; AI with CI A/Prof Sarah Palmer
- 2018 – 2019: CREID Early-Mid Career Collaboration Grants, \$16,706, *“Meta-transcriptomic” sequencing to enhance pathogen genomics*; Co-CI with Dr Phil Britton, Dr Verlaine Timms and Dr Jason Kwong
- 2017 – 2018: Marie Bashir Institute for Infectious Diseases and Biosecurity (Zoonoses node), Seed Funding, \$10,000, *Development of a high throughput sequencing pipeline to enhance the response to outbreaks of Ross River virus in Australia*; CI
- 2017 – 2021: University of Sydney, DVC-R Grant Challenge HPC allocations, \$343,784 in-kind support, *Revealing the Australian Virome*, Co-CI with Prof Eddie Holmes, Dr Mang Shi and Dr Jan Buchmann
- 2017 – 2018: University of Sydney Research Excellence Initiative Grant (SREI 2020), \$148,500, *Centre for Pathogen Discovery*, Co-CI (CI, Prof Eddie Holmes, University of Sydney)
- 2016 – 2017: Marie Bashir Institute for Infectious Diseases and Biosecurity (Anti-Microbial Resistance node), Seed Funding, \$17,000, *Detecting emergent antiviral resistance in hepatitis C virus*; AI (CI, Dr Mark Douglas, Westmead Hospital)
- 2016 – 2017: Singapore General Hospital, Research Grant, \$24,995, *The prevalence of naturally occurring HCV resistance-associated variants amongst treatment-naïve Hepatitis C patients*; Co-CI (CI, Dr Kun Lee Lim, SGH)
- 2015 – 2016: University of Sydney, HMR+ Implementation Fund, \$153,913, *Exploiting genomics to understand pathogen evolution in external infection transmission/evolution and within the normal, obese and immunosuppressed host*; Co-CI (CI, Prof Tony Cunningham, University of Sydney)
- 2014 – 2017: National Health and Medical Research Council, Peter Doherty - Australian Biomedical Fellowship, \$304,596, *Virus genetics and clinical outcome*; CI

PUBLICATION METRICS

Citations taken from Google Scholar

- Peer review papers: 34
- Total citations: 1286
- h-index: 14
- i10-index: 20

PEER REVIEW JOURNAL ARTICLES

34. Geoghegan J, Pirotta V, Harvey E, Smith A, Buchhmann J, Ostrowski M, **Eden JS**, Harcourt R, Holmes EC. Virological sampling of inaccessible wildlife with drones. *Viruses*. [Accepted]
33. Lun JH, Hewitt J, Sitabkhan A, **Eden JS**, Tuipulotu DE, Netzler NE, Morrell L, Merif J, Jones R, Huang B, Warrilow D, Ressler KA, Ferson MJ, Dwyer D, Kok J, Rawlinson WD, Deere D, Crosbie ND, White PA. Emerging Noroviruses Identified by Clinical and Wastewater. *Emerging Microbes & Infections*. 7(1):50.
32. Shi M, Lin XD, Chen X, Tian JH, Chen LJ, Li K, Wang W, **Eden JS**, Shen JJ, Liu L, Holmes EC, Zhang YZ. The Origin of Vertebrate RNA Viruses. *Nature*. 556(7700):197.
31. Patterson Ross Z, Klunk J, Fornaciari G, Giuffra V, Duchene S, Duggan AT, Poinar D, Douglas MW, **Eden JS**, Holmes EC, Poinar HN. The paradox of HBV evolution as revealed from a 16th century mummy. *Plos Pathog*. 2018;14(1):e1006750.

30. Qi W, Jia W, Liu D, Li J, Bi Y, Xie S, Li B, Hu T, Du Y, Xing L, Zhang J, Zhang F, Wei X, **Eden JS**, Li H, Tian H, Li W, Su G, Lao G, Xu C, Xu B, Liu W, Zhang G, Ren T, Holmes EC, Cui J, Shi W, Gao GF, Liao M. Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. *J Virol.* 2018;92(2).
29. **Eden JS**, Chisholm RH, Bull RA, White PA, Holmes EC, Tanaka MM. Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. *Virus Evolution.* 2017;3(2):vex018.
28. **Eden JS**, Rose K, Ng J, Shi M, Wang Q, Sintchenko V, Holmes EC. Francisella tularensis ssp. holarctica in Ringtail Possums, Australia. *Emerging Infectious Diseases.* 2017;23(7):1198-201.
27. Hiener B, Horsburgh BA, **Eden JS**, Barton K, Schlub TE, Lee E, von Stockenstrom S, Odevall L, Milush JM, Liegler T, Sinclair E, Hoh R, Boritz EA, Douek D, Fromentin R, Chomont N, Deeks SG, Hecht FM, Palmer S. Identification of Genetically Intact HIV-1 Proviruses in Specific CD4(+) T Cells from Effectively Treated Participants. *Cell Reports.* 2017;21(3):813-22.
26. Kerr PJ, Cattadori IM, Rogers MB, Fitch A, Geber A, Liu J, Sim DG, Boag B, **Eden JS**, Ghedin E, Read AF, Holmes EC. Genomic and phenotypic characterization of myxoma virus from Great Britain reveals multiple evolutionary pathways distinct from those in Australia. *Plos Pathog.* 2017;13(3):e1006252.
25. Le Pendu J, Abrantes J, Bertagnoli S, Guitton JS, Le Gall-Recule G, Lopes AM, Marchandeau S, Alda F, Almeida T, Celio AP, Barcena J, Burmakina G, Blanco E, Calvete C, Cavadini P, Cooke B, Dalton K, Delibes Mateos M, Deptula W, **Eden JS**, Wang F, Ferreira CC, Ferreira P, Foronda P, Goncalves D, Gavier-Widen D, Hall R, Hukowska-Szematowicz B, Kerr P, Kovaliski J, Lavazza A, Mahar J, Malogolovkin A, Marques RM, Marques S, Martin-Alonso A, Monterroso P, Moreno S, Mutze G, Neimanis A, Niedzwiedzka-Rystwej P, Peacock D, Parra F, Rocchi M, Rouco C, Ruvoen-Clouet N, Silva E, Silverio D, Strive T, Thompson G, Tokarz-Deptula B, Esteves P. Proposal for a unified classification system and nomenclature of lagoviruses. *Journal of General Virology.* 2017;98(7):1658-66.
24. Liu J, Cattadori IM, Sim DG, **Eden JS**, Holmes EC, Read AF, Kerr PJ. Reverse Engineering Field Isolates of Myxoma Virus Demonstrates that Some Gene Disruptions or Losses of Function Do Not Explain Virulence Changes Observed in the Field. *J Virol.* 2017;91(20).
23. Pollett S, Trovao NS, Tan Y, **Eden JS**, Halpin RA, Bera J, Das SR, Wentworth D, Ocana V, Mendocilla SM, Alvarez C, Calisto ME, Garcia J, Halsey E, Ampuero JS, Nelson MI, Leguia M. The transmission dynamics and diversity of human metapneumovirus in Peru. *Influenza and Other Respiratory Viruses.* 2017.
22. Rose K, Agius J, Hall J, Thompson P, **Eden JS**, Srivastava M, Tiernan B, Jenkins C, Phalen D. Emergent multisystemic Enterococcus infection threatens endangered Christmas Island reptile populations. *Plos One.* 2017;12(7):e0181240.
21. Shi M, Neville P, Nicholson J, **Eden JS**, Imrie A, Holmes EC. High-Resolution Metatranscriptomics Reveals the Ecological Dynamics of Mosquito-Associated RNA Viruses in Western Australia. *J Virol.* 2017;91(17):e00680-17.
20. Duchene S, Duchene DA, Di Giallonardo F, **Eden JS**, Geoghegan JL, Holt KE, Ho SY, Holmes EC. Cross-validation to select Bayesian hierarchical models in phylogenetics. *BMC Evolutionary Biology.* 2016;16(1):115.
19. Lim KL, Hewitt J, Sitabkhan A, **Eden JS**, Lun J, Levy A, Merif J, Smith DW, Rawlinson WD, White PA. A multi-site study of norovirus molecular epidemiology in Australia and New Zealand, 2013-2014. *Plos One.* 2016;11(4):e0145254.

18. Mahar JE, Nicholson L, **Eden JS**, Duchene S, Kerr PJ, Duckworth J, Ward VK, Holmes EC, Strive T. Benign Rabbit Caliciviruses Exhibit Evolutionary Dynamics Similar to Those of Their Virulent Relatives. *J Virol*. 2016;90(20):9317-29.
17. Shi M, Lin XD, Tian JH, Chen LJ, Chen X, Li CX, Qin XC, Li J, Cao JP, **Eden JS**, Buchmann J, Wang W, Xu J, Holmes EC, Zhang YZ. Redefining the invertebrate RNA virosphere. *Nature*. 2016;540(7634):539-43.
16. Alhammad YM, Maharajh S, Butcher R, **Eden JS**, White PA, Pournourios P, Drummer HE. Longitudinal Sequence and Functional Evolution within Glycoprotein E2 in Hepatitis C Virus Genotype 3a Infection. *Plos One*. 2015;10(5):e0126397.
15. **Eden JS**, Kovaliski J, Duckworth JA, Swain G, Mahar JE, Strive T, Holmes EC. Comparative phylodynamics of rabbit hemorrhagic disease virus in Australia and New Zealand. *J Virol*. 2015;89(18):9548-58.
14. **Eden JS**, Read AJ, Duckworth JA, Strive T, Holmes EC. Resolving the origin of rabbit hemorrhagic disease virus: Insights from an investigation of the viral stocks released in Australia. *J Virol*. 2015;89(23):12217-20.
13. **Eden JS**, Hewitt J, Lim KL, Boni MF, Merif J, Greening G, Ratcliff RM, Holmes EC, Tanaka MM, Rawlinson WD, White PA. The emergence and evolution of the novel epidemic norovirus GII.4 variant Sydney 2012. *Virology*. 2014;450-451:106-13.
12. Eltahla AA, Lim KL, **Eden JS**, Kelly AG, Mackenzie JM, White PA. Nonnucleoside inhibitors of norovirus RNA polymerase: Scaffolds for rational drug design. *Antimicrob Agents Ch*. 2014;58(6):3115-23.
11. Cui J, **Eden JS**, Holmes EC, Wang LF. Adaptive evolution of bat dipeptidyl peptidase 4 (DPP4): Implications for the origin and emergence of Middle East respiratory syndrome coronavirus. *Viol J*. 2013;10:304.
10. **Eden JS**, Tanaka MM, Boni MF, Rawlinson WD, White PA. Recombination within the pandemic norovirus GII.4 lineage. *J Virol*. 2013;87(11):6270-82.
9. Eltahla AA, Lackovic K, Marquis C, **Eden JS**, White PA. A fluorescence-based high-throughput screen to identify small compound inhibitors of the genotype 3a hepatitis C virus RNA polymerase. *J Biomol Screen*. 2013;18(9):1027-34.
8. Lim KL, **Eden JS**, Oon LL, White PA. Molecular epidemiology of norovirus in Singapore, 2004-2011. *J Med Virol*. 2013;85(10):1842-51.
7. van Beek J, Ambert-Balay K, Botteldoorn N, **Eden JS**, Fonager J, Hewitt J, Iritani N, Kroneman A, Vennema H, Vinje J, White PA, Koopmans M, NoroNet. Indications for worldwide increased norovirus activity associated with emergence of a new variant of genotype II.4, late 2012. *Eurosurveillance*. 2013;18(1):8-9.
6. Bull RA, **Eden JS**, Luciani F, McElroy K, Rawlinson WD, White PA. Contribution of Intra- and Interhost Dynamics to Norovirus Evolution. *J Virol*. 2012;86(6):3219-29.
5. **Eden JS**, Lim KL, White PA. Complete genome of the human norovirus GIV.1 strain Lake Macquarie virus. *J Virol*. 2012;86(18):10251-2.
4. White PA, **Eden JS**, Hansman GS. Molecular epidemiology of noroviruses and sapoviruses and their role in Australian outbreaks of acute gastroenteritis. *Microbiology Australia*. 2012;33(2):70-3.
3. **Eden JS**, Sharpe LJ, White PA, Brown AJ. Norovirus RNA-dependent RNA polymerase is phosphorylated by an important survival kinase, Akt. *J Virol*. 2011;85(20):10894-8.
2. Bull RA, **Eden JS**, Rawlinson WD, White PA. Rapid evolution of pandemic noroviruses of the GII.4 lineage. *Plos Pathog*. 2010;6(3):e1000831.
1. **Eden JS**, Bull RA, Tu E, Mclver CJ, Lyon MJ, Marshall JA, Smith DW, Musto J, Rawlinson WD, White PA. Norovirus GII.4 variant 2006b caused epidemics of acute gastroenteritis in

Australia during 2007 and 2008. *J Clin Virol.* 2010;49(4):265-71.