

Liam Brierley

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Current Employment:

Research Fellow, University of Glasgow	May 2024 – May 2029
<ul style="list-style-type: none">• Five-year research post through MRC Career Development Award fellowship• Affiliate Researcher with School of Biodiversity, One Health & Veterinary Medicine• Establishing research group with aims of advancing computational virology by integrating state-of-the-art machine learning and new data sources to investigate fundamental questions around viral evolution and applied questions of public health interest around zoonotic virus emergence.	

Previous Employment:

Research Fellow, University of Liverpool	Nov 2022 – Apr 2024
<ul style="list-style-type: none">• 18-month position with line management responsibility for postdoctoral research associates.• Supervised three PhD students and was primary supervisor to an MRes project.	

MRC Skills Development Fellow, University of Liverpool	Oct 2019 – Oct 2022
<ul style="list-style-type: none">• Competitive fellowship (2 internal places) with extensive training allowance.• Responsible for teaching on MSc Health Data Science in guest lectures/workshops for DASC501, DASC508 modules, as well as departmental courses (co-lead of 'Introduction to R' workshop).• Trained in course design via Wellcome 'How to design and delivering genomics training' scheme.	

Lecturer in Statistics, sigma Maths & Stats Support Centre, Coventry University	2017 – 2019
<ul style="list-style-type: none">• Teaching focused-role with responsibility for undergraduate lectures, practicals, research projects, and assessment as well as workshops and short course teaching in statistical topics.• Supervised four final year undergraduate research projects and mentored as personal tutor.	

Biostatistician/Epidemiologist, University of Edinburgh	Feb 2017 – Aug 2017
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Research Assistant, Institute of Zoology, Zoological Society of London	2011 – 2012
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Education:

PGCert Academic Practice in Higher Education, Coventry University	2018 – 2019
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PhD, University of Edinburgh	2012 – 2016
<ul style="list-style-type: none">• Thesis: 'The ecology of emerging diseases: virulence and transmissibility of human RNA viruses' Supervisors: Dr Amy Pedersen, Prof. Mark Woolhouse; Funded by NERC.	

MSc Modern Epidemiology (Distinction), Imperial College London 2010 – 2011

- Thesis: 'Bats as viral hosts, from taxonomic and spatial perspectives'
Supervisor: Prof. Kate Jones (Institute of Zoology, Zoological Society of London)

MA (Hons) Natural Sciences (Class I), Magdalene College, University of Cambridge 2007 – 2010

- Dissertation: 'Rodent species richness as a risk factor for zoonotic infectious disease emergence'.

Awards/Grants:

- MRC Mid-Range Equipment Award (£503,603 GBP; Co-lead) Glasgow, 2025 - 2026
- DASA Microbial Forensic Capability Competition (£245,850 GBP; Co-lead) Glasgow, 2024 - 2025
- MRC CVR-HZI Collaborative Development Fund (£23,289 GBP) Glasgow, 2024 - 2025
- MRC Career Development Award (£1,724,119 GBP) Glasgow, 2024 - 2029
- Pandemic Institute/CSL Seqirus Collaboration Fund (£495,394 GBP) Liverpool, 2022 - 2024
- Wellcome Trust Institutional Strategic Support Fund Contract Supplement (£13,604 GBP) 2022
- FEMS Congress Attendance Grant (\$575 USD) 2021
- NIHR HPRU-EIZ & CEIDR COVID-19 Strategic Research Fund (£38,100 GBP; Co-I) 2020
- MRC Skills Development Fellowship (£235,657 GBP) Liverpool, 2019 - 2022
- NERC PhD Doctoral Training Award (3.5 years) Edinburgh, 2012 - 2015
- MSc Modern Epidemiology Dissertation Prize Imperial, 2011
- Santander UK Nationals' Masters Scholarship (£5000 GBP) Imperial, 2010
- Thomas Wall Trust Award (£1000 GBP) 2010
- Bundy Scholarship (£250 GBP) Magdalene College, Cambridge, 2010
- Christie Prize for Natural Sciences Magdalene College, Cambridge, 2010

Wider Professional Involvement:

- Academic Honorary Partnership with UK Health Security Agency (2024-)
- *Scientific Data*: Editorial Board Member; *Frontiers in Virology*: Associate Editor
- Peer reviews include *Sci Rep*, *Proc R Soc B*, *Phil Trans R Soc B*, *PLOS Biol*, *PLOS Comput Biol* (see <https://www.webofscience.com/wos/author/record/HPG-1144-2023> for extended list)
- 5-years grant review experience via **British Ecological Society Review College (2020-)**
- MRC Career Development Fellowship Award Reviewer (2021)
- Fellow of the Royal Statistical Society and Officer of the Merseyside Local Group (2020: Secretary, 2021-24: Chair); Committee member of the Celebrating Diversity SIG (2024-)
- Member of the British Ecological Society
- Fellow of the Higher Education Academy

Media & Science Communication:

- Solo interactive outreach shows 2017 - present
- 'A Virus To End Humanity': a pandemic scenario show exploring what might shape the risks of the next pandemic and how scientists can understand them featuring audience interactivity. Performed at the Cabaret of Dangerous Ideas, Edinburgh Fringe Festival, St Andrews Science Discovery Day and at several local skeptics/science society branches (Birmingham, Coventry, Bournemouth, Leicester, Wycombe, St Andrews).
 - 'War, Pestilence, Death and ..Statistics?!': an interactive show featuring games to explore statistical concepts like survivorship bias and relative risk through morbid stories from human history. Performed at Cabaret of Dangerous Ideas, Edinburgh Fringe Festival, various skeptics/science society branches (Birmingham, Warwickshire, Merseyside, Glasgow), and internationally (Melbourne, Sydney).
- Other sci-comm presentations:
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| NatureScot Young Employee Network: 'Statistics in the media' | 21 Aug 2025 |
| Ignite Liverpool: 'Eurovision: the winning (statistical) formula?' | 3 May 2023 |
| Royal Veterinary College: 'COVID-19: Will good weather decrease infection rates?' | 28 Jul 2020 |
| Skeptics in the Pub Online: 'Origins of the novel coronavirus (SARS-CoV-2)' | 28 Mar 2020 |
| Pint of Science Warwickshire: 'Life or death: can you really trust the stats?' | 21 May 2019 |
| 72 nd World Science Fiction Convention, London | 14 – 18 Aug 2014 |
| 'Where do new and deadly viruses come from?' (Joan & Harry Harrison Memorial Prize Winner) | |
- Podcasts
- | | |
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| The Skeptic Zone - Episode #842 | 24 Nov 2024 |
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- Statistical Ambassadorship, Royal Statistical Society 2016 - present
- Trained in media and public engagement for statistics communication by Sir David Spiegelhalter.
 - Co-analysed data for media organisations, including The Guardian and 'Panorama'.
 - Analysed data for and featured in BBC Bitesize Articles: '[Is there a formula for winning Eurovision? The experts speak](#)', '[Can the Eurovision running order affect a song's chances?](#)'
- Bright Club Edinburgh, Bright Club Glasgow 2015 – 2017, 2024 - present
- Co-organiser, trainer, and regular performer for science-themed stand-up comedy evenings.

Academic blog posts:

- Lorenzo-Arribas, A., **Brierley, L.**, and Reynolds, P. 2024. Reclaiming Narratives. The Royal Statistical Society, <https://rss.org.uk/news-publication/news-publications/2024/general-news/rss-celebrating-diversity-group-commemorates-2024/>
- Toader, A-M., and **Brierley, L.** 2023. Where do AI, data science, and computer games intersect? Real World Data Science, <https://realworlddatascience.net/viewpoints/posts/2023/08/17/data-science-and-games.html>
- Brierley, L.** 2023. Influencers for Influenza? How health researchers could use social media as a data source. University of Liverpool Institute of Population Health blog, <https://www.liverpool.ac.uk/population-health/blog/iph-february-2023-blogs/influencersforinfluenza/>
- Brierley, L.**, Fagre, A., Han, B., and Carlson, C.J. 2021. Can AI help us trace Omicron's origins? Verena blog, <https://www.viralemergence.org/blog/can-ai-help-us-trace-omicrons-origins>
- Brierley, L.** 2020. Using open-access tools (taxize, rentrez) to find coronaviruses, their genetic sequences, and their hosts. rOpenSci blog, <https://ropensci.org/blog/2020/11/10/coronaviruses-and-hosts/>
- Jones, K., and **Brierley, L.** 2016. Bats, people, and a complex web of disease transmission. ESRC STEPS centre blog. <https://steps-centre.org/blog/bats-people/>

Publications:

[square brackets indicate equal contribution]

- Maruzani, R., Fowler, A., **Brierley, L.**, and Jorgensen, A. Predicting high confidence ctDNA somatic variants with ensemble machine learning models. *Scientific Reports*, 15: 18384.
- Maruzani, R., **Brierley, L.**, Jorgensen, A., and Fowler, A. Benchmarking UMI-aware and standard variant callers for low frequency ctDNA variant detection. *BMC Genomics*, 25: 827.
- Farrell, M.J., Le Guillarme, N., **Brierley, L.**, Hunter, B., Scheepens, D., Willoughby, A., Yates, A., and Mideo, N. 2024. The changing landscape of text mining - a review of approaches for ecology and evolution. *Proceedings of the Royal Society B*, 291(2027): 20240423.
- Lu, L., Zhang, F., **Brierley, L.**, Robertson, G., Chase-Topping, M., Lycett, S., and Woolhouse, M.E.J. 2024. Temporal dynamics, discovery, and emergence of human-transmissible RNA viruses. *Molecular Biology and Evolution*, 41(1): msad272.
- Hufsky, F., Abecasis, A.B., Babaian, A., Beck, S., **Brierley, L.**, Dellicour, S., Eggeling, C., Elena, S.F., Gieraths, U., Ha, A.D., Harvey, W., Jones, T.C., Lamkiewicz, K., Lovate, G.L., Lücking, D., Machyna, M., Nishimura, L., Nocke, M.K., Renard, B.Y., Sakaguchi, S., Sakellaridi, L., et al. 2023. The International Virus Bioinformatics Meeting 2023. *Viruses*, 15(10): 2031.
- Hawkins, M.J., Vaselli, N.M., Charalampopoulos, D., **Brierley, L.**, Elliot, A.J., Buchan, I., and Hungerford, D. 2023. Network embedding unveils the hidden interactions in the mammalian virome. *Viruses*, 15(8): 1625.
- Poisot, T., Ouellet, M-A., Mollentze, N., Farrell, M.J., Becker, D.J., **Brierley, L.**, Albery, G.F., Gibb, R.J., Seifert, S.N., and Carlson, C.J. 2023. Network embedding unveils the hidden interactions in the mammalian virome. *Patterns*, 4(6): 100738.
- Farrell, M.J., **Brierley, L.**, Willoughby, A., Yates, A., and Mideo, N. 2022. Past and future use of text mining in ecology & evolution. *Proceedings of the Royal Society B*, 289(1975): 20212721.
- Carlson, C.J., Gibb, R., Albery, G.F., **Brierley, L.**, Connor, R.C., Dallas, T.A., Eskew, E.A., Fagre, A., Farrell, M.J., Frank, H., Muylaert, R., Poisot, T., Rasmussen, A., Ryan, S.J., and Seifert, S.N. 2022. The global virome in one network (VIRION): an atlas of vertebrate-virus associations. *mBio*, 13(2): e02985-21.
- Brierley, L.**, Nanni, F., Polka, J.K., Dey, G., Palfy, M., Fraser, N., and Coates, J.A. 2022. Tracking changes between preprint posting and journal publication during a pandemic. *PLOS Biology*, 20(2): e3001285.
- Gibb, R., Albery, G.F., Mollentze, N., Eskew, E.A., **Brierley, L.**, Ryan, S.J., Seifert, S.N., and Carlson, C.J. 2022. Mammal virus diversity estimates are unreliable at the species level. *Biology Letters*, 18(1): 20210427.
- Albery, G.F., Becker, D.J., **Brierley, L.**, Brook, C.E., Christofferson, R.C., Cohen, L.E., Dallas, T.A., Eskew, E.A., Fagre, A., Farrell, M.J., Glennon, E., Guth, S., Joseph, M.B., Mollentze, N., Neely, B.A., Poisot, T., Rasmussen, A.L., Ryan, S.J., Sjodin, A.R., Seifert, S., Sorrell, E.M., and Carlson, C.J. 2021. The science of the host-virus network. *Nature Microbiology*, 6(12): 1483-1492.
- Gibb, R., Albery, G.F., Becker, D.J., **Brierley, L.**, Connor, R., Dallas, T.A., Eskew, E.A., Farrell, M.J., Rasmussen, A.L., Ryan, S.J., Sweeny, A., Carlson, C.J., and Poisot, T. 2021. Data proliferation, reconciliation, and synthesis in viral ecology. *BioScience*, 71(11): 1148-1156.
- Brierley, L.**, and Fowler, A. 2021. Predicting the animal hosts of coronaviruses from compositional biases of spike protein and whole genome sequences through machine learning. *PLOS Pathogens*, 17(4): e1009149.
- [Fraser, N., **Brierley, L.**, Dey, G., Polka, J.K., Palfy, M., Nanni, F., and Coates, J.A. 2021. The evolving role of preprints in the dissemination of COVID-19 research and their impact on the science communication landscape. *PLOS Biology*, 19(4): e3000959.

- Brierley, L.** 2021. Lessons from the influx of preprints during the early COVID-19 pandemic. *Lancet Planetary Health*, 5(3): e115-117.
- [Metelmann, S., Pattni, K., **Brierley, L.**], Cavalerie, L., Caminade, C., Blagrove, M.S.C., Turner, J., Sharkey, K.J., and Baylis, M. 2021. Impact of climatic, demographic and disease control factors on the transmission dynamics of COVID-19 in large cities worldwide. *One Health*, 12: 100221.
- Zhang, F., Chase-Topping, M., Guo, C-G., van Bunnik, B.A.D., **Brierley, L.**, and Woolhouse, M.E.J. 2020. Global discovery of human-infective RNA viruses: A modelling analysis. *PLOS Pathogens*, 16(11): e1009079.
- Brierley, L.**, Pedersen, A.B., and Woolhouse, M.E.J. 2019. Tissue tropism and transmission ecology predict virulence of human RNA viruses. *PLOS Biology*, 17(11): e3000206.
- McGurnaghan, S.J., **Brierley, L.**, Caparrotta, T.M., McKeigue, P.M., Blackbourn, L.A.K., Wild, S.H., Leese, G., McCrimmon, R.J., McKnight, J.A., Pearson, E.R., Petrie, J.R., Sattar, N., and Colhoun, H.M. 2019. The effect of dapagliflozin on glycaemic control and other cardiovascular disease risk factors in type 2 diabetes mellitus patients: a real-world observational study. *Diabetologia*, 62(4): 621-632.
- Woolhouse, M.E.J., and **Brierley, L.** 2018. Epidemiological characteristics of human-infective RNA viruses. *Scientific Data*, 5: 180017.
- Woolhouse, M.E.J., **Brierley, L.**, McCaffery, C., and Lycett, S. 2016. Assessing the epidemic potential of RNA and DNA viruses. *Emerging Infectious Diseases*, 22(12): 2037-2044.
- Brierley, L.**, Vonhof, M.J., Olival, K.J., Daszak, P., and Jones, K.E. 2016. Quantifying global drivers of zoonotic bat viruses: a process-based perspective. *The American Naturalist*, 187(2): E53-E64.
- Woolhouse, M.E.J., Adair, K., and **Brierley, L.** 2013. RNA viruses: a case study of the biology of emerging infectious diseases. *Microbiology Spectrum*, 1: OH-0001-2012.
- Grace, D., Mutua, F., Ochungo, P., Kruska, R., Jones, K., **Brierley, L.**, Lapar, L., Said, M., Herrero, M., Phuc, P.M., Thao, N.B., Akuku, I., and Ongutu, F. 2012. Mapping of poverty and likely zoonoses hotspots. Zoonoses Project 4. Report to the UK Department for International Development. Nairobi, Kenya: ILRI.

Preprints:

- Brierley, L.**, Mould-Quevedo, J., and Baylis, M. An AI for an AI: identifying zoonotic potential of avian influenza viruses via genomic machine learning. <https://doi.org/10.1101/2025.09.16.676011>
- Hawkins, M.J., **Brierley, L.**, Hughes, D.M., Elliot, A.J., Buchan, I., and Hungerford, D. COVID-19 and new-onset autoimmune mediated gastrointestinal illness: a naturalistic cohort study from England. https://papers.ssrn.com/sol3/papers.cfm?abstract_id=5278544
- [Hayes, S., Hilton, J.], Mould-Quevedo, J., Donnelly, C., Baylis, M., and **Brierley, L.** Ecology and environment predict spatially stratified risk of H5 highly pathogenic avian influenza clade 2.3.4.4b in wild birds across Europe. <https://doi.org/10.1101/2024.07.17.603912v2>
- Kockelbergh, H., Evans, S.C., **Brierley, L.**, Green, P.L., Jorgensen, A.L., Soilleux, E.J., and Fowler, A. Evaluating the utility of amino acid similarity-aware kmers to represent TCR repertoires for classification. <https://doi.org/10.1101/2024.12.06.626025>

Invited presentations:	*upcoming
The Pandemic Institute Scientific Meeting, Liverpool <i>'An AI for an AI: Identifying zoonotic potential of avian influenza viruses via genomic machine learning'</i>	1 - 2 Oct 2025
UKRI One Health Computational Network Symposium, University of Glasgow <i>'Inferring viral evolution through machine learning'</i>	24 Apr 2025
Department of Health Data Science, University of Liverpool MSc Guest Lecture: <i>'Statistical measures of genome composition and codon usage biases'</i>	27 Mar 2025
Big Data Institute, Li Ka Shing Centre, University of Oxford DTP Guest Lecture: <i>'Application of machine learning to viral sequences and macroevolution'</i>	29 Nov 2024
Infectious Disease Modelling Section, University of Melbourne Seminar: <i>'The 'where' and the 'who' of virus emergence and evolution'</i>	18 Oct 2024
Joint UNIversities Pandemic and Epidemiology Research (JUNIPER) Consortium (online) Seminar: <i>'Inferring the next zoonotic spillover of avian influenza directly from genomic machine learning'</i>	8 May 2024
School of Biodiversity, One Health, and Veterinary Medicine, University of Glasgow. Seminar: <i>'Which tissues, which hosts, which places: macroecology & evolution of viral emergence'</i>	6 July 2023
Microbiology Society Annual Conference 2023, Birmingham. <i>'Inferring host potential directly from viral genomes through computational learning'</i>	17 – 20 April 2023
Royal Statistical Society International Conference 2022, Aberdeen. <i>'Statistics of Strange Species: Which animals are emerging viruses likely to come from?'</i>	12 – 15 Sep 2022
Royal Statistical Society Young Statisticians' Meeting 2022 (online). Plenary talk: <i>'How can we predict the next pandemic?'</i>	4 - 5 Aug 2022
Royal Statistical Society Glasgow Local Group. <i>'Paper planes, pints, and other props: communicating stats to the public through interactivity'</i>	8 Dec 2021
Data Mining & Machine Learning Group, University of Liverpool. Seminar: <i>'Combining machine learning and genomic approaches to predict RNA virus emergence'</i>	12 Feb 2020
Institute of Biomedical Science Congress 2019, Birmingham. <i>'Insights into the future: emerging viruses'</i>	22 - 25 Sep 2019
Cambridge Disease Dynamics Unit, University of Cambridge. Seminar: <i>'Can host and virus ecology predict virulence of emerging RNA viruses?'</i>	11 Apr 2019
5 th Boyd Orr Symposium: <i>'From viral genotype to phenotype'</i> , Glasgow. <i>'Ecological risk factors for virulence in human RNA viruses'</i>	23 Oct 2014

Contributed presentations: *upcoming

- 11th International Symposium on Avian Influenza, St Johns. 24 – 26 Jun 2025
Poster: '*Uncovering the contribution of environmental and ecological factors to spatial risk of 2.3.4.4b HPAI in wild birds*' & Poster:
'*An AI for an AI: can the next zoonotic avian influenza spillover be identified straight from its genome?*'
- Influenza Update Meeting 2024, Glasgow. 2 - 3 Dec 2024
Poster: '*Uncovering the contribution of environmental and ecological factors to predicted highly pathogenic avian influenza risks in wild birds*' &
'*An AI for an AI: can the next zoonotic avian influenza spillover be identified straight from its genome?*'
- 17th Int'l Symposium on Veterinary Epidemiology and Economics, Sydney. 11 - 15 Nov 2024
Uncovering the contribution of environmental and ecological factors to predicted highly pathogenic avian influenza risks in wild birds' &
'*An AI for an AI: can the next zoonotic avian influenza spillover be identified straight from its genome?*'
- OPTIONS XII for the Control of Influenza, Brisbane. 29 Sep - 2 Oct 2024
Poster: '*Uncovering the contribution of environmental and ecological factors to predicted highly pathogenic avian influenza risks in wild birds*' & Poster:
'*An AI for an AI: can the next zoonotic avian influenza spillover be identified straight from its genome?*'
- 2024 Ecology & Evolution of Infectious Disease Conference, Stanford, CA. 24 - 27 Jun 2024
'*An AI for an AI: can the next zoonotic avian influenza spillover be identified straight from its genome?*'
- British Ecological Society Annual Meeting 2023, Belfast. 12 – 15 Dec 2023
'*Wild bird ecology and environment can predict landscape-level risks of avian influenza in Europe*'
- Epidemics9 (Elsevier), Bologna. 28 Nov – 1 Dec 2023
Poster: '*Modelling the zoonotic capabilities of avian influenza via genomic machine learning*'
- Ecological and Evolutionary Drivers of Pathogen Emergence Symposium, Exeter. 13 – 14 Jun 2023
'*Trade-offs and consequences of parasite specialism from tissue to taxa*'
- EVBC International Virus Bioinformatics Meeting 2023, Valencia. 24 – 26 May 2023
'*Modelling the zoonotic capabilities of avian influenza via genomic machine learning*'
- Royal Statistical Society International Conference 2022, Aberdeen. 12 – 15 Sep 2022
Workshop: '*Don't panic! The Ambassadors' guide to communicating statistics*'
- EMBO Workshop: Codon usage: Function, mechanism, and evolution, Edinburgh. 8 – 11 Apr 2022
Poster: '*Codon usage biases as informative machine learning features to predict coronavirus origins*'
- BES & SFE² joint Annual Meeting (Ecology Across Borders) 2021, Liverpool. 12 – 15 Dec 2021
'*Building a comparative database of pathogen tropisms from published literature*'

Royal Statistical Society International Conference 2021, Manchester. 'Generating data on pathogen tropisms from published literature' & Workshop: 'Don't panic! The Ambassadors' guide to communicating statistics'	6 - 9 Sep 2021
ASM & FEMS World Microbe Forum 2021 (online) e-poster: 'Predicting the animal hosts of coronaviruses from genomic data through machine learning'	20 - 24 Jun 2021
18th Annual Ecology & Evolution of Infectious Disease Conference (online) e-poster: 'Predicting the animal hosts of coronaviruses from genomic data through machine learning'	14 - 17 Jun 2021
British Ecological Society Annual Meeting 2020 (online) 'Predicting the animal hosts of coronaviruses from genomic data through machine learning'	14 - 18 Dec 2020
European R Users' Meeting 2020 (online) 'Using open-access data to derive genome composition of emerging viruses'	17 - 19 Jun 2020
British Ecological Society Annual Meeting, Birmingham. <i>Tropism and transmission ecology predict virulence of human RNA viruses'</i>	17 - 19 Dec 2018
13 th Annual Ecology & Evolution of Infectious Disease Conference, Athens, GA. 'Host range of RNA viruses predicts transmission and virulence of human infections'	26 - 29 May 2015
British Society for Parasitology Spring Meeting, Liverpool. 'Host range of RNA viruses predicts transmission and virulence of human infections'	16 - 18 Apr 2015
2 nd Edinburgh Ecology Network Symposium, Edinburgh. 'Can viral ecology predict virulence of human RNA viruses?'	27 Feb 2015
European Wildlife Disease Association Conference, Edinburgh. 'Are threats to wild species associated with virus sharing with humans?'	26 - 29 Aug 2014
From emerging to pandemic viruses (Conférences Jacques Monod), Roscoff. Poster: 'Risk factors for virulence in human RNA viruses'	2 - 6 Apr 2014
Epidemics4 (Elsevier), Amsterdam. Poster: 'Risk factors for virulence in human RNA viruses'	19 - 22 Nov 2013