

# Gytis Dudas

Institute of Biotechnology, Life Sciences Center, Vilnius University  
Saulėtekio al. 7, LT-10257, Vilnius, Lithuania  
✉ gytis.dudas@gmc.vu.lt  
🌐 Personal website

## Curriculum Vitae

### Postgraduate career

- 2021– Principal Investigator (senior researcher), *Life Sciences Centre (Institute of Biotechnology), University of Vilnius*, Vilnius, Lithuania.
- 2020– Remote consultant, *Ring Therapeutics*, Cambridge, MA, USA.
- 2018– Remote consultant, *CZ Biohub*, San Francisco, CA, USA.
- 2018– Remote consultant, *The Scripps Research Institute*, San Diego, CA, USA.
- 2016–2018 Postdoctoral fellow, *Fred Hutchinson Cancer Research Center*, Seattle, WA, USA, Mentor: Trevor Bedford.

### Education

- 2011–2016 Doctor of Philosophy, “Inference of Evolutionary and Ecological Processes from Reticulate Evolution in RNA Viruses”, *University of Edinburgh*, Edinburgh, UK. Supervisor: Prof. Andrew Rambaut, secondary supervisor: Prof. Andrew Leigh-Brown; Thesis examiners: Prof. Oliver G Pybus, Prof. Paul Sharp.
- 2007–2011 BSc in Biological Sciences with Honours in Evolutionary Biology, *University of Edinburgh*, Edinburgh, UK. First Class, Ashworth Prize and Class Medal

### Publications

- 2023 42. Tang M, **Dudas G**, Bedford T, Minin VN., *Fitting stochastic epidemic models to gene genealogies using linear noise approximation*, *Annals of Applied Statistics* 17(1): 1-22.
- 2022 41. [<sup>1</sup> Brito AF, Semenova E, **Dudas G**], Hassler GW, Kalinich CC, Kraemer MUG, ..., Suchard MA, Grubaugh ND, Baele G, Faria NR, *Global disparities in SARS-CoV-2 genomic surveillance*, *Nature Communications* 13: 7003.
- 2022 40. Klitting R, Kafetzopoulou LE, Thiery W, **Dudas G**, Gryseels S, ..., Suchard MA, Lemey P, Andersen KG, Dellicour S., *Predicting the evolution of Lassa Virus endemic area and population at risk over the next decades*, *Nature Communications* 13: 5596.
- 2022 39. **Dudas G**, Batson J, *Accumulated metagenomic studies reveal recent migration, whole genome evolution, and taxonomic incompleteness of orthomyxoviruses*, bioRxiv: 2022.08.31.505987.
- 2022 38. Tsitsiklis A, Osborne CM, Kamm J, Williamson K, Kalantar K, **Dudas G**, ..., DeRisi JL, Mourani PM, Langelier CR, *Lower respiratory tract infections in children requiring mechanical ventilation: a multicentre prospective surveillance study incorporating airway metagenomics*, *The Lancet Microbe* 3(4): e284–e293.

<sup>1</sup>[ ] denotes equal contribution

- 2022 37. Kaleta T, Kern L, Hong SL, ..., **Dudas G**, ..., Baele G, Panning M, Fuchs J, *Antibody escape and global spread of SARS-CoV-2 lineage A.27*, Nature Communications 13: 1152.
- 2021 36. [**Dudas G**], Hong SL, Potter B, Calvignac-Spencer S, Niatou-Singa FS, Tombolomako TB, Fuh-Neba T, ..., Griškevičius L, [Baele G], *Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions*, Nature Communications 12: 5769.
- 2021 35. Chazot N, Condamine FL, **Dudas G**, Peña C, Kodandaramaiah U, Matos-Maraví P, ..., Wahlberg N., *Conserved ancestral tropical niche but different continental histories explain the latitudinal diversity gradient in brush-footed butterflies*, Nature Communications 12: 5717.
- 2021 34. Zeller M, Gangavarapu K, Anderson C, Smither AR, Vanchiere JA, Rose R, Snyder DJ, **Dudas G**, Watts A, Matteson NL, Robles-Sikisaka R, ..., Kamil JP, Garry RF, Suchard MA, Andersen KG, *Emergence of an early SARS-CoV-2 epidemic in the United States*, Cell 184, 4939–4952.
- 2021 33. Pautienius A, **Dudas G**, Simkute E, Grigas J, Zakiene I, Paulauskas A, Armonaite A, Zienius D, Slyzius E, Stankevicius A, *Bulk Milk Tank Samples Are Suitable to Assess Circulation of Tick-Borne Encephalitis Virus in High Endemic Areas*, Viruses 13(9):1772.
- 2021 32. Arze CA, Springer S, **Dudas G**, Patel S, Bhattacharyya A, Swaminathan H, ..., Andersen KG, Yozwiak NL, *Global genome analysis reveals a vast and dynamic anellovirus landscape within the human virome*, Cell Host & Microbe 29(8): 1305-1315.e6.
- 2021 31. Pirnay JP, Selhorst P, Hong SL, Cochez C, Potter B, Maes P, Petrillo M, **Dudas G**, ..., Soentjens P, Baele G, *Variant Analysis of SARS-CoV-2 Genomes from Belgian Military Personnel Engaged in Overseas Missions and Operations*, Viruses 13(7): 1359.
- 2021 30. [Batson J, **Dudas G**, Haas-Stapleton E, Kistler A, Li LM, Logan P, Ratnasari K, Retallack H]., *Single mosquito metatranscriptomics identifies vectors, emerging pathogens and reservoirs in one assay*, eLife 10:e68353.
- 2021 29. **Dudas G**, Huber G, Wilkinson M, Yllanes D., *Polymorphism of Genetic Ambigrams*, Virus Evolution 2021: veab038.
- 2020 28. Karcher MD, Carvalho LM, Suchard MA, **Dudas G**, Minin VN., *Estimating effective population size changes from preferentially sampled genetic sequences*, PLoS Comput Biol 16(10): e1007774.
- 2020 27. Müller NF, Stolz U, **Dudas G**, Stadler T, Vaughan TG., *Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses*, PNAS 117(29): 17104-17111.
- 2019 26. **Dudas G**, Bedford T., *The ability of single genes vs full genomes to resolve time and space in outbreak analysis*, BMC Evolutionary Biology 19(1): 1-17.
- 2019 25. Müller NF, **Dudas G**, Stadler T., *Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations*, Virus Evolution 5(2): vez030.

- 2018 24. Dellicour S, Baele G, **Dudas G**, Faria NR, Pybus OG, Suchard MA, Rambaut A, Lemey P., *Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak*, Nature Communications 9: 2222.
- 2018 23. Chu DKW, Hui Kenrie PY, ..., **Dudas G**, ..., Drosten C, Chevalier V, Peiris M, *MERS coronaviruses from camels in Africa exhibit region-dependent genetic diversity*, PNAS 115(12): 3144-3149.
- 2018 22. Whitmer SLM, Ladner JT, ..., **Dudas G**, ..., Palacios G, Ströher U, *Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors*, Cell Reports 22(5): 1159-1168.
- 2018 21. **Dudas G**, Carvalho LM, Rambaut A, Bedford T, *MERS-CoV spillover at the camel-human interface*, eLife 7: e31257.
- 2017 20. Langat P, Raghwanji J, **Dudas G**, ..., Russell C, Pybus O, Kellam P, McCauley J, Watson S, *Genome-wide evolutionary dynamics of influenza B viruses on a global scale*, PLOS Pathogens 13(12): e1006749.
- 2017 19. [Grubaugh ND, Ladner JT, Moritz KUG, **Dudas G**, Tan AL, Gangavarapu K, Wiley MR, White S, Thézé J], ..., Sabeti PC, Gillis LD, Michael SF, Bedford T, Pybus OG, Isern S, Palacios G, Andersen KG, *Multiple introductions of Zika virus into the United States revealed through genomic epidemiology*, Nature 546(7656): 401-405.
- 2017 18. **Dudas G**, Carvalho LM, Bedford T, Tatem AJ, Baele G, Faria N, Park D, Ladner J, Arias A, ..., Suchard M, Lemey P, Rambaut A, *Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic*, Nature 544(7650): 309-315.
- 2017 17. Black A, Potter B, **Dudas G**, Feldstein L, Grubaugh ND, Andersen KG, Ellis BR, Ellis EM, Bedford T, *Genetic characterization of the Zika virus epidemic in the US Virgin Islands*, bioRxiv: 113100.
- 2016 16. Holmes EC, **Dudas G**, Rambaut A, Andersen KG, *The Evolution of Ebola virus: Insights from the 2013-2016 Epidemic*, Nature 538(7624): 193-200.
- 2016 15. Whitmer SLM, Albariño C, Shepard SS, **Dudas G**, ..., Nichol ST, Ströher U, *Preliminary Evaluation of the Effect of Investigational Ebola Virus Disease Treatments on Viral Genome Sequences*, Journal of Infectious Diseases: jiw177.
- 2016 14. Rambaut A, **Dudas G**, Carvalho LM, Park DJ, Yozwiak NL, Holmes EC, Andersen KG, *Comment on "Mutation rate and genotype variation of Ebola virus from Mali case sequences"*, Science 353(6300): 658-658.
- 2016 13. Arias A, Watson SJ, Asogun D, ..., **Dudas G**, ..., Pybus OG, Rambaut A, Kellam P, Goodfellow I, Cotten M, *Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases*, Virus Evolution 2 (1): vew016.
- 2016 12. Lewis NS, Russell CA, Langat P, ..., **Dudas G**, ..., Watson SJ, Brown IH, Vincent AL, *The global antigenic diversity of swine influenza A viruses*, eLife 5: e12217.
- 2016 11. Quick J, Loman NJ, Duraffour S, Simpson JT, Severi E, Cowley L ..., **Dudas G**, ..., Günther S, Carroll MW, *Real-time, portable genome sequencing for Ebola surveillance*, Nature 530(7589): 228-232.
- 2016 10. **Dudas G**, Rambaut A, *MERS-CoV recombination: implications about the reservoir and potential for adaptation*, Virus Evolution 2(1): vev023.
- 2015 9. Ladner JT, Wiley MR, Mate S, **Dudas G**, ... Palacios G, *Evolution and Spread of Ebola Virus in Liberia, 2014-2015*, Cell Host & Microbe 18(6): 659-669.

- 2015 8. [Park DJ, **Dudas G**, Wohl S, Goba A, Whitmer SLM], ..., Sabeti PC, *Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone*, Cell 161(7): 1516-1526.
- 2015 7. Carroll MW, Matthews DA, Hiscox JA, ... **Dudas G**, ... Günther S, *Temporal and spatial analysis of the 2014-2015 Ebola virus outbreak in West Africa*, Nature 524(7563): 97-101.
- 2015 6. **Dudas G**, Obbard DJ, *Are arthropods at the heart of virus evolution?*, eLife 4: e06837.
- 2015 5. **Dudas G**, Bedford T, Lycett S, Rambaut A, *Reassortment between Influenza B Lineages and the Emergence of a Coadapted PB1–PB2–HA Gene Complex*, Molecular Biology and Evolution 32(1): 162-172.
- 2014 4. Obbard DJ, **Dudas G**, *The genetics of host–virus coevolution in invertebrates*, Current Opinion in Virology 8: 73-78.
- 2014 3. Gire SK, Goba A, Andersen KG, ... **Dudas G**, ... Sabeti PC, *Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak*, Science 345(6202): 1369-1372.
- 2014 2. **Dudas G**, Rambaut A, *Phylogenetic analysis of Guinea 2014 EBOV Ebolavirus outbreak*, PLOS Currents Outbreaks 6.
- 2014 1. Bedford T, Suchard MA, Lemey P, **Dudas G**, Gregory V, ..., Rambaut A, *Integrating influenza antigenic dynamics with molecular evolution*, eLife 3: e01914.

## Funding

2023- EMBO Installation Grant, 3 years, 150 000 EUR.

## Professional service

2021-2022 Co-author and chief data analyst for Lithuania's pandemic SARS-CoV-2 genomic surveillance project. The project generated >39 000 SARS-CoV-2 genomes February 2021 - May 2022 averaging  $\approx 2.0\%$  (between 0.2% and 28% in a given month) of all COVID-19 cases in Lithuania.

2021-2022 Advisory council of independent experts to the Lithuanian government tasked with advising the government on COVID-19 prevention, diagnostics, treatment, and application of other means of epidemic control.

2016-2018 Social media editor (on Twitter) for Virus Evolution.

*Ad hoc* referee BMC Bioinformatics, Cell Reports, Nature Communications, Nature Ecology & Evolution, Nature Medicine, Nature Microbiology, PLoS Currents Outbreaks, eLife, PLoS Neglected Tropical Diseases, BMC Genome Medicine, Molecular Biology and Evolution, Infection, Genetics and Evolution, The Journal of Infectious Diseases, PLOS Pathogens, PeerJ, Proceedings of the Royal Society B, Scientific Reports, Virology Journal, Virus Evolution.

## Postgraduate student supervision

2023 Brygida Serebriakova (MSc)

2023 Viktorija Juknevičiūtė (MSc)

## Postgraduate student supervision (informal)

2018-2021	Karthik Gangavarapu (PhD)
2017-2021	Barney I Potter (research assistant)
2016-2018	Sidney M Bell (PhD)

## Presentations

2022,	Vilnius	Invited oral presentation at a joint Lithuanian-CNRS Symposium on Health, "Emergence and spread of SARS-CoV-2 lineage B.1.620 with variant of concern-like mutations and deletions"
2022,	Seattle	Invited oral presentation at Fred Hutchinson Cancer Center computational biology seminar, "The RNA virus research revolution slumbering in accumulated metagenomic data"
2022,	San Francisco	Invited oral presentation at CZ Biohub internal seminar series, "The RNA virus research revolution slumbering in accumulated metagenomic data"
2022,	Vilnius	Invited oral presentation at Lithuanian Biochemical Society's conference Biochemistry in the Big Data Age, "Small victories of the Lithuanian SARS-CoV-2 genomic surveillance programme"
2021,	Vilnius	Invited oral presentation at EVOdrops Workshop 5, "SARS-CoV-2 in Lithuania"
2021,	Vilnius	Invited oral presentation (remote) at Vilnius University Hospital Santaros Klinikos conference COVID-19 infekcija: iššūkiai, patirtys ir ateities perspektyva, "Lietuvos SARS-CoV-2 sekoskaitos projekto pasiekimai" [in Lithuanian]
2021,	Cambridge	Invited (remote) talk at University of Cambridge Department of Virology, "MERS-CoV spillover at the camel-human interface"
2020,	Seattle	Invited (remote) talk at University of Washington Department of Genome Sciences, "Single mosquito metatranscriptomics in California"
2019,	London	Informal presentation at Imperial College London, "Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic"
2019,	Basel	Invited talk at ETH Zürich, "Beyond (two) button phylogenetics"
2019,	Phoenix	Invited talk at Arizona State University, "Reconstructing the history and drivers of viral epidemics from genomes of emerging RNA viruses"
2019,	Flagstaff	Invited talk at Northern Arizona University, "MERS-CoV spillover at the camel-human interface"
2018,	Edinburgh	Invited talk at ARTIC network meeting, "MERS-CoV spillover at the camel-human interface"
2018,	San Diego	Invited talk at UC San Diego HIV Institute, "Reconstructing the history and drivers of viral epidemics from genomes of Zika, MERS-CoV, and Ebola viruses"
2018,	San Francisco	Invited talk at BioHub, "Reconstructing the history and drivers of viral epidemics from virus genomes"
2018,	Bellevue	Oral presentation at the 6th Annual Disease Modeling Symposium, "Genomic epidemiology and population genetics of emerging RNA viruses"
2018,	Tucson	Invited talk at BIO5 Institute, "MERS-CoV spillover at the camel-human interface"

- 2018, Tucson Invited talk at University of Arizona, "Reconstructing the history and drivers of viral epidemics from virus genomes"
- 2017, Seattle Invited talk at University of Washington Institute for Health Metrics and Evaluation, "MERS-CoV spillover at the camel-human interface"
- 2017, Baltimore Invited talk at 19<sup>th</sup> Annual International Meeting of the Institute of Human Virology, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- 2017, Edinburgh Oral presentation at ARTIC network meeting, "Reproducible visualisation using Jupyter notebooks"
- 2017, Hong Kong Oral presentation at Next Generation Informatics for Global Health: Disease Dynamics and Digital Epidemiology, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- 2017, Cambridge Invited talk at Broad Institute, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- 2017, Boston Invited talk at Harvard T.H. Chan School of Public Health, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- 2017, Atlanta Oral presentation at the MIDAS Network Meeting, "Virus genomes reveal factors that spread and sustained the Ebola epidemic"
- 2016, Seattle Oral presentation for Combi Seminar series, "Virus genomes reveal the factors that spread and sustained the West African Ebola epidemic"
- 2016, Cambridge Oral presentation at Virus Genomics and Evolution, "Pattern and determinants of the geographic dissemination of Ebola virus in West Africa 2013-2016"
- 2015, Zürich Invited talk at University of Zürich, "Lessons about virus biology from molecular clocks"
- 2015, Vienna Oral presentation at SMBE 2015, "Population genetics of Ebola virus in West Africa"
- 2015, Lisbon Oral presentation at Forecasting Evolution?, "Population genetics of Ebola virus in West Africa"
- 2015, online Invited talk at Phyloseminar.org, "Ebola virus epidemiology, transmission, and viral evolution from four months of sequencing in Sierra Leone"
- 2015, Seattle Invited talk at Fred Hutchinson Cancer Research Center, "Reticulate evolution: unlikely lessons about RNA viruses and their hosts"
- 2014, Oxford Invited talk at University of Oxford, "Phylodynamics of co-circulating influenza virus lineages"
- 2014, London Invited talk at Imperial College London, "Phylodynamics of co-circulating influenza virus lineages"
- 2013, Amsterdam Oral presentation at Epidemics 4, "Inter-subtype reassortment patterns in influenza B reveal selective maintenance of co-reassorting segment complexes"
- 2012, Glasgow Oral presentation at Popgroup 46, "Antagonistic interactions between co-circulating subtypes of human influenza viruses"
- 2012, Dublin Poster at SMBE 2012, "Phylodynamics of influenza viruses before, during and after the 2009 swine flu pandemic"

## Teaching

2022, Vilnius University Parts of Molecular Evolution course for BSc/MSc students.

## Awards

2018 SciPy John Hunter Excellence in Plotting Prize, 1st place, for “History of Ebola Virus Epidemic in West Africa 2013-2015”, a matplotlib-based phylogeographic visualisation.

2017 Young Investigator Award to attend “Next Generation Informatics for Global Health: Disease Dynamics and Digital Epidemiology” in Hong Kong.

2016 Mahan postdoctoral fellowship, Fred Hutchinson Cancer Research Center.

2015 SMBE Young Investigator Travel Award to attend the SMBE 2015 meeting in Vienna.

2015 Wellcome Trust Travel Grant to attend the “Forecasting Evolution?” meeting in Lisbon.

## Workshops

2020, Salt Lake City BioVis@IEEE Challenges Workshop, part of VIS 2020 virtual conference, domain expert speaker.

2015, University of Birmingham “PoreCamp: A bootcamp to learn about operating the Oxford Nanopore MinION”, attendee.

2015, University of Zürich “Temporal tree calibration in BEAST”, organiser.

## Outreach

TV3 “Mokslininkas prabilo apie didžiausią problemą dėl COVID-19: virusas gali kelti riziką net šimtmečiais”, *online article, news website of a television channel*, interview.  
2022 Aug 20

Vilnius University “Genominė epidemiologija: kaip atrodo protrūčiai iš virusų perspektyvos”, *a showcase of research carried out at Vilnius University*, invited talk.  
2022 Mar 18

Kavinė Fantastiška “Kaip sukurti baisiausią pasaulyje virusą”, *monthly Lithuanian language podcast about science, fantasy, and science fiction*, invited talk.  
2022 Mar 17

Mokslo Sriuba “Kaip mutuoja virusai?”, *Lithuanian language pop-science show*, consulting.  
2022 Feb 28

Vilniaus Knygų Mugė “Ar mokslininkai pralaimi sąmokslų teorijoms?”, *Vilnius Book Fair*, member of discussion panel.  
2022 Feb 24

Biologų Sandrauga “Genominė epidemiologija: ‘teorinė biologija’ užkrečiamųjų ligų kontrolėje”, *organisation for extracurricular activities for highschool students interested in biology*, invited talk.  
2022 Feb 04

- LRT / VU “Mokslas be pamokslų. Koronaviruso evoliucija: ko laukti?”, *joint Vilnius University and Lithuanian National Radio and Television podcast*, interview.  
2022 Jan 06
- VLE “COVID-19 atmainos”, *online article in the Universal Lithuanian Encyclopedia*, contributed article.  
2021 Sep 21
- Nacionalinė Moksleivių Akademinė “Evoliucija populiacijos lygmeniu: kertinės idėjos”, “Šiuolaikinis mokslo atsakas į epidemijas”, *a series of lectures for the National Student Academy, a Lithuanian non-profit public education organisation*, lectures.  
2021 Feb 19
- LRT Mokslininkas Gytis Dudas apie pačius įdomiausius ir pavojingiausius virusus: mirtiniausių galima sutikti ir Lietuvoje, *Lithuanian National Radio and Television*, interview.  
2021 Jan 24
- Išmani Lietuva Virusų detektyvas: ar galime užkirsti kelią pandemijoms?, *Lithuanian innovation conference*, invited talk.  
2020 Oct 14
- NYLA podcast Koronavirusas: ką jau žinome, o ko dar ne, *Lithuanian language podcast*, interview.  
2020 Jul 23
- Nature News How countries are using genomics to help avoid a second coronavirus wave, *science news*, background consultant.  
2020 May 27
- FiveThirtyEight Genetic Tracking Helped Us Fight Ebola. Why Can't It Halt COVID-19?, *politics and economics news*, interview.  
2020 Apr 15
- LRT Dar neseniai pasaulis kovojo su mirtinu Ebolos virusu: kaip pavyko suvaldyti epidemiją neturint veikiančios vakcinos, *Lithuanian National Radio and Television*, interview.  
2020 Mar 25
- NYLA podcast Gyventi su COVID-19. Kalba mokslininkai, *Lithuanian language podcast*, interview.  
2020 Mar 15
- Moteris magazine Ebolos virusą perpratęs Gytis Dudas: “Lietuvoje vis dar jauti, kad gali kažką pakeisti”, *Lithuanian language magazine*, interview.  
2019 Mar 22
- NYLA podcast Perpratęs ebolą: Gytis Dudas, *Lithuanian language podcast*, interview.  
2018 Dec 14
- Hutch News MERS remains primarily a camel virus – for now, *Fred Hutchinson Cancer Research Center newsletter*, interview.  
2018 Jan 16
- Vancouver Bioinformatics Users Group Virus genomes reveal factors that spread and sustained the West African Ebola virus epidemic, *bioinformatics users meeting*, invited talk.  
2018 Jan 11
- Cascadia Users of Geospatial Open Source Spring Fling Reconstructing the history of the Ebola epidemic, *open source geography and software meeting*, invited talk.  
2017 May 20



- The Washington Post The March for Science could save lives, *daily newspaper*, editorial covering research.  
2017 Apr 19
- GenomeWeb Ebola Genomes Help Reconstruct Virus' Spread During West African Outbreak, *online science newsletter*, interview.  
2017 Apr 12
- Hutch News A big-picture look at the world's worst Ebola epidemic, *Fred Hutchinson Cancer Research Center newsletter*, interview.  
2017 Apr 12
- BioPOD April 2015 episode, *podcast*, interview.  
2015 Apr
- Eu:Sci podcast Episode 101, *podcast*, interview.  
2014 Nov 12
- The Scotsman Edinburgh plays a part in solving Ebola crisis, *Local newspaper*, interview.  
2014 Oct 31
- NERC news NERC-funded student helps analyse Ebola genome sequence, *Natural Environment Research Council newsletter*, interview.  
2014 Sep 05
- SciDev.net Ongoing Ebola outbreak highlights research shortcomings, *online science news portal*, interview.  
2014 Jun 04