CURRICULUM VITAE

for

Ussery, David W.

Department of Physiological Sciences
College of Veterinary Medicine
Oklahoma State University
https://ussery.org/

1. PERSONAL

David Wayne Ussery

2. DEGREES

Post-doctoral Fellow, Institute for Molecular Medicine, The John Radcliffe Hospital, University of Oxford, England	1992 - 1996
Ph.D. in Biochemistry and Molecular Biology, The University of Cincinnati College of Medicine, Cincinnati, Ohio	1986 - 1993
M.Sc. in Physical Chemistry, The University of New Mexico, Albuquerque, New Mexico.	1982 - 1986
B.A. in Chemistry, William Jewell College, Liberty, Missouri, USA	1978 - 1982

3. DEGREES CREDENTIALS

none.

4. APPOINTMENTS (INCLUDING JOINT) & PROMOTIONS AT OSU

Professor	2025 - present
INTERACT Director	2025 - present
McCasland Foundation Professorship	2026 - present

5. MEMBERSHIPS AND AFFILIATIONS

Founding Member, Genomic Standards Consortium (GSC)	2005 - present
Member, American Association for the Advancement of Science	1985 - present
Advisory Board, EcoCyc, SRI, Palo Alto, California	2013 - 2017
Member, German Genome Linguistics Consortium	2002 - 2008

6. PREVIOUS POSITIONS RELEVANT TO OSU EMPLOYMENT

Professor, Department of Biomedical Informatics, UAMS 2016 - 2025
Professor, Department of Physiology and Cell Biology, UAMS 2016 - 2025
Helen G. Adams / ARA Endowed Chair in Bioinformatics, UAMS 2017 - 2025

Visiting International Professor, Dept. Clinical Diagnostics, St. Olav's Hospital 2012 - 2018
Norwegian University of Science and Technology (NTNU), Trondheim, Norway

Comparative Genomics Group Leader, Biosciences Division, Oak Ridge 2013 - 2016
National Labs (ORNL), Oak Ridge, Tennessee, USA

Professor (20%), Center for Biological Sequence Analysis (CBS), Department of 2013 - 2015
Systems Biology, The Technical University of Denmark, Kgs. Lyngby, Denmark

Associate Professor, Center for Biological Sequence Analysis (CBS), Dept. of 2002 - 2013
Systems Biology, The Technical University of Denmark, Kgs. Lyngby, Denmark

Professor II (20%), Centre for Molecular Biology & Neuroscience, Institute of 2004 - 2011
Medical Microbiology, Rikshospitalet University Hospital, Oslo, Norway

Associate Research Professor, Center for Biological Sequence Analysis, (CBS) 1998 - 2002
Institute of Biotechnology, The Technical University of Denmark,
Kgs. Lyngby, Denmark

9. TEACHING ACTIVITIES

Visiting Assistant Professor, Department of Biology, Roanoke College, Salem, Virginia, USA 1997 - 1998

Assistant Research Professor, Center for Biological Sequence Analysis, Dept. Chemistry, The Technical University of Denmark, Lyngby, Denmark 1997

Visiting Scientist, Department of Pharmacology, Microbiolgy & Food Hygiene, Norwegian College of Vetinary Medicine, Oslo, Norway 1996 - 1997

Postdoctoral Research Fellow, Imperial Cancer Research Fund, Institute of 1992 - 1996

7. LEAVES

Molecular Medicine, The John Radcliffe Hospital, Oxford University,

8. RECOGNITIONS

Headington, Oxford, United Kingdom

none.

McCasland Foundation Professorship in Physiological Sciences, DVM, OSU 2026

ScholarGPS award for lifetime ranking in top 0.05% of scholars worldwide 2025

ScholarGPS award for lifetime ranking in top 0.2% of scholars worldwide 2022

Helen G. Adams Endowed Professorship in Biomedical Informatics at UAMS 2017

Arkansas Research Alliance Fellow award ($500,000) 2016

Made “editor’s choice” for Ebolavirus comparative genomics paper 2015

Member of “Faculty of a thousand” (F1000) 2011

Published most highly cited paper of the year in industrial microbiology 2009

Made list of BioMedCentral “hot 100” most cited authors 2007

9.1 Scheduled Instructional Activity

CBSC 5110: **Special Topics in High-throughput Genomics**
Mondays & Wednesdays: room 101, McElroy Hall, 9:30 – 10:20 p.m., spring 2026

9.2 Unscheduled Instructional Activity

- Supervising Aakash Bhattacharyya, from Central High School, for a science fair project for spring 2026. (Aakash won 4th place in computational biology division last year at the International Science Fair).

- Supervised Josef Gantner [junior, majoring in microbiology] on bioinformatics project (December 2025 - January 2026).

9.3 Course and Program Development

- Completed OSU-ITLE's Artificial Intelligence for Instructor's course, October, 2025.

- Led team of 3 faculty members from the CBSC graduate program, in ITLE's "AI Integration Platform program", Autumn, 2025.

9.4 Teaching Materials

- Wrote first textbook on comparative genomics, based on 10 years' of teaching
- Did more than 30 one-week workshops on comparative genomics (see below)
- Taught genomics / bioinformatics courses since 1997 (see below)

9.5 Other Teaching-Related Activities: Previous teaching activities, 1982 - 2025

Taught graduate level courses in Bioinformatics	1998 - 2025
UAMS courses taught	2016 - 2025
BMIG 5101 "Foundations in BMI: Sequences", Course director	2018 - 2025
BMIG 5210 "Genomics & Metagenomics", Course director	2018 - 2025
BMIG 6050 "Research Design", Course director	2019 - 2025
BMIG 5002 "BioMedicine for Informaticists", Co-Director	2018 - 2025
BMIG 5003 "Computational Methods in Biomedical Informatics"	2019 - 2025
BIOC 6102 "Special Topics in Biochemistry", guest lecture	2021 - 2025
PCOL 5120 "Grant writing / Ethics 3" Small group leader	2019 - 2025
PCOL 5121 "Grant writing / Ethics 4" Guest lecture and small group leader	2020 - 2025
PCOL 6101 "Systems Therapeutics", Guest lecture	2019 - 2025
BMIG 5110 "Project Rotations in BMI"	2018 - 2025
BMIG 6215 "Special Topics / student research in BMI"	2019 - 2025
BMIG 6800 "Dissertation Research"	2019 - 2025

Clinical Informatics Fellow "Bioinformatics rotation" (required)	2020 - 2025
Clinical Informatics Fellow "Metagenomics rotation" (optional)	2020 - 2025
Guest lectures for INBRAE orientation for new UAMS Ph.D. students	2019 - 2025
Guest lectures for the Arkansas Summer Research Institute	2021 - 2025

Taught one-week workshops on Comparative Microbial Genomics	2005 - 2025
INBRE – UALR/UAMS (Little Rock, USA)	March of 2017 - 2019; 2021-2024
UA Fayetteville, Arkansas, USA,	July, 2017
Kathmandu, Nepal	March, 2013
CDC, Atlanta, Georgia, USA	August, 2012
Trondheim, Norway	05/2012; 05/2015; 04/2016; 05/2017
Alicante, Spain	December, 2011
Tunis, Tunisia	December, 2010
Granada, Spain	October, 2010
Oxford, England	September, 2010
Rabat, Morocco	April, 2010; April, 2013
Northern Arizona University, Flagstaff, Arizona, USA	July, 2009
Oslo, Norway	October, 2006
Petropolis, Brazil	08/2006; 08/2007; 08/2009
Bangkok, Thailand	03/2005; 06/2008; 03/2010; 06/2011; 08/2016; 05/2017; 11/2017; 12/2019

Previous courses taught (before coming to UAMS in 2016).	1982 - 2014
Taught bioinformatics at The Technical University of Denmark (DTU)	1997 - 2014
Organized and taught bioinformatics journal club at DTU	1998 - 2008
Taught 'Scientific Communication" course at DTU	2001 - 2014
Taught Introductory Biology and Genetics at Roanoke College, Virginia.	1997 - 1998
Taught Molecular Biology course at Norwegian Veterinary College of Med.	1996 - 1997
Gave tutorials at Magdalen College, University of Oxford	1993 - 1995
Taught biochemistry / molecular biology at UC College of Medicine	1986 - 1991
Teaching assistant, organic and biochemistry labs at U. New Mexico	1982 - 1986

10. SUPERVISION AND ADVISORY ACTIVITIES

10.0 High-School Student Supervision

- Supervising Aakash Bhattacharyya, from Central High School, for a science fair project for spring 2026. (Aakash won 4th place in computational biology division last year (2025) at the International Science Fair).

10.1 Undergraduate Student Supervision

- At OSU - Supervised Josef Gantner [junior, majoring in microbiology] on bioinformatics project (December 2025 - January 2026).

Undergraduate students mentored at UAMS **2017 - 2025**

Summer Undergraduate Research Fellowship (SURF) students: 2017 - 2021

Bobby Tu, from Cornell University, Ithaca, New York 2021
"Genomics of SARS-CoV-2 Alpha and Delta variants".

Matthew Thompson, from Harding University, Searcy, Arkansas 2019
"Alignment-free Construction of Pan-genomes".

Ana Swearingen, from Harding University, Searcy, Arkansas 2018
"High Molecular Weight DNA Extraction for Oxford Nanopore Sequencing ".

Connor Purvis, from Harding University, Searcy, Arkansas 2017
"Impact of respiratory syncytial virus and influenza virus infection on the diversity of gut microbiome in children".

10.2 Clinical trainee (intern/resident) supervision

None.

10.3 Graduate Theses Supervised

Graduate students mentored in the UAMS Graduate Program **2016 - 2025**

__1_ Ph.D. student ***Brian Scott Delavan***, (graduated 30 April, 2025) 2021 - 2025
"Application of Bioinformatic Tools to Tuberculosis Surveillance at the Arkansas Department of Health".

__2_ M.Sci. student ***Sudip Panday***, (graduated 12 November, 2024) 2022 - 2024
"Mash based analysis reveals unprecedented diversity in *Salmonella*".

__3_ Ph.D. student ***Kaleb Abram***, (graduated April, 2023) 2017 - 2023
"Unifying traditional microbiology and sequence-based bacterial taxonomies".

__4_ Ph.D. student ***Sangam Kandel*** (graduated 23 February, 2023) 2021 - 2023
"SARS-CoV-2 genomics in Arkansas".

__5_ Ph.D. student ***Duah Alkam***, (graduated 28 January, 2021) 2017 - 2021
"Using genome-wide screens to identify-critical *Staphylococcus aureus* genes"

__6_ Ph.D. student ***Visanu Wanchai***, (graduated 30 November, 2020) 2016 - 2020
"What is Life? Conservation of functional domains and domain architectures in life forms ".

__7_ Ph.D. student ***Skylar Connor***, (graduated 30 July, 2020) 2017 - 2020
"Towards a Better Resolution in Microbial Taxonomy: 16S rRNA trees vs. ribosomal protein trees"

UT Knoxville Genome Science and Technology (GST) program

__8_ Ph.D. student ***Carissa Bleker***, (graduated in August, 2020) 2016 - 2020
"Data-Driven Analytics for High-Throughput Biological Applications".
(Mike Langston, UTK main thesis advisor)

__9_ Ph.D. student ***Suresh Poudel*** (graduated in August, 2017) 2013 - 2017
"Proteomics of *Clostridium thermocellum*"
(Bob Hettich, ORNL / UTK main thesis advisor)

_10_ Ph.D. student ***Bikash Bogati*** (graduated in June, 2021) 2015 - 2021
"To survive some of us must stop growing: ZorO stasis in Enterohemorrhagic Escherichia coli"
(Elizabeth Fozo, UTK, main thesis advisor)

__11_ Ph.D. ***Qian Zhang***, (graduated in May, 2016) 2013 - 2016
"High-throughput clustering of genomes".
(Qian got her M.Sci. degree, and in the Ph.D. program at U. Washington, Seattle.)

CBS (Denmark) Ph.D. students **[2004-2016]**

All of the below Ph.D. students have graduated in 3 to 3.5 years, and have published at least three first-author papers

_12_ Ph.D. student ***Thomas Pedersen*** 2012 - 2016
"Comprehensive Proteomics of *Streptococcus thermophilus* in Industrial Dairy Products".

_13_ Ph.D. student ***Asli Ismihan Özen*** 2012 - 2016
"Phylogenomics Approaches for Functional Discovery".

_14_ Ph.D. student ***Tammi Vesth*** 2011 - 2013
"Determining and comparing protein function in Bacterial genome sequences".
https://orbit.dtu.dk/en/publications/determining-and-comparing-protein-function-in-bacterial-genome-se/

_15_ Ph.D. student ***Marlene Hansen*** 2010 - 2013
"High-throughput Characterization of *Campylobacter* genomes for epidemiological studies".

_16_ Ph.D. student ***Shinny Pimlapas Leekitcharoenphon*** 2010 - 2013
"High-throughput Characterization of Salmonella genomes for epidemiological studies".

_17_ Ph.D. student ***Rolf Sommer Kaas*** 2010 - 2013
"High-throughput Characterization of Escherichia coli and Shigella genomes for epidemiological studies".

_18_ Ph.D. student ***Oksana Lukjancenko*** 2010 - 2013
"Analysis of pan-genome content and its application in microbial identification".
https://orbit.dtu.dk/en/publications/analysis-of-pan-genome-content-and-its-application-in-microbial-i/

_19_ Ph.D. student ***Martin Holm Rau*** 2009 - 2012
"*Pseudomonas aeruginosa* host-adaptation in cystic fibrosis patients".

_20_ Ph.D. student ***Maria Seier-Petersen*** 2009 - 2011
"Response to Biocides in *Salmonella, E. coli, and S. aureus*".

_21_ Ph.D. student ***Kristoffer Kiil*** 2007 - 2010
"Prediction of Bacterial Protein Function".

_22_ Ph.D. student ***Peter F. Hallin*** 2007 - 2009
"Operon Prediction in Bacterial Genomes".

_23_ Ph.D. student ***Tim T. Binnewies***, 2005 - 2007
"Computational Modeling of Bacterial Pathogenesis".

_24_ Ph.D. student ***Hanni Wallinbrock***. 2004 - 2006
"DNA Microarrays in Comparative Genomics and Transcriptomics".

Norwegian Ph.D. students supervised **[2003-2014]**

Students supervised at CBS (Denmark) and the University of Oslo [UiO], Norway or at St. Olaf's Hospital, NTNU (Norges Teknisk-Naturvitenskaplige Universitet, or The Norwegian University of Science and Technology), in Trondheim, Norway.

_25_ Ph.D. student ***Kjersti Haugum*** 2011 - 2014
"Genomic heterogeneity among non-O157 Shiga toxin-producing *Escherichia coli* (STEC) from patients with and without haemolytic uremic syndrome (HUS)".
Clinic of Laboratory Medicine, Department of Medical Microbiology, St. Olavs Hospital, Trondheim University Hospital, Trondheim, Norway.

_26_ Ph.D. student ***Brynildsrud Ola Brønstad*** 2011 - 2013
"Small RNAs in bacterial genomes".
Norwegian School of Veterinary Science, Dept Food Safety & Infect Biol, Oslo, Norway.

_27_ Ph.D. student ***Hilde Vinje*** 2011 - 2013
"From Bacterial Genome Sequence to Taxonomy".
Biostatistics group / IKBM, Norwegian University of Life Science, Ås, Norway.

_28_ Ph.D. student ***Øystein Tenfjord Engelsen*** 2006 - 2010
"Estimating Gene Families in Bacterial Genomes".
Biostatistics group / IKBM, Norwegian University of Life Science, Ås, Norway.

_29_ Ph.D. student ***Camilla Seks*** 2005 - 2008
"Public health risk of the ubiquitous reservoir of Shiga toxin-encoding *Escherichia coli* in animals".
Norwegian School of Veterinary Science, Dept Food Safety & Infect Biol, Oslo, Norway.

.....

_30_ Ph.D. student ***Jon Bohlin*** 2004 - 2008
"Mathematical models in bioinformatics and infectious disease dynamics".
Norwegian School of Veterinary Science, Dept Food Safety & Infect Biol, Oslo, Norway.

.....

_31_ Ph.D. student ***Karin Lageson*** 2003 - 2008
"Ribosomal RNAs in prokaryotes: mapping and characterization".
CMBN, IMM, Rikshospitalet, Oslo, Norway.

Masters Students educated in Denmark **(2000 - 2013)**
All of the master's students below have published at least one paper as part of their master's thesis project.

.....

_32_ ***Emilie Glad Bak*** 2013
"Subtyping of Listeria monocytogenes".

.....

_33_ ***Sandra Anderson*** 2013
"Identification of unknown metagenomic species".

.....

_34_ ***Dan Jensen*** 2012
"Identification of genetic markers for prediction of bacterial lifestyle characteristics".

.....

_35_ ***Annika Jacobsen*** 2012
"Variation in Antiterminator Q in Verocytotoxin Phages".

.....

_36_ ***Niklas J. Cvetanovski*** 2011
"Comparison of probiotic bacterial core genes in Human Microbiome Samples".

.....

_37_ ***Asli Ismihan Özen*** 2011
"Taxonomy from Genomic Sequences".

.....

_38_ ***Tammi Vesth*** 2011
"Artificial Neural Networks to predict function in bacterial genomes".

.....

_39_ ***Marlene Hansen*** 2010
"Biofilm Formation and Genome Annotation of *Achromobacter xylosoxidans* - An emerging Cystic Fibrosis Pathogen".

.....

_40_ ***Anja Stausgaard*** 2010
"Modeling Bacterial Virulence in *S. aureus*".

.....

_41_ ***Oksana Lukjancenko*** 2009
"Design of a high-density 116 genome-based microarray for enteric bacteria".

.....
_42_ ***Mamuna Afzal*** 2009
"Immunological Analysis of *Mycobacterium avium* Subsp. Paratuberculosis Ejlskov 2007 09".

.....
_43_ ***Soad Abidi*** 2009
"Comparative Genomics of Mycobacterium avium Subsp. Paratuberculosis Ejlskov 2007 09".

.....
_44_ ***Mervat El-Minaoui*** 2008
"Comparative Genomics of *Pseudomonas*".

.....
_45_ ***Mads Albaek*** 2008
"Comparison of 51 *Burkholderia* genomes".

.....
_46_ ***Marcello Bertalan*** 2007
"Comparative Genomics of *Bacteroides fragilis*".

.....
_47_ ***Kristoffer Kiil*** 2006
"Operon Prediction in *Streptomyces coelicolor*".

.....
_48_ ***Peter F. Hallin*** 2006
"Design and application of a high density microarray for expression analysis in *Campylobacter jejuni*".

.....
_49_ ***Heng Wu*** 2005
"Prediction of rRNA operons in bacterial genomes".

.....
_50_ ***Haakan Ohlsson*** 2003
"Prediction of promoters based on DNA structures".

.....
_51_ ***Vera van Noort*** 2002
"Genome annotation in *Escherichia coli*".

.....
_52_ ***Carsten Friis*** 2000
"DNA structures in Bacterial Chromosomes".

.....

10.4 Post-Doctoral Supervision

- ***Dr. Veniamin Borin*** https://scholar.google.com/citations?hl=en&user=LBMUqooAAAAJ 2025 - present
Dr. Borin is currently funded by an NIH R01 grant (GM148886), "Biophysical Model of Enzyme Catalysis: Conformational Sub-states, Solvent Coupling and Energy Networks", that I am now the PI for. His project involves using molecular dynamics simulations to model the active sites of novel Squalene-Hopene Cyclase (SHC) enzymes developed by directed evolution.

- ***Dr. Ranabir Majumder*** https://scholar.google.com/citations?hl=en&user=d2nYs-MAAAAJ 2025 - present
Dr. Majumder is also currently funded by an NIH R01 grant (GM148886), "Biophysical Model of Enzyme Catalysis: Conformational Sub-states, Solvent Coupling and Energy Networks", that I am now the PI for. Ranabir's project involves using structural 'metadynamics' -modeling how protein structures change with time, using a combination of molecular dynamics simulations as well as now also using deep-learning/protein language model components as an extension of comparative genomics and sequence-based structural modeling.

Previous post-docs (before joining OSU in 2025) **1999 - 2020**

Dr. Zulema Udaondo 2017 - 2020

Dr. Adriana Cabal 2009 - 2010

Dr. Matloob Qureshi 2009 - 2010

Dr. Stefano Borini 2008 - 2010

Dr. Tom Coeyne 2006 - 2007

Dr. Anne Petersen 2004 - 2005

Dr. Peder Worning 1999 - 2005

Dr. Lise Petersen 1999 - 2001

10.5 Other Advisory Activities (Mentor for Early Career Faculty)

Assistant Professor Se-Ran Jun (now Associate Professor at UAMS) 2016 - 2024

Associate Professor Intawat Nookaew (now full Professor at UAMS) 2016 - 2024

Assistant Professor Michael Robeson II (now Associate Professor at UAMS) 2017 - 2024

Assistant Professor Nandini Mukherjee (now Associate Professor at UAMS) 2018 - 2022

11 - 18 PUBLICATIONS & FUNDING

Publications ***1984 - present***

Web page with full list of publications: https://ussery.org/Pubs_full_Dec2025.html

ORCID:
https://orcid.org/0000-0003-3632-5512

GoogleScholar:
https://scholar.google.com/citations?user=aws0djcAAAAJ&hl=en
As of 26 December, 2025: 319 papers; 32,7347 citations; h-index = 72; i10 index = 178 articles.

NCBI "MyBibliography" page
https://www.ncbi.nlm.nih.gov/myncbi/1-76oZYFPumk7/bibliography/public/

"Exaly project" rankings page
https://exaly.com/author/8920020/david-w-ussery/rankings
As of 26 December, 2025, most cited author of the year, for eight different journals.

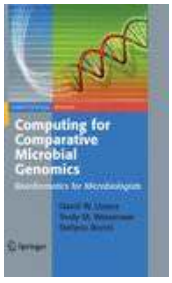
Scholar GPS ranking page:
https://scholargps.com/scholars/39389209849759/david-w-ussery
As of 26 December, 2025, lifetime ranking in top 0.02%

Frontiers impact page
https://loop.frontiersin.org/people/106537/impact
As of 26 December, 2025, 72,390 views from 267 publications.

*legends: * = > student/post-doc co-authors; cited > 10x (178 articles); cited > 100x (55 articles); cited > 1000x (8 articles).*

11. BOOKS & Chapters in Books

11.1 - Authored book:



David Wayne Ussery, Trudy M. Wassenaar, *Stefano Borini*, "**Computing for Comparative Microbial Genomics: Bioinformatics for Microbiologists**", (Springer, 2009). https://link.springer.com/book/10.1007/978-1-84800-255-5. Cited 66x.

11.2 - Edited books:

- none -

11.3 - Authored Book Chapters:

1. **Adriana Cabal*, Trudy M Wassenaar, **David W Ussery**, (2018). "Gender Differences in the Gut Microbiome and How These Affect Cardiovascular Diseases", Chapter 7 in **Gender Differences in the Pathogenesis and Management of Heart Disease**, (Springer International Publishing AG, 2018). https://doi.org/10.1007/978-3-319-71135-5_7. Cited 15x

2. Trudy M. Wassenaar, **Visanu Wanchai, *Duah Alkam*, Intawat Nookaew, and **David W. Ussery**, (2018)."Conservation of Two-Component Signal Transduction Systems in *E. coli*, *Salmonella*, and Across 100,000 Bacteria of Various Bacterial Phyla". Chapter 7 in **Molecular Mechanisms of Microbial Evolution**, P. H. Rampelotto (ed.); Springer International Publishing AG, part of Springer Nature (2018). Grand Challenges in Biology and Biotechnology. https://doi.org/10.1007/978-3-319-69078-0_7

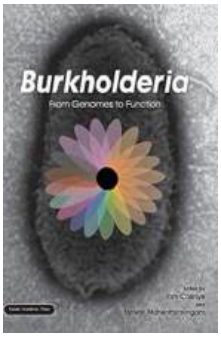
3. Trudy M. Wassenaar, Se-Ran Jun, **Visanu Wanchai, *Preecha Patumcharoenpol*, Intawat Nookaew, **Katrina Schlum*, Michael R. Leuze, and **David W. Ussery**, (2017). "Insights from Comparative Genomics of the Genus *Salmonella*", Chapter 1 in: **Current Topics in *Salmonella* and Salmonellosis**, (Mihai Mares, editor, InTechOpen, published by Ion Ionescu de la Brad University of Agricultural Sciences and Veterinary Medicine of Iași, Romania; 2017). http://dx.doi.org/10.5772/67131

4. **David Ussery**, (2017). "Science in The Abolition of Man: Can Science Rescue Itself ?", Chapter 7 in: **Contemporary Perspectives on C.S. Lewis' The Abolition of Man: History, Philosophy, Education, and Science**, Tim Mosteller and Gayne John Anacker (eds) (Bloomsbury Academic, London, 2017) https://doi.org/10.5040/9781474296465.ch-007

5. **Asli Ismihan Ozen*, **David Wayne Ussery**, (2015)."Genome Atlases, Potential Applications in Study of Metagenomes"; chapter in: **ENCYCLOPEDIA OF METAGENOMICS - Genes, Genomes and Metagenomes. Basics, Methods, Databases and Tools** (K.E. Nelson, editor, Springer Science+Business Media New York, pages 219-222). https://doi.org/10.1007/978-1-4899-7478-5_686

6. **Asli I. Ozen, *Tammi Vesth,* **David W. Ussery**, (2013). "From Genome Sequence to Taxonomy - A Skeptic's View", Chapter 8 in **The Prokaryotes**, 4th edition, (Springer Berlin Heidelberg, pages 209-227; 2013). https://doi.org/10.1007/978-3-642-30194-0_11

7. **Pimlapas Leekitcharoenphon*, Gregory S. Buzard, and **David W. Ussery**, (2013). "Comparative Genomics in the Genus *Burkholderia*", Chapter 2 in B**urkholderia: Molecular Microbiology and Genomics** (Horizon Press, 2013). https://doi.org/10.21775/9781912530069. Cover image.



8. Trudy M. Wassenaar, **Tim T. Binnewies, *Peter F. Hallin*, and **David W. Ussery,** (2010). "Tools for comparison of bacterial genomes", Chapter 74 in: **Handbook of Hydrocarbon and Lipid Microbiology**, (K. N. Timmis (ed.), Springer-Verlag, Heidelberg, Germany, 2010; pages 4,313 - 4,317). https://doi.org/10.1007/978-3-540-77587-4_337.

9. Trudy M. Wassenaar, **Jon Bohlin, *Tim T. Binnewies*, **David W. Ussery**, (2009). "Genome comparison of bacterial pathogens", Chapter 1 in **Genome Dynamics, volume 6 - Microbial Pathogenomics**, (Karger AG publishers, Basel, 2009). https://doi.org/10.1159/000235759

10. **David W. Ussery**, "Physical Maps of Chromosomes", **The Encyclopedia of Life Sciences**, John Wiley & Sons, Ltd., Chichester, England, (2009). https://doi.org/10.1002/9780470015902.a0001425

11. David W. Ussery, **Kristoffer Kiil, *Karin Lagesen*, Thomas Sicheritz-Ponten, **Jon Bohlin*, and Trudy M. Wassenaar, (2009). "The genus *Burkholderia*: analysis of 56 genomic sequences", Chapter 14 in **Genome Dynamics, volume 6 - Microbial Pathogenomics**, (Karger AG publishers, Basel, 2009). https://doi.org/10.1159/000235768
Cited 77x

12. **Kristoffer Kiil, *Tim T. Binnewies, *Hanni Willenbrock*, Susse Kirkelund Hansen, **Lei Yang, *Lars Jelsbak*, **David W. Ussery**, and **Carsten Friis*, (2009). "Comparative genomics of *Pseudomonas*", Chapter 1 in ***Pseudomonas*: Model Organism, Pathogen, Cell Factory**, (Edited by Bernd H. A. Rehm; Wiley-VCH Press, 2009). https://doi.org/10.1002/9783527622009.ch1

13. Jens Klockgether, Dieco Würdemann, Lutz Wiehlmann, **Tim T. Binnewies*, **David W. Ussery,** and Burkhard Tümmler, "Genome Diversity of *Pseudomonas aeruginosa*", Chapter 2 in: ***Pseudomonas*: Genetics and Molecular Biology,** (editor: Pierre Cornelis; Horizon Press, London, 2008; pages 19-42). https://doi.org/10.21775/9781910190036
Cited 13x

14. **Kristoffer Kiil, *Tim T. Binnewies, *Hanni Willenbrock*, Susse Kirkelund Hansen, **Lei Yang, *Lars Jelsbak,* **David W. Ussery**, and **Carsten Friis,* "Comparative genomics of *Pseudomonas*", Chapter 1 in: ***Pseudomonas*: Model organism, pathogen, cell factory**, (Wiley-VCH Press, 2008; pages 1-23). https://doi.org/10.1002/9783527622009.ch1
Cited 21x

15. **Phatthanaphong Wanchanthuek, *Peter F. Hallin, *Rodrigo Gouveia-Oliveira*, and **David W. Ussery**, "Structural features of fungal genomes", Chapter 3 in: **Topics in Current Genetics: Comparative genomics using fungi as a model**, **15**:47-77, (2006). (P. Sunnerhagen and J. Piskur, eds., Springer Verlag, Heidelberg). https://doi.org/10.1007/4735_112

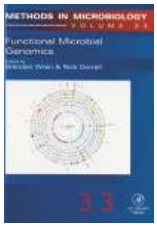
16. Mensur Dlakic, **David Ussery**, and Søren Brunak, "DNA bendability and nucleosome positioning in transcriptional regulation", Chapter 14 in: **DNA Conformation in**

Transcription, (Takashi Ohyama, editor; Landes Bioscience, Georgetown, Texas, 2005; pages 189-202.). https://link.springer.com/content/pdf/10.1007/0-387-29148-2.pdf#page=193
Cited 13x

17. **David W. Ussery**, (2004). "Darwin's Transparent Box: Biochemical Evidence for Evolution", Chapter 4 in **WHY INTELLIGENT DESIGN FAILS – A Scientific Critique of the New Creationism,** (Rutgers University Press, New Brunswick, New Jersey, 2004; pages 48-57). https://www.rutgersuniversitypress.org/why-intelligent-design-fails/9780813538723. Link to book on Amazon: https://a.co/d/dk6GKKA

18. **Lars Juhl Jensen, *Marie Skovgaard*, Thomas Sicheritz-Ponten, **Niclas Tu Hansen, *Helle Johansson, *Merete Kjær Jørgensen, *Kristoffer Kiil, *Peter F. Hallin* and **David Ussery**, "Comparative genomics of four Pseudomonas species", Chapter 5 in **THE *PSEUDOMONADS* VOL I. GENOMICS, LIFE STYLE AND MOLECULAR ARCHITECTURE** (Juan L. Ramos, editor, Kluwer Academic / Plenum Publishers, New York, pages 139-164, 2004). https://doi.org/10.1007/978-1-4419-9086-0_5

19. **Marie Skovgaard, *Lars Juhl Jensen, *Carsten Friis, *Hans-Henrik Stærfeldt, *Peder Worning*, Søren Brunak, and **David Ussery**, "The Atlas Visualisation of Genome-wide Information", **Methods in Microbiology**, **33**:49-63, (2002). https://doi.org/10.1016/S0580-9517(02)33004-6
Cover image.
Cited 21x



20. **David W. Ussery**, "DNA Structure: A-, B-, and Z-DNA Families", **The Encyclopedia of Life Sciences**, Macmillan Publishers, (2002), page e003122. https://doi.org/10.1038/npg.els.0003122.
Cited 128x

21. **David W. Ussery**, "DNA Denaturation", **The Encyclopedia of Genetics**, pages 517-521, (2001). https://doi.org/10.1006/rwgn.2001.0353. Cited 23x

22. **David W. Ussery**, "Genome Databases", **The Encyclopedia of Genetics**, pages 550-553, (2001). https://doi.org/10.1006/rwgn.2001.0313

23. Sinden,R.R., Pearson,C.E., Potaman,V.N., and **Ussery,D.W.,** (1998). "DNA: Structure and Function", Chapter 1 in: **Advances in Genome Biology**, (Verma, R. D., editor, Vol. 5, pages 1-141, 1998). https://doi.org/10.1016/S1067-5701(98)80019-3.
Cited 1605x.

12. PAPERS IN REFEREED JOURNALS

24. *Jin J., Rahmatallah Y., Gomez-Acevedo H., Park Y. M., **Ussery D. W.**, Jakoet E., Orloff M. S., "A Tracts of Homozygosity Approach Identifies Methylation-Regulated CSMD1 Expression Targets in Non-Small Cell Lung Cancers Related to Smoking Behavior", Cancer Epidemiology, Biomarkers & Prevention, (2025); **34**(12):2247–2258. doi: https://doi.org/10.1158/1055-9965.EPI-25-0159. PubMed PMID: 41036856.

25. Boysen G., Alexandrov L. B., Rahbari R., Nookaew I., **Ussery D.**, Chao M. R., Hu C. W., Cooke M. S., "Investigating the origins of the mutational signatures in cancer", Nucleic Acids Research, (2025); **53**(1). doi: https://doi.org/10.1093/nar/gkae1303. PubMed PMID: 39778866; PMCID: PMC11707540.

26. *Bhattacharyya A., *Panday S., **Ussery D.,** "Rapid assessment of clinical severity for salmonellosis cases via protein family domain analysis and machine learning", Academia Molecular Biology and Genomics, (2025); **2**(2). Epub 20250630. doi: https://doi.org/10.20935/acadmolbiogen7776. PubMed PMID: 40964454; PMCID: PMC12440251.

27. Wassenaar T. M., Harville T., *Chastain J., Wanchai V.*, **Ussery D. W.**, "DNA structural features and variability of complete MHC locus sequences", Frontiers in Bioinformatics, (2024); **4**:1392613. Epub 20240703. doi: https://doi.org/10.3389/fbinf.2024.1392613. PubMed PMID: 39022183; PMCID: PMC11251971.

28. **Kandel S.*, Hartzell S. L., Ingold A. K., Turner G. A., Kennedy J. L., **Ussery D. W.,** "Genomic surveillance of SARS-CoV-2 using long-range PCR primers", Frontiers in Microbiology, (2024); **15**:1272972. Epub 20240214. doi: https://doi.org/10.3389/fmicb.2024.1272972. PubMed PMID: 38440140; PMCID: PMC10910555.

29. Wong L., Randolph C., Kanwischer E., Ingold A., Boyanton B. L., Jr., Taylor J., Frenner R. A., Harley S. E., Bird J. T., Thurman T. J., Kandel S., **Ussery D. W.**, Byrum S. D., Dinwiddie D., Domman D., Chalwadi U. K., Kennedy J., "Severe Acute Respiratory Syndrome Coronavirus-2 Lambda Variant Collected from a Child from Arkansas and Sequenced", Microbiology Resource Announcements, (2023); **12**(3):e0000723. Epub 20230213. doi: https://doi.org/10.1128/mra.00007-23. PubMed PMID: 36779742; PMCID: PMC10019291.

30. Wassenaar T. M., **Ussery D. W.**, Rosel A. C., "Big data in genomic research for big questions with examples from covid-19 and other zoonoses", Journal of Applied Microbiology, (2023); **134**(1). doi: https://doi.org/10.1093/jambio/lxac055. PubMed PMID: 36626787.
Cited 20x

31. **Kandel S.*, Hartzell S. L., Ingold A. K., Turner G. A., Kennedy J. L., **Ussery D. W. ,** "Genomic Surveillance of SARS-CoV-2 Using Long-Range PCR Primers", bioRxiv, (2023). Epub 20230711. doi: https://doi.org/10.1101/2023.07.10.548464. PubMed PMID: 37502853; PMCID: PMC10369864.

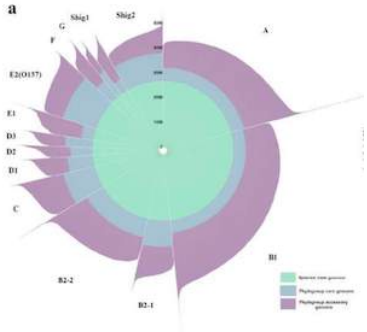
32. Wassenaar T. M., **Wanchai V.*, **Ussery D. W.,** "Comparison of Monkeypox virus genomes from the 2017 Nigeria outbreak and the 2022 outbreak", Journal of Applied Microbiology, 2022;133(6):3690–3698. Epub 20221011. doi: https://doi.org/10.1111/jam.15806. PubMed PMID: 36074056; PMCID: PMC9828465.

33. Wassenaar T. M., **Wanchai V.*, Buzard G., **Ussery D. W.,** "The first three waves of the Covid-19 pandemic hint at a limited genetic repertoire for SARS-CoV-2", FEMS Microbiology Reviews, (2022); **46**(3). doi: https://doi.org/10.1093/femsre/fuac003. PubMed PMID: 35076068; PMCID: PMC9075578.
Cited 18x

34. Jenjaroenpun P., Wongsurawat T., **Wadley T. D.*, Wassenaar T. M., Liu J., Dai Q., Wanchai V., Akel N. S., Jamshidi-Parsian A., Franco A. T., Boysen G., Jennings M. L., **Ussery D. W.**, He C., Nookaew I., "Decoding the epitranscriptional landscape from native RNA sequences", Nucleic Acids Research, (2021); **49**(2):e7. doi: https://doi.org/10.1093/nar/gkaa620. PubMed PMID: 32710622; PMCID: PMC7826254.
Cited 295x

35. **Alkam D.*, Wongsurawat T., Nookaew I., Richardson A. R., **Ussery D.**, Smeltzer M. S., Jenjaroenpun P., "Is amplification bias consequential in transposon sequencing (TnSeq) assays? A case study with a *Staphylococcus aureus* TnSeq library subjected to PCR-based and amplification-free enrichment methods", Microbial Genomics, (2021); **7**(10). doi: https://doi.org/10.1099/mgen.0.000655. PubMed PMID: 34596508; PMCID: PMC8627206.

36. *Abram K., *Udaondo Z., *Bleker C., *Wanchai V., Wassenaar T. M., Robeson M. S., 2nd, **Ussery D. W. ,** "Mash-based analyses of *Escherichia coli* genomes reveal 14 distinct phylogroups", Nature Communications Biology, (2021); **4**(1):117. Epub 20210126. doi: https://doi.org/10.1038/s42003-020-01626-5. PubMed PMID: 33500552; PMCID: PMC7838162.
Cited 125x



37. Gautam B., Gyanwali G., **Ussery D. W.**, "Assessment of Bacterial Load in Polyethylene Terephthalate (PET) Bottled Water Marketed in Kathmandu Valley, Nepal", International Journal of Polymer Science, (2021); Article ID 6681249, 10 pages. https://doi.org/10.1155/2021/6681249.
Cited 14x

38. Jenjaroenpun P., Wanchai V., Ono-Moore K. D., Laudadio J., James L. P., Adams S. H., Prior F., Nookaew I., **Ussery D. W.**, Wongsurawat T., "Two SARS-CoV-2 Genome Sequences of Isolates from Rural U.S. Patients Harboring the D614G Mutation, Obtained Using Nanopore Sequencing", Microbiology Resource Announcements, (2021); **10**(1). Epub 20201217. doi: https://doi.org/10.1128/MRA.01109-20. PubMed PMID: 33334896; PMCID: PMC8407695.
Cited 16x

39. Wongsurawat T., Jenjaroenpun P., De Loose A., **Alkam D.*, **Ussery D. W.**, Nookaew I., Leung Y. K., Ho S. M., Day J. D., Rodriguez A, "A novel Cas9-targeted long-read assay for simultaneous detection of IDH1/2 mutations and clinically relevant MGMT methylation in fresh biopsies of diffuse glioma", Acta Neuropathologica Communications, (2020); **8**(1):87. Epub 20200620. doi: https://doi.org/10.1186/s40478-020-00963-0. PubMed PMID: 32563269; PMCID: PMC7305623.
Cited 44x

40. Wassenaar T. M., Jun S. R., Robeson M., **Ussery D. W.,** "Comparative genomics of hepatitis A virus, hepatitis C virus, and hepatitis E virus provides insights into the evolutionary history of *Hepatovirus* species". MicrobiologyOpen, (2020); **9**(2):e973. Epub 20191119. doi: https://doi.org/10.1002/mbo3.973. PubMed PMID: 31742930; PMCID: PMC7002107.

41. **Wanchai V.*, Nookaew I., **Ussery D. W.,** "ProdMX: Rapid query and analysis of protein functional domain based on compressed sparse matrices", Computational and Structural Biotechnology Journal, (2020); **18**:3890–3896. Epub 20201124. doi: https://doi.org/10.1016/j.csbj.2020.10.023. PubMed PMID: 33335686; PMCID: PMC7719867.

42. **Udaondo Z.*, Jenjaroenpun P., Wongsurawat T., Meyers E., Anderson C., Lopez J., Mohan M., Tytarenko R., Walker B., **Ussery D.**, Kothari A., Jun S. R., "Two Cases of Vancomycin-Resistant *Enterococcus faecium* Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing", Open Forum Infectious Diseases, (2020); **7**(6):ofaa180. Epub 20200523. doi: https://doi.org/10.1093/ofid/ofaa180. PubMed PMID: 32550237; PMCID: PMC7291683.
Cited 13x

43. Patel L., Shukla T., Huang X., **Ussery D. W.**, Wang S., "Machine Learning Methods in Drug Discovery", Molecules, (2020); **25**(22). Epub 20201112. doi: https://doi.org/10.3390/molecules25225277. PubMed PMID: 33198233; PMCID: PMC7696134.
Cited 484x

44. **Kandel S.*, Sripiboon S., Jenjaroenpun P., **Ussery D. W.,** Nookaew I., Robeson M. S., 2nd, Wongsurawat T., "16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand", Microbiology Resource Announcements, (2020); **9**(24). Epub 20200611. doi: https://doi.org/10.1128/MRA.00248-20. PubMed PMID: 32527771; PMCID: PMC7291096.
Cited 11x

45. Jenjaroenpun P., Wongsurawat T., **Udaondo Z.*, Anderson C., Lopez J., Mohan M., Tytarenko R., Walker B., Nookaew I., **Ussery D.**, Kothari A., Jun S. R., "Complete Genome Sequences of Four Isolates of Vancomycin-Resistant *Enterococcus faecium* with the vanA Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia", Microbiology Resource Announcements, (2020); **9**(6). Epub 20200206. doi: https://doi.org/10.1128/MRA.01380-19. PubMed PMID: 32029568; PMCID: PMC7005116.

46. Cleveland M. H., Anekella B., Brewer M., Chin P. J., Couch H., Delwart E., Huggett J., Jackson S., Martin J., Monpoeho S., Morrison T., Ng S. H. S., **Ussery D**., Khan A. S. , "Report of the 2019 NIST-FDA workshop on standards for next generation sequencing detection of viral adventitious agents in biologics and biomanufacturing", Biologicals, (2020); **64**:76–82. Epub 20200222. doi: https://doi.org/10.1016/j.biologicals.2020.02.003. PubMed PMID: 32094072; PMCID: PMC9987593.
Cited 18x

47. Wongsurawat T., Nakagawa M., Atiq O., Coleman H. N., Jenjaroenpun P., Allred J. I., Trammel A., Puengrang P., **Ussery D. W.,** Nookaew I., "An assessment of Oxford Nanopore sequencing for human gut metagenome profiling: A pilot study of head and neck cancer patients", Journal of Microbiological Methods, (2019); **166**:105739. Epub 20191015. doi: https://doi.org/10.1016/j.mimet.2019.105739. PubMed PMID: 31626891; PMCID: PMC6956648.

48. Wongsurawat T., Jenjaroenpun P., Taylor M. K., Lee J., Tolardo A. L., Parvathareddy J., **Kandel S., *Wadley T. D.*, Kaewnapan B., Athipanyasilp N., Skidmore A., Chung D., Chaimayo C., Whitt M., Kantakamalakul W., Sutthent R., Horthongkham N., **Ussery D.** W., Jonsson C. B., Nookaew I., "Rapid Sequencing of Multiple RNA Viruses in Their Native Form", Frontiers in Microbiology, (2019); **10**:260. Epub 20190225. doi: https://doi.org/10.3389/fmicb.2019.00260. PubMed PMID: 30858830; PMCID: PMC6398364.
Cited 84x

49. Wassenaar T. M., **Wanchai V.*, Buzard G. S., **Ussery D. W.,** "*In silico* Selection of Amplification Targets for Rapid Polymorphism Screening in *Ebola* Virus Outbreaks", Frontiers in Microbiology, (2019); **10**:857. Epub 20190426. doi: https://doi.org/10.3389/fmicb.2019.00857. PubMed PMID: 31080442; PMCID: PMC6497787.

50. **Wadley T. D.*, Jenjaroenpun P., Wongsurawat T., **Ussery D. W.,** Nookaew I., "Complete Genome and Plasmid Sequences of *Escherichia coli* Type Strain ATCC 11775", Microbiology Resource Announcements, (2019); **8**(9). Epub 20190228. doi: https://doi.org/10.1128/MRA.00046-19. PubMed PMID: 30834378; PMCID: PMC6395863.

51. **Udaondo Z.*, Wongsurawat T., Jenjaroenpun P., Anderson C., Lopez J., Mohan M., Tytarenko R., Walker B., Nookaew I., **Ussery D.**, Kothari A., Jun S. R., "Draft Genome Sequences of 48 Vancomycin-Resistant *Enterococcus faecium* Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection", Microbiology Resource

Announcements, (2019); **8**(15). Epub 20190411. doi: https://doi.org/10.1128/MRA.00222-19. PubMed PMID: 30975810; PMCID: PMC6460033.

52. Gurley B. J., Miousse I. R., Nookaew I., Ewing L. E., Skinner C. M., Jenjaroenpun P., Wongsurawat T., Kennon-McGill S., Avula B., Bae J. Y., McGill M. R., **Ussery D.**, Khan I. A., Koturbash I., "Decaffeinated Green Tea Extract Does Not Elicit Hepatotoxic Effects and Modulates the Gut Microbiome in Lean B6C3F(1) Mice", Nutrients, (2019); **11**(4). Epub 20190403. doi: https://doi.org/10.3390/nu11040776. PubMed PMID: 30987244; PMCID: PMC6521095.
Cited 28x

53. Gomez-Acevedo H., Patterson J. D., Sardar S., Gokden M., Das B. C., **Ussery D. W.**, Rodriguez A, "SMARC-B1 deficient sinonasal carcinoma metastasis to the brain with next generation sequencing data: a case report of perineural invasion progressing to leptomeningeal invasion", BMC Cancer, (2019); 19(1):827. Epub 20190822. doi: https://doi.org/10.1186/s12885-019-6043-0. PubMed PMID: 31438887; PMCID: PMC6704572.

54. Bavineni M., Wassenaar T. M., Agnihotri K., **Ussery D. W.**, Luscher T. F., Mehta J. L., "Mechanisms linking preterm birth to onset of cardiovascular disease later in adulthood", Eur Heart J., (2019); **40**(14):1107–1112. doi: https://doi.org/10.1093/eurheartj/ehz025. PubMed PMID: 30753448; PMCID: PMC6451766.
Cited 107x

55. Amann R. I., Baichoo S., Blencowe B. J., Bork P., Borodovsky M., Brooksbank C., Chain P. S. G., Colwell R. R., Daffonchio D. G., Danchin A., de Lorenzo V., Dorrestein P. C., Finn R. D., Fraser C. M., Gilbert J. A., Hallam S. J., Hugenholtz P., Ioannidis J. P. A., Jansson J. K., Kim J. F., Klenk H. P., Klotz M. G., Knight R., Konstantinidis K. T., Kyrpides N. C., Mason C. E., McHardy A. C., Meyer F., Ouzounis C. A., Patrinos A. A. N., Podar M., Pollard K. S., Ravel J., Munoz A. R., Roberts R. J., Rossello-Mora R., Sansone S. A., Schloss P. D., Schriml L. M., Setubal J. C., Sorek R., Stevens R. L., Tiedje J. M., Turjanski A., Tyson G. W., **Ussery D. W.**, Weinstock G. M., White O., Whitman W. B., Xenarios I., "Consent insufficient for data release-Response", Science, (2019); **364**(6439):446. doi: https://doi.org/10.1126/science.aax7509. PubMed PMID: 31048484.

56. Amann R. I., Baichoo S., Blencowe B. J., Bork P., Borodovsky M., Brooksbank C., Chain P. S. G., Colwell R. R., Daffonchio D. G., Danchin A., de Lorenzo V., Dorrestein P. C., Finn R. D., Fraser C. M., Gilbert J. A., Hallam S. J., Hugenholtz P., Ioannidis J. P. A., Jansson J. K., Kim J. F., Klenk H. P., Klotz M. G., Knight R., Konstantinidis K. T., Kyrpides N. C., Mason C. E., McHardy A. C., Meyer F., Ouzounis C. A., Patrinos A. A. N., Podar M., Pollard K. S., Ravel J., Munoz A. R., Roberts R. J., Rossello-Mora R., Sansone S. A., Schloss P. D., Schriml L. M., Setubal J. C., Sorek R., Stevens R. L., Tiedje J. M., Turjanski A., Tyson G. W., **Ussery D. W.**, Weinstock G. M., White O., Whitman W. B., Xenarios I., "Toward unrestricted use of public genomic data", Science, (2019); **363**(6425):350–352. doi: https://doi.org/10.1126/science.aaw1280. PubMed PMID: 30679363.
Cited 68x

57. **Alkam D.*, Jenjaroenpun P., Wongsurawat T., Udaondo Z., Patumcharoenpol P., Robeson M., Haselow D., Mason W., Nookaew I., **Ussery D.**, Jun S. R., "Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016", Infection, Genetics and Evolution, (2019); **75**:103965. Epub 20190715. doi: https://doi.org/10.1016/j.meegid.2019.103965. PubMed PMID: 31319177; PMCID: PMC6832845.

58. Wongsurawat T., Jenjaroenpun P., Athipanyasilp N., Kaewnapan B., Leelahakorn N., Angkasekwinai N., Kantakamalakul W., Sutthent R., **Ussery D. W.**, Horthongkham N., Nookaew I., "Genome Sequences of Zika Virus Strains Recovered from Amniotic Fluid, Placenta, and Fetal Brain of a Microcephaly Patient in Thailand, 2017", Microbiology Resource Announcements, (2018); **7**(11). Epub 20180920. doi: https://doi.org/10.1128/MRA.01020-18. PubMed PMID: 30533643; PMCID: PMC6256666.
Cited 11x

59. Wongsurawat T., Athipanyasilp N., Jenjaroenpun P., Jun S. R., Kaewnapan B., Wassenaar T. M., Leelahakorn N., Angkasekwinai N., Kantakamalakul W., **Ussery D. W.**, Sutthent R., Nookaew I., Horthongkham N., "Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand", Emerging Infectious Diseases, (2018); **24**(9):1758–1761. Epub 20180917. doi: https://doi.org/10.3201/eid2409.180416. PubMed PMID: 29985788; PMCID: PMC6106416.
Cited 90x

60. Jenjaroenpun P., Wongsurawat T., Pereira R., Patumcharoenpol P., **Ussery D. W.**, Nielsen J., Nookaew I., "Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of *Saccharomyces cerevisiae* CEN.PK113-7D", Nucleic Acids Research, (2018); **46**(7):e38. doi: https://doi.org/10.1093/nar/gky014. PubMed PMID: 29346625; PMCID: PMC5909453.
Cited 142x

61. **Cabal A.*, Jun S. R., Jenjaroenpun P., **Wanchai V.*, Nookaew I., Wongsurawat T., Burgess M. J., Kothari A., Wassenaar T. M., **Ussery D. W.,** "Genome-Based Comparison of Clostridioides difficile: Average Amino Acid Identity Analysis of Core Genomes", Microbial Ecology, (2018); **76**(3):801–813. Epub 20180214. doi: https://doi.org/10.1007/s00248-018-1155-7. PubMed PMID: 29445826; PMCID: PMC6132499.
Cited 13x

62. Apopa P. L., Alley L., Penney R. B., Arnaoutakis K., Steliga M. A., Jeffus S., Bircan E., Gopalan B., **Jin J., *Patumcharoenpol P.,* Jenjaroenpun P., Wongsurawat T., Shah N., Boysen G., **Ussery D.**, Nookaew I., Fagan P., Bebek G., Orloff M. S., "PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin.", Frontiers in Microbiology, (2018); **9**:1757. Epub 20180806. doi: https://doi.org/10.3389/fmicb.2018.01757. PubMed PMID: 30127774; PMCID: PMC6087756.
Cited 124x

63. **Zhang Q.*, Jun S. R., Leuze M., **Ussery D.**, Nookaew I., "Viral Phylogenomics Using an Alignment-Free Method: A Three-Step Approach to Determine Optimal Length of k-mer", Scientific Reports, (2017); **7**:40712. Epub 20170119. doi: https://doi.org/10.1038/srep40712. PubMed PMID: 28102365; PMCID: PMC5244389.
Cited 72x

64. **Wanchai V., *Patumcharoenpol P.*, Nookaew I., **Ussery D.,** "dBBQs: dataBase of Bacterial Quality scores", BMC Bioinformatics, (2017); **18**(Suppl 14):483. Epub 20171228. doi: https://doi.org/10.1186/s12859-017-1900-9. PubMed PMID: 29297289; PMCID: PMC5751761. Cited 10x

65. *Poudel S.*, Giannone R. J., Rodriguez M., Jr., Raman B., Martin M. Z., Engle N. L., Mielenz J. R., Nookaew I., Brown S. D., Tschaplinski T. J., **Ussery D.,** Hettich R. L., "Integrated omics analyses reveal the details of metabolic adaptation of *Clostridium thermocellum* to lignocellulose-derived growth inhibitors released during the deconstruction of switchgrass", Biotechnology for Biofuels, (2017); **10**:14. Epub 20170110. doi: https://doi.org/10.1186/s13068-016-0697-5. PubMed PMID: 28077967; PMCID: PMC5223564.
Cited 50x

66. Jun S. R., Wassenaar T. M., **Wanchai V., *Patumcharoenpol P.*, Nookaew I., **Ussery D. W.,** "Suggested mechanisms for Zika virus causing microcephaly: what do the genomes tell us?", BMC Bioinformatics, (2017); **18**(Suppl 14):471. Epub 20171228. doi: https://doi.org/10.1186/s12859-017-1894-3. PubMed PMID: 29297281; PMCID: PMC5751795.
Cited 28x

67. **Alkam D.*, Wongsurawat T., Jenjaroenpun P., Connor S., Hobbs C., Wassenaar T. M., Jun S. R., Nookaew I., **Ussery D.,** "Three Complete Genome Sequences of Genotype G Mumps Virus from the 2016 Outbreak in Arkansas, USA", Genome Announcements, (2017); **5**(32). Epub 20170810. doi: https://doi.org/10.1128/genomeA.00555-17. PubMed PMID: 28798162; PMCID: PMC5552971.

68. Pedersen T. L., Nookaew I., Ussery D. W., Månsson M., "PanViz: interactive visualization of the structure of functionally annotated pangenomes", Bioinformatics, (2017); **33**(7):1081–1082. doi: https://doi.org/10.1093/bioinformatics/btw761. PubMed PMID: 28057677; PMCID: PMC5859990.
Cited 36x

69. Wassenaar T. M., **Ussery D. W.**, Ingmer H., "The qacC Gene Has Recently Spread between Rolling Circle Plasmids of *Staphylococcus*, Indicative of a Novel Gene Transfer Mechanism", Frontiers in Microbiology, (2016); **7**:1528. Epub 20160927. doi: https://doi.org/10.3389/fmicb.2016.01528. PubMed PMID: 27729906; PMCID: PMC5037232.
Cited 30x

70. **Leekitcharoenphon P.*, Hendriksen R. S., Le Hello S., Weill F. X., Baggesen D. L., Jun S. R., **Ussery D. W.**, Lund O., Crook D. W., Wilson D. J., Aarestrup F. M., "Global Genomic Epidemiology of *Salmonella enterica* Serovar Typhimurium DT104", Applied and

Environmental Microbiology, (2016); **82**(8):2516–2526. Epub 20160404. doi: https://doi.org/10.1128/AEM.03821-15. PubMed PMID: 26944846; PMCID: PMC4959494.
Cited 148x

71. Jun S. R., Wassenaar T. M., Nookaew I., Hauser L., Wanchai V., Land M., Timm C. M., Lu T. Y., Schadt C. W., Doktycz M. J., Pelletier D. A., **Ussery D. W**., "Diversity of *Pseudomonas* Genomes, Including *Populus*-Associated Isolates, as Revealed by Comparative Genome Analysis", Applied and Environmental Microbiology, (2016); **82**(1):375–383. Epub 20151030. doi: https://doi.org/10.1128/AEM.02612-15. PubMed PMID: 26519390; PMCID: PMC4702629. Cited 90x

72. Wassenaar T. M., **Ussery D**., Nielsen L. N., Ingmer H., "Review and phylogenetic analysis of qac genes that reduce susceptibility to quaternary ammonium compounds in *Staphylococcus* species", European Journal of Microbiology and Immunology, (2015); **5**(1):44–61. Epub 20150326. doi: https://doi.org/10.1556/EUJMI-D-14-00038. PubMed PMID: 25883793; PMCID: PMC4397847.
Cited 225x

73. Timm C. M., Campbell A. G., Utturkar S. M., Jun S. R., Parales R. E., Tan W. A., Robeson M. S., Lu T. Y., Jawdy S., Brown S. D., **Ussery D. W.**, Schadt C. W., Tuskan G. A., Doktycz M. J., Weston D. J., Pelletier D. A., "Metabolic functions of *Pseudomonas fluorescens* strains from *Populus deltoides* depend on rhizosphere or endosphere isolation compartment", Frontiers in Microbiology, (2015); **6**:1118. Epub 20151014. doi: https://doi.org/10.3389/fmicb.2015.01118. PubMed PMID: 26528266; PMCID: PMC4604316.
Cited 78x

74. Thompson C. C., Amaral G. R., Campeao M., Edwards R. A., Polz M. F., Dutilh B. E., **Ussery D. W**., Sawabe T., Swings J., Thompson F. L., "Microbial taxonomy in the post-genomic era: rebuilding from scratch?", Archives of Microbiology, (2015); **197**(3):359–370. Epub 20141223. doi: https://doi.org/10.1007/s00203-014-1071-2. PubMed PMID: 25533848.
Cited 139x

75. Land M., Hauser L., Jun S. R., Nookaew I., Leuze M. R., Ahn T. H., Karpinets T., Lund O., Kora G., Wassenaar T., Poudel S., **Ussery D. W.**, "Insights from 20 years of bacterial genome sequencing", Functional & Integrative Genomics, (2015); **15**(2):141–161. Epub 20150227. doi: https://doi.org/10.1007/s10142-015-0433-4. PubMed PMID: 25722247; PMCID: PMC4361730.
Cited 1020x.

76. Jun S. R., Leuze M. R., Nookaew I., Uberbacher E. C., Land M., Zhang Q., **Wanchai V.*, Chai J., Nielsen M., Trolle T., Lund O., Buzard G. S., Pedersen T. D., Wassenaar T. M., **Ussery D. W**., "*Ebolavirus* comparative genomics", FEMS Microbiology Reviews, (2015); **39**(5):764–778. Epub 20150714. doi: https://doi.org/10.1093/femsre/fuv031. PubMed PMID: 26175035; PMCID: PMC4551310.
Cited 75x

77. Espinoza-Valles I., Vora G. J., Lin B., Leekitcharoenphon P., Gonzalez-Castillo A., **Ussery D.,** Hoj L., Gomez-Gil B., "Unique and conserved genome regions in *Vibrio harveyi* and related species in comparison with the shrimp pathogen *Vibrio harveyi* CAIM 1792", Microbiology (Reading). (2015); **161**(9):1762–1779. Epub 20150721. doi: https://doi.org/10.1099/mic.0.000141. PubMed PMID: 26198743.

78. Beatson S. A., Ben Zakour N. L., Totsika M., Forde B. M., Watts R. E., Mabbett A. N., Szubert J. M., Sarkar S., Phan M. D., Peters K. M., Petty N. K., Alikhan N. F., Sullivan M. J., Gawthorne J. A., Stanton-Cook M., Nhu N. T., Chong T. M., Yin W. F., Chan K. G., Hancock V., **Ussery D. W**., Ulett G. C., Schembri M. A., "Molecular analysis of asymptomatic bacteriuria *Escherichia coli* strain VR50 reveals adaptation to the urinary tract by gene acquisition", Infection and Immunity, (2015); **83**(5):1749–1764. Epub 20150209. doi: https://doi.org/10.1128/IAI.02810-14. PubMed PMID: 25667270; PMCID: PMC4399054.
Cited 37x

79. Ali A., Naz A., Soares S. C., Bakhtiar M., Tiwari S., Hassan S. S., Hanan F., Ramos R., Pereira U., Barh D., Figueiredo H. C., **Ussery D. W**., Miyoshi A., Silva A., Azevedo V., "Pan-genome analysis of human gastric pathogen *H. pylor*i: comparative genomics and pathogenomics approaches to identify regions associated with pathogenicity and prediction of potential core therapeutic targets", BioMed Research International, (2015); **2015**:139580. Epub 20150129. doi: https://doi.org/10.1155/2015/139580. PubMed PMID: 25705648; PMCID: PMC4325212.
Cited 75x

80. Nielsen H. B., Almeida M., Juncker A. S., Rasmussen S., Li J., Sunagawa S., Plichta D. R., Gautier L., Pedersen A. G., Le Chatelier E., Pelletier E., Bonde I., Nielsen T., Manichanh C., Arumugam M., Batto J. M., Quintanilha Dos Santos M. B., Blom N., Borruel N., Burgdorf K. S., Boumezbeur F., Casellas F., Dore J., Dworzynski P., Guarner F., Hansen T., Hildebrand F., Kaas R. S., Kennedy S., Kristiansen K., Kultima J. R., Leonard P., Levenez F., Lund O., Moumen B., Le Paslier D., Pons N., Pedersen O., Prifti E., Qin J., Raes J., Sorensen S., Tap J., Tims S., **Ussery D. W**., Yamada T., Meta H. I. T. Consortium, Renault P., Sicheritz-Ponten T., Bork P., Wang J., Brunak S., Ehrlich S. D., Meta H. I. T. Consortium, "Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes", Nature Biotechnology, (2014); **32**(8):822–828. Epub 20140706. doi: https://doi.org/10.1038/nbt.2939. PubMed PMID: 24997787.
Cited 1286x.

81. **Lukjancenko O.*, **Ussery D. W**., "*Vibrio* chromosome-specific families", Frontiers in Microbiology, (2014); **5**:73. Epub 20140318. doi: https://doi.org/10.3389/fmicb.2014.00073. PubMed PMID: 24672511; PMCID: PMC3957060.
Cited 36x

82. Larsen M. V., Cosentino S., *Lukjancenko O.*, Saputra D., Rasmussen S., Hasman H., Sicheritz-Ponten T., Aarestrup F. M., **Ussery D. W**., Lund O., "Benchmarking of methods for genomic taxonomy", Journal of Clinical Microbiology, (2014); **52**(5):1529–1539. Epub 20140226. doi: https://doi.org/10.1128/JCM.02981-13. PubMed PMID: 24574292; PMCID: PMC3993634.
Cited 428x

83. Land M. L., Hyatt D., Jun S. R., Kora G. H., Hauser L. J., **Lukjancenko O.*, **Ussery D. W.,** "Quality scores for 32,000 genomes", Standards in Genomic Sciences, (2014); **9**:20. Epub 20141208. doi: https://doi.org/10.1186/1944-3277-9-20. PubMed PMID: 25780509; PMCID: PMC4334873.
Cited 58x

84. **Haugum K.*, Johansen J., Gabrielsen C., Brandal L. T., Bergh K., **Ussery D. W**., Drablos F., Afset J. E., "Comparative genomics to delineate pathogenic potential in non-O157 Shiga toxin-producing *Escherichia col*i (STEC) from patients with and without haemolytic uremic syndrome (HUS) in Norway", PLoS One, (2014); **9**(10):e111788. Epub 20141031. doi: https://doi.org/10.1371/journal.pone.0111788. PubMed PMID: 25360710; PMCID: PMC4216125.
Cited 54x

85. Field D., Sterk P., Kottmann R., De Smet J. W., Amaral-Zettler L., Cochrane G., Cole J. R., Davies N., Dawyndt P., Garrity G. M., Gilbert J. A., Glockner F. O., Hirschman L., Klenk H. P., Knight R., Kyrpides N., Meyer F., Karsch-Mizrachi I., Morrison N., Robbins R., San Gil I., Sansone S., Schriml L., Tatusova T., **Ussery D**., Yilmaz P., White O., Wooley J., Caporaso G., "Genomic standards consortium projects", Standards in Genomic Sciences, (2014); **9**(3):599–601. Epub 20140215. doi: https://doi.org/10.4056/sigs.5559680. PubMed PMID: 25197446; PMCID: PMC4148985.

86. **Vesth T., *Ozen A., *Andersen S. C., *Kaas R. S., *Lukjancenko O., *Bohlin J.*, Nookaew I., Wassenaar T. M., **Ussery D. W.**, "*Veillonella*, Firmicutes: Microbes disguised as Gram negatives, Standards in Genomic Sciences, (2013); **9**(2):431–448. Epub 20131215. doi: https://doi.org/10.4056/sigs.2981345. PubMed PMID: 24976898; PMCID: PMC4062629.
Cited 79x

87. **Lukjancenko O.*, Thomsen M. C., Larsen M. V., **Ussery D. W**., "PanFunPro: PAN-genome Analysis Based on FUNctional PROfiles", F1000 Research,(2013); **2**:265. doi: https://doi.org/10.12688/f1000research.2-265.v1.
Cited 31x

88. **Vesth T., *Lagesen K., *Acar O.*, **Ussery D**., "CMG-biotools, a free workbench for basic comparative microbial genomics", PLoS One, (2013); **8**(4):e60120. Epub 20130405. doi: https://doi.org/10.1371/journal.pone.0060120. PubMed PMID: 23577086; PMCID: PMC3618517.
Cited 130x

89. **Jensen D. B.*, **Ussery D. W.**, "Bayesian prediction of microbial oxygen requirement", F1000 Research, (2013); **2**:184. Epub 20130913. doi: https://doi.org/10.12688/f1000research.2-184.v1. PubMed PMID: 26913185; PMCID: PMC4743139.

90. **Holch A., *Webb K., *Lukjancenko O.*, **Ussery D.**, Rosenthal B. M., Gram L., "Genome sequencing identifies two nearly unchanged strains of persistent *Listeria monocytogenes* isolated at two different fish processing plants sampled 6 years apart", Applied and Environmental Microbiology, (2013); **79**(9):2944–2951. Epub 20130222. doi: https://doi.org/10.1128/AEM.03715-12. PubMed PMID: 23435887; PMCID: PMC3623136.
Cited 163x

91. **Cook H.*, **Ussery D. W.**, "Sigma factors in a thousand *E. coli* genomes", Environmental Microbiology, (2013); **15**(12):3121–3129. Epub 20130829. doi: https://doi.org/10.1111/1462-2920.12236. PubMed PMID: 23992563.
Cited 52x

92. **Bohlin J., *Brynildsrud O., *Vesth T., *Skjerve E.*, **Ussery D. W.**, "Amino acid usage is asymmetrically biased in AT- and GC-rich microbial genomes", PLoS One, (2013); **8**(7):e69878. Epub 20130726. doi: https://doi.org/10.1371/journal.pone.0069878. PubMed PMID: 23922837; PMCID: PMC3724673.
Cited 35x

93. Acevedo-Rocha C. G., Fang G., Schmidt M., **Ussery D. W.**, Danchin A., "From essential to persistent genes: a functional approach to constructing synthetic life", Trends in Genetics, (2013); **29**(5):273–279. Epub 20121206. doi: https://doi.org/10.1016/j.tig.2012.11.001. PubMed PMID: 23219343; PMCID: PMC3642372.
Cited 130x

94. Ali A., Soares S. C., Barbosa E., Santos A. R., Barh D., Bakhtiar S. M., Hassan S. S., **Ussery D. W.**, Miyoshi S. A., Azevedo V., "Microbial Comparative Genomics: An Overview of Tools and Insights Into The Genus *Corynebacterium*", Journal of Bacteriology and Parasitology, (2013); **167**:2. doi: http://dx.doi.org/10.4172/2155-9597.1000167.
Cited 26x

95. Zakham F., Aouane O., **Ussery D.**, Benjouad A., Ennaji M. M., "Computational genomics-proteomics and Phylogeny analysis of twenty one *Mycobacterial* genomes (Tuberculosis & non Tuberculosis strains)", Microbial Informatics and Experimentation, (2012); **2**(1):7. Epub 20120828. doi: https://doi.org/10.1186/2042-5783-2-7. PubMed PMID: 22929624; PMCID: PMC3504576.

96. **Ussery D. W.**, Gordon S. V., "Two novel methods for using genome sequences to infer taxonomy", Microbiology (Reading). (2012); 158(Pt 6):1414. Epub 20120413. doi: https://doi.org/10.1099/mic.0.059816-0. PubMed PMID: 22504434.

97. Snipen L. G., **Ussery D. W.**, "A domain sequence approach to pangenomics: applications to *Escherichia coli*", F1000Research, (2012); **1**:19. Epub 20121001. doi: https://doi.org/

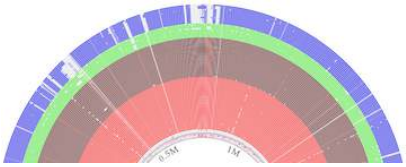
10.12688/f1000research.1-19.v2. PubMed PMID: 24555018; PMCID: PMC3901455.
Cited 20x

98. Snipen L., Wassenaar T. M., Altermann E., Olson J., Kathariou S., Lagesen K., Takamiya M., Knochel S., **Ussery D. W.**, Meinersmann R. J., "Analysis of evolutionary patterns of genes in *Campylobacter jejuni* and *C. coli*", Microbial Informatics and Experimentation, (2012); **2**(1):8. Epub 20120828. doi: https://doi.org/10.1186/2042-5783-2-8. PubMed PMID: 22929701; PMCID: PMC3502170.
Cited 14x

99. Rodriguez-Valera F., **Ussery D. W.**, "Is the pan-genome also a pan-selectome?" F1000Research, (2012); **1**:16. Epub 20120921. doi: https://doi.org/10.12688/f1000research.1-16.v1. PubMed PMID: 24358823; PMCID: PMC3782348.
Cited 50x

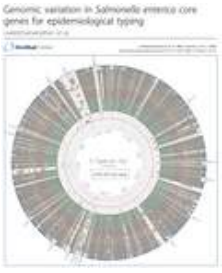
100. **Ozen A. I.*, **Ussery D. W.**, "Defining the *Pseudomonas* genus: where do we draw the line with *Azotobacter*?", Microbial Ecology, (2012); **63**(2):239–248. Epub 20110803. doi: https://doi.org/10.1007/s00248-011-9914-8. PubMed PMID: 21811795; PMCID: PMC3275731.
Cited 191x

101. Mekalanos J. J., Robins W., **Ussery D. W.**, Davis B. M., Schadt E., Waldor M. K., "Non-O1 *Vibrio cholerae* unlinked to cholera in Haiti", Proceedings of the National Academy of Sciences (PNAS), (2012); **109**(47):E3206; author reply E3207. Epub 20121003. doi: https://doi.org/10.1073/pnas.1212443109. PubMed PMID: 23035253; PMCID: PMC3511112.
Cited 10x



102. **Lukjancenko O.*, **Ussery D. W.**, Wassenaar T. M., "Comparative genomics of *Bifidobacterium, Lactobacillus* and related probiotic genera", Microbial Ecology, (2012); **63**(3):651–673. Epub 20111027. doi: https://doi.org/10.1007/s00248-011-9948-y. PubMed PMID: 22031452; PMCID: PMC3324989.
Cited 138x

103. **Leekitcharoenphon P., *Lukjancenko O., *Friis C.*, Aarestrup F. M., **Ussery D. W.**, "Genomic variation in *Salmonella enterica* core genes for epidemiological typing", BMC Genomics, (2012); **13**:88. Epub 20120312. doi: https://doi.org/10.1186/1471-2164-13-88. PubMed PMID: 22409488; PMCID: PMC3359268.
Cited 121x
Cover image.



104. Larsen M. V., Cosentino S., Rasmussen S., Friis C., Hasman H., Marvig R. L., Jelsbak L., Sicheritz-Ponten T., **Ussery D. W.**, Aarestrup F. M., Lund O., "Multilocus sequence typing of total-genome-sequenced bacteria", Journal of Clinical Microbiology, (2012);

50(4):1355–1361. Epub 20120111. doi: https://doi.org/10.1128/JCM.06094-11. PubMed PMID: 22238442; PMCID: PMC3318499.
Cited 2584x.

105. Kroger C., Dillon S. C., Cameron A. D., Papenfort K., Sivasankaran S. K., Hokamp K., Chao Y., Sittka A., Hebrard M., Handler K., Colgan A., **Leekitcharoenphon P.*, Langridge G. C., Lohan A. J., Loftus B., Lucchini S., **Ussery D. W.**, Dorman C. J., Thomson N. R., Vogel J., Hinton J. C., "The transcriptional landscape and small RNAs of *Salmonella enterica* serovar Typhimurium, Proceedings of the National Academy of Sciences (PNAS), (2012); **109**(20):E1277–1286. Epub 20120425. doi: https://doi.org/10.1073/pnas.1201061109. PubMed PMID: 22538806; PMCID: PMC3356629.
Cited 495x

106. **Kaas R. S., *Friis C.*, **Ussery D. W.**, Aarestrup F. M., "Estimating variation within the genes and inferring the phylogeny of 186 sequenced diverse *Escherichia coli* genomes", BMC Genomics, (2012); **13**:577. Epub 20121031. doi: https://doi.org/10.1186/1471-2164-13-577. PubMed PMID: 23114024; PMCID: PMC3575317.
Cited 292x

107.**Jensen D. B., *Vesth T. C., *Hallin P. F., *Pedersen A. G.*, **Ussery D. W.,** "Bayesian prediction of bacterial growth temperature range based on genome sequences", BMC Genomics, (2012); **13** (Suppl 7):S3. Epub 20121213. doi: https://doi.org/10.1186/1471-2164-13-S7-S3. PubMed PMID: 23282160; PMCID: PMC3521210.
Cited 24x

108. Gonzaga A., Martin-Cuadrado A. B., Lopez-Perez M., Megumi Mizuno C., Garcia-Heredia I., Kimes N. E., Lopez-Garcia P., Moreira D., **Ussery D**., Zaballos M., Ghai R., Rodriguez-Valera F., "Polyclonality of concurrent natural populations of Alteromonas macleodi", Genome Biology and Evolution, (2012); **4**(12):1360–1374. doi: https://doi.org/10.1093/gbe/evs112. PubMed PMID: 23212172; PMCID: PMC3542563.
Cited 55x

109. Dillon S. C., Espinosa E., Hokamp K., **Ussery D. W.**, Casadesus J., Dorman C. J., "LeuO is a global regulator of gene expression in *Salmonella enterica* serovar Typhimurium", Molecular Microbiology, (2012); **85**(6):1072–1089. Epub 20120723. doi: https://doi.org/10.1111/j.1365-2958.2012.08162.x. PubMed PMID: 22804842.
Cited 84x

110. **Bohlin J.*, van Passel M. W., Snipen L., Kristoffersen A. B., **Ussery D**., Hardy S. P., "Relative entropy differences in bacterial chromosomes, plasmids, phages and genomic islands", BMC Genomics, (2012); **13**:66. Epub 20120210. doi: https://doi.org/10.1186/1471-2164-13-66. PubMed PMID: 22325062; PMCID: PMC3305612.
Cited 26x

111. Ali A., Soares S. C., Santos A. R., Guimaraes L. C., Barbosa E., Almeida S. S., Abreu V. A., Carneiro A. R., Ramos R. T., Bakhtiar S. M., Hassan S. S., **Ussery D. W.**, On S., Silva A.,

Schneider M. P., Lage A. P., Miyoshi A., Azevedo V., "*Campylobacter fetus* subspecies: comparative genomics and prediction of potential virulence targets", Gene, (2012); 508(2):145–156. Epub 20120806. doi: https://doi.org/10.1016/j.gene.2012.07.070. PubMed PMID: 22890137.
Cited 74x

112. Zakham F., Belayachi L., **Ussery D.**, Akrim M., Benjouad A., El Aouad R., Ennaji M. M., "*Mycobacterial* species as case-study of comparative genome analysis", Cellular and Molecular Biology (Noisy-le-grand). (2011); **57** Suppl:OL1462–1469. Epub 20110208. doi: https://doi.org/10.1170/167. PubMed PMID: 21396338.
Cited 37x

113. Takamiya M., Ozen A., Rasmussen M., Alter T., Gilbert T., **Ussery D. W.**, Knochel S., "Genome Sequence of *Campylobacter jejuni* strain 327, a strain isolated from a turkey slaughterhouse", Standards in Genomic Sciences, (2011); **4**(2):113–122. Epub 20110425. doi: https://doi.org/10.4056/sigs.1313504. PubMed PMID: 21677848; PMCID: PMC3111999.

114. Karlsson F. H., **Ussery D. W**., Nielsen J., Nookaew I., "A closer look at *Bacteroides*: phylogenetic relationship and genomic implications of a life in the human gut", Microbial Ecology, (2011); **61**(3):473–485. Epub 20110111. doi: https://doi.org/10.1007/s00248-010-9796-1. PubMed PMID: 21222211.
Cited 178x

115.Jacobsen A., Hendriksen R. S., Aaresturp F. M., **Ussery D. W.**, *Friis C.*, "The *Salmonella enterica* pan-genome", Microbial Ecology, (2011); **62**(3):487–504. Epub 20110604. doi: https://doi.org/10.1007/s00248-011-9880-1. PubMed PMID: 21643699; PMCID: PMC3175032.
Cited 258x

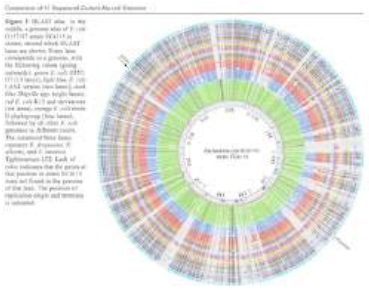
116. Field D., Amaral-Zettler L., Cochrane G., Cole J. R., Dawyndt P., Garrity G. M., Gilbert J., Glockner F. O., Hirschman L., Karsch-Mizrachi I., Klenk H. P., Knight R., Kottmann R., Kyrpides N., Meyer F., San Gil I., Sansone S. A., Schriml L. M., Sterk P., Tatusova T., **Ussery D. W.**, White O., Wooley J., "The Genomic Standards Consortium", PLoS Biology, (2011); **9**(6):e1001088. Epub 20110621. doi: https://doi.org/10.1371/journal.pbio.1001088. PubMed PMID: 21713030; PMCID: PMC3119656.
Cited 218x

117. Brede D. A., Snipen L. G., **Ussery D. W**., Nederbragt A. J., Nes I. F., "Complete genome sequence of the commensal *Enterococcus faecalis* 62, isolated from a healthy Norwegian infant", Journal of Bacteriology, (2011); **193**(9):2377–2378. Epub 20110311. doi: https://doi.org/10.1128/JB.00183-11. PubMed PMID: 21398545; PMCID: PMC3133060.
Cited 72x

118. **Vesth T.*, Wassenaar T. M., Hallin P. F., Snipen L., *Lagesen K.*, **Ussery D. W**., "On the origins of a *Vibrio* species", Microbial Ecology, (2010); **59**(1):1–13. doi: https://doi.org/

10.1007/s00248-009-9596-7. PubMed PMID: 19830476; PMCID: PMC2807590.
Cited 66x

119. Snipen L., **Ussery D. W.**, "Standard operating procedure for computing pangenome trees", Standards in Genomic Sciences, (2010); **2**(1):135–141. Epub 20100128. doi: https://doi.org/10.4056/sigs.38923. PubMed PMID: 21304685; PMCID: PMC3035256.
Cited 94x



120. **Lukjancenko O.*, Wassenaar T. M., **Ussery D. W.**, "Comparison of 61 sequenced *Escherichia coli* genomes", Microbial Ecology, (2010); **60**(4):708–720. Epub 20100711. doi: https://doi.org/10.1007/s00248-010-9717-3. PubMed PMID: 20623278; PMCID: PMC2974192.
Cited 721x

121. Lavin J. L., Ramirez L., **Ussery D. W.**, Pisabarro A. G., Oguiza J. A., "Genomic analysis of two-component signal transduction proteins in basidiomycetes", Journal of Molecular Microbiology and Biotechnology, (2010); **18**(2):63–73. Epub 20100123. doi: https://doi.org/10.1159/000277654. PubMed PMID: 20110730.
Cited 17x

122. Lavin J. L., *Binnewies T. T.*, Pisabarro A. G., **Ussery D. W.**, Garcia-Lobo J. M., Oguiza J. A., "Differences in two-component signal transduction proteins among the genus *Brucella*: implications for host preference and pathogenesis", Veterinary Microbiology, (2010); **144**(3-4):478–483. Epub 20100128. doi: https://doi.org/10.1016/j.vetmic.2010.01.007. PubMed PMID: 20153589.
Cited 21x

123. **Lagesen K.*, **Ussery D. W.**, Wassenaar T. M., "Genome update: the 1000th genome--a cautionary tale", Microbiology (Reading). (2010); **156**(Pt 3):603–608. Epub 20100121. doi: https://doi.org/10.1099/mic.0.038257-0. PubMed PMID: 20093288.

124. *Friis C., Wassenaar T. M., Javed M. A., Snipen L., **Lagesen K.*, **Hallin P. F.*, Newell D. G., Toszeghy M., Ridley A., Manning G., **Ussery D. W.**, "Genomic characterization of *Campylobacter jejuni* strain M1", PLoS One, (2010); **5**(8):e12253. Epub 20100826. doi: https://doi.org/10.1371/journal.pone.0012253. PubMed PMID: 20865039; PMCID: PMC2928727.
Cited 129x

125. Davenport C., **Ussery D. W.**, Tummler B., "Comparative genomics of green sulfur bacteria", Photosynthesis Research, (2010); **104**(2-3):137–152. Epub 20100123. doi: https://doi.org/10.1007/s11120-009-9515-2. PubMed PMID: 20099081.
Cited 16x

126. **Bohlin J.*, Snipen L., Hardy S. P., Kristoffersen A. B., **Lagesen K.*, Donsvik T., Skjerve E., **Ussery D. W.**, "Analysis of intra-genomic GC content homogeneity within prokaryotes",

BMC Genomics, (2010); **11**:464. Epub 20100806. doi: https://doi.org/10.1186/1471-2164-11-464. PubMed PMID: 20691090; PMCID: PMC3091660.
Cited 65x

127. **Bohlin J.*, Snipen L., Cloeckaert A., *Lagesen K.*, **Ussery D.**, Kristoffersen A. B., Godfroid J., "Genomic comparisons of *Brucella* spp. and closely related bacteria using base compositional and proteome based methods", BMC Evolutionary Biology, (2010); **10**:249. Epub 20100813. doi: https://doi.org/10.1186/1471-2148-10-249. PubMed PMID: 20707916; PMCID: PMC2928237.
Cited 55x

128. Wortman J. R., Gilsenan J. M., Joardar V., Deegan J., Clutterbuck J., Andersen M. R., Archer D., Bencina M., Braus G., Coutinho P., von Dohren H., Doonan J., Driessen A. J., Durek P., Espeso E., Fekete E., Flipphi M., Estrada C. G., Geysens S., Goldman G., de Groot P. W., Hansen K., Harris S. D., Heinekamp T., Helmstaedt K., Henrissat B., Hofmann G., Homan T., Horio T., Horiuchi H., James S., Jones M., Karaffa L., Karanyi Z., Kato M., Keller N., Kelly D. E., Kiel J. A., Kim J. M., van der Klei I. J., Klis F. M., Kovalchuk A., Krasevec N., Kubicek C. P., Liu B., Maccabe A., Meyer V., Mirabito P., Miskei M., Mos M., Mullins J., Nelson D. R., Nielsen J., Oakley B. R., Osmani S. A., Pakula T., Paszewski A., Paulsen I., Pilsyk S., Pocsi I., Punt P. J., Ram A. F., Ren Q., Robellet X., Robson G., Seiboth B., van Solingen P., Specht T., Sun J., Taheri-Talesh N., Takeshita N., **Ussery D**., vanKuyk P. A., Visser H., van de Vondervoort P. J., de Vries R. P., Walton J., Xiang X., Xiong Y., Zeng A. P., Brandt B. W., Cornell M. J., van den Hondel C. A., Visser J., Oliver S. G., Turner G., "The 2008 update of the *Aspergillus nidulans* genome annotation: a community effort", Fungal Genetics and Biology, (2009); **46** Suppl 1(Suppl 1):S2–13. Epub 20081225. doi: https://doi.org/10.1016/j.fgb.2008.12.003. PubMed PMID: 19146970; PMCID: PMC2826280.

129. Wassenaar T. M., **Bohlin J.*, **Binnewies T. T.*, **Ussery D. W**., "Genome comparison of bacterial pathogens", GENOME DYNAMICS - Microbial Pathogenomics, (2009); **6**:1–20. Epub 20090819. doi: https://doi.org/10.1159/000235759. PubMed PMID: 19696490.
Cited 18x

130. Wang K., **Ussery D. W**., Brunak S., "Analysis and prediction of gene splice sites in four *Aspergillus* genomes", Fungal Genetics and Biology, (2009); **46** Suppl 1:S14–18. Epub 20081010. doi: https://doi.org/10.1016/j.fgb.2008.09.010. PubMed PMID: 18948220.
Cited 48x

131. **Ussery D. W**., **Kiil K.*, **Lagesen K.*, Sicheritz-Ponten T., **Bohlin J.*, Wassenaar T. M., "The genus *Burkholderia*: analysis of 56 genomic sequences", GENOME DYNAMICS - Microbial Pathogenomics, (2009); **6**:140–157. Epub 20090819. doi: https://doi.org/10.1159/000235768. PubMed PMID: 19696499.

132. Thompson C. C., Vicente A. C., Souza R. C., Vasconcelos A. T., **Vesth T.*, Alves N., Jr., **Ussery D. W**., Iida T., Thompson F. L., "Genomic taxonomy of *Vibrios*", BMC Evolutionary Biology, (2009); **9**:258. Epub 20091027. doi: https://doi.org/

10.1186/1471-2148-9-258. PubMed PMID: 19860885; PMCID: PMC2777879.
Cited 218x

133. Snipen L., Almoy T., **Ussery D. W.**, "Microbial comparative pan-genomics using binomial mixture models", BMC Genomics, (2009); **10**:385. Epub 20090819. doi: https://doi.org/10.1186/1471-2164-10-385. PubMed PMID: 19691844; PMCID: PMC2907702.
Cited 147x

134. **Hallin P. F., *Staerfeldt H. H., *Rotenberg E., *Binnewies T. T.*, Benham C. J., **Ussery D. W.**, "GeneWiz browser: An Interactive Tool for Visualizing Sequenced Chromosomes", Standards in Genomic Sciences, (2009); **1**(2):204–215. Epub 20090925. doi: https://doi.org/10.4056/sigs.28177. PubMed PMID: 21304658; PMCID: PMC3035224.
Cited 21x

135. Garrity G. M., Thompson L. M., **Ussery D. W.**, Paskin N., Baker D., Desmeth P., Schindel D. E., Ong P. S., "Studies on monitoring and tracking genetic resources: an Executive Summary.", Standards in Genomic Sciences, (2009); **1**(1):78–86. Epub 20090720. doi: https://doi.org/10.4056/sigs.1491. PubMed PMID: 21304641; PMCID: PMC3035216.
Cited 25x

136. **Bohlin J.*, Skjerve E., **Ussery D. W.**, "Analysis of genomic signatures in prokaryotes using multinomial regression and hierarchical clustering", BMC Genomics, (2009); **10**:487. Epub 20091021. doi: https://doi.org/10.1186/1471-2164-10-487. PubMed PMID: 19845945; PMCID: PMC2770534.
Cited 31x

137. **Bohlin J.*, Hardy S. P., **Ussery D. W.**, "Stretches of alternating pyrimidine/purines and purines are respectively linked with pathogenicity and growth temperature in prokaryotes", BMC Genomics, (2009); **10**:346. Epub 20090731. doi: https://doi.org/10.1186/1471-2164-10-346. PubMed PMID: 19646265; PMCID: PMC2728739.

138. Garrity G. M., Thompson L. M., Ussery D. W., Paskin N., Baker D., Desmeth P., Schindel D. E., Ong P. S., "Studies on Monitoring and Tracking Genetic Resources", peer-reviewed technical report that was commissioned by the Convention on Biological Diversity (21 January, 2009 [UNEP/CBD/ABS/GTLE/2/INF/4] https://www.cbd.int/doc/meetings/abs/abswg-07/information/abswg-07-inf-02-en.pdf.

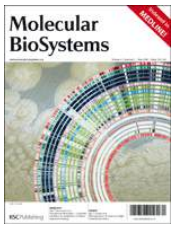
139.Reva O. N., **Hallin P. F., *Willenbrock H.*, Sicheritz-Ponten T., Tummler B., **Ussery D. W.**, "Global features of the *Alcanivorax borkumensis* SK2 genome", Environmental Microbiology, (2008); **10**(3):614–625. Epub 20071212. doi: https://doi.org/10.1111/j.1462-2920.2007.01483.x. PubMed PMID: 18081853.
Cited 37x

140. Lee K. B., De Backer P., Aono T., Liu C. T., Suzuki S., Suzuki T., Kaneko T., Yamada M., Tabata S., Kupfer D. M., Najar F. Z., Wiley G. B., Roe B., *Binnewies T. T.*, **Ussery D. W.**,

D'Haeze W., Herder J. D., Gevers D., Vereecke D., Holsters M., Oyaizu H., "The genome of the versatile nitrogen fixer *Azorhizobium caulinodans* ORS571", BMC Genomics, (2008); **9**:271. Epub 20080604. doi: https://doi.org/10.1186/1471-2164-9-271. PubMed PMID: 18522759; PMCID: PMC2443382.
Cited 160x

141. Hancock V., Seshasayee A. S., **Ussery D. W.**, Luscombe N. M., Klemm P., "Transcriptomics and adaptive genomics of the asymptomatic bacteriuria *Escherichia coli* strain 83972", Molecular Genetics and Genomics, (2008); **279**(5):523–534. doi: https://doi.org/10.1007/s00438-008-0330-9. PubMed PMID: 18317809; PMCID: PMC2329726.
Cited 44x

142. **Hallin P. F., *Binnewies T. T.*, **Ussery D. W.**, "The Genome BLASTatlas - A GeneWiz Extension for Visualization of Whole-Genome Homology", Molecular Biosystems, (2008); **4**(5):363–371. Epub 20080317. doi: https://doi.org/10.1039/b717118h. PubMed PMID: 18414733.
Cover image.
Cited 72x



143. Garrity G. M., Field D., Kyrpides N., Hirschman L., Sansone S. A., Angiuoli S., Cole J. R., Glockner F. O., Kolker E., Kowalchuk G., Moran M. A., **Ussery D.**, White O., "Toward a standards-compliant genomic and metagenomic publication record", OMICS: A Journal of Integrative Biology, (2008); **12**(2):157–160. doi: https://doi.org/10.1089/omi.2008.A2B2. PubMed PMID: 18564916.

144. Field D., Garrity G., Gray T., Morrison N., Selengut J., Sterk P., Tatusova T., Thomson N., Allen M. J., Angiuoli S. V., Ashburner M., Axelrod N., Baldauf S., Ballard S., Boore J., Cochrane G., Cole J., Dawyndt P., De Vos P., DePamphilis C., Edwards R., Faruque N., Feldman R., Gilbert J., Gilna P., Glockner F. O., Goldstein P., Guralnick R., Haft D., Hancock D., Hermjakob H., Hertz-Fowler C., Hugenholtz P., Joint I., Kagan L., Kane M., Kennedy J., Kowalchuk G., Kottmann R., Kolker E., Kravitz S., Kyrpides N., Leebens-Mack J., Lewis S. E., Li K., Lister A. L., Lord P., Maltsev N., Markowitz V., Martiny J., Methe B., Mizrachi I., Moxon R., Nelson K., Parkhill J., Proctor L., White O., Sansone S. A., Spiers A., Stevens R., Swift P., Taylor C., Tateno Y., Tett A., Turner S., **Ussery D.**, Vaughan B., Ward N., Whetzel T., San Gil I., Wilson G., Wipat A., "The minimum information about a genome sequence (MIGS) specification", Nature Biotechnology, (2008); **26**(5):541–547. doi: https://doi.org/10.1038/nbt1360. PubMed PMID: 18464787; PMCID: PMC2409278.
Cited 1430x.

145. Boyd E. F., Cohen A. L., Naughton L. M., **Ussery D. W.**, *Binnewies T. T.*, Stine O. C., Parent M. A., "Molecular analysis of the emergence of pandemic *Vibrio parahaemolyticus*", BMC Microbiology, (2008); **8**:110. Epub 20080630. doi: https://doi.org/10.1186/1471-2180-8-110. PubMed PMID: 18590559; PMCID: PMC2491623.
Cited 203x

146. **Bohlin J.*, Skjerve E., **Ussery D. W.**, "Reliability and applications of statistical methods based on oligonucleotide frequencies in bacterial and archaeal genomes", BMC Genomics, (2008); **9**:104. Epub 20080228. doi: https://doi.org/10.1186/1471-2164-9-104. PubMed PMID: 18307761; PMCID: PMC2289816.
Cited 51x

147. **Bohlin J.*, Skjerve E., **Ussery D. W.**, "Investigations of oligonucleotide usage variance within and between prokaryotes", PLoS Computational Biology, (2008); **4**(4):e1000057. Epub 20080418. doi: https://doi.org/10.1371/journal.pcbi.1000057. PubMed PMID: 18421372; PMCID: PMC2289840.
Cited 82x

148. Wassenaar T. M., Gamieldien J., Shatkin J., Luber P., Moyer N., Carpenter T., **Ussery D. W.**, "The importance of virulence prediction and gene networks in microbial risk assessment", Human and Ecological Risk Assessment, (2007); **13**:1-15. doi: https://doi.org/10.1080/10807030701226855.

149. **Willenbrock H.*, **Ussery D. W.**, "Prediction of highly expressed genes in microbes based on chromatin accessibility", BMC Molecular Biology, (2007); **8**:11. Epub 20070213. doi: https://doi.org/10.1186/1471-2199-8-11. PubMed PMID: 17295928; PMCID: PMC1805505.
Cited 24x

150. **Willenbrock H., *Hallin P. F.*, Wassenaar T. M., **Ussery D. W.**, "Characterization of probiotic *Escherichia coli* isolates with a novel pan-genome microarray", Genome Biology, (2007); **8**(12):R267. doi: https://doi.org/10.1186/gb-2007-8-12-r267. PubMed PMID: 18088402; PMCID: PMC2246269.
Cited 117x

151. Pel H. J., de Winde J. H., Archer D. B., Dyer P. S., Hofmann G., Schaap P. J., Turner G., de Vries R. P., Albang R., Albermann K., Andersen M. R., Bendtsen J. D., Benen J. A., van den Berg M., Breestraat S., Caddick M. X., Contreras R., Cornell M., Coutinho P. M., Danchin E. G., Debets A. J., Dekker P., van Dijck P. W., van Dijk A., Dijkhuizen L., Driessen A. J., d'Enfert C., Geysens S., Goosen C., Groot G. S., de Groot P. W., Guillemette T., Henrissat B., Herweijer M., van den Hombergh J. P., van den Hondel C. A., van der Heijden R. T., van der Kaaij R. M., Klis F. M., Kools H. J., Kubicek C. P., van Kuyk P. A., Lauber J., Lu X., van der Maarel M. J., Meulenberg R., Menke H., Mortimer M. A., Nielsen J., Oliver S. G., Olsthoorn M., Pal K., van Peij N. N., Ram A. F., Rinas U., Roubos J. A., Sagt C. M., Schmoll M., Sun J., **Ussery D.**, Varga J., Vervecken W., van de Vondervoort P. J., Wedler H., Wosten H. A., Zeng A. P., van Ooyen A. J., Visser J., Stam H., "Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88", Nature Biotechnology, (2007); **25**(2):221–231. Epub 20070128. doi: https://doi.org/10.1038/nbt1282. PubMed PMID: 17259976. Cited 1430x.

152. Miller W. G., Parker C. T., Rubenfield M., Mendz G. L., Wosten M. M., **Ussery D. W.**, Stolz J. F., *Binnewies T. T., Hallin P. F.*, Wang G., Malek J. A., Rogosin A., Stanker L. H.,

Mandrell R. E., "The complete genome sequence and analysis of the epsilonproteobacterium *Arcobacter butzleri*", PLoS One. (2007); **2**(12):e1358. Epub 20071226. doi: https://doi.org/10.1371/journal.pone.0001358. PubMed PMID: 18159241; PMCID: PMC2147049.
Cited 286x

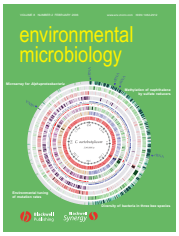
153. Lavin J. L., *Kiil K.*, Resano O., **Ussery D. W.**, Oguiza J. A., "Comparative genomic analysis of two-component regulatory proteins in *Pseudomonas syringae*", BMC Genomics, (2007); **8**:397. Epub 20071031. doi: https://doi.org/10.1186/1471-2164-8-397. PubMed PMID: 17971244; PMCID: PMC2222644.
Cited 43x

154. **Lagesen K.*, **Hallin P.*, Rodland E. A., *Staerfeldt H. H.*, Rognes T., **Ussery D. W.,** "RNAmmer: consistent and rapid annotation of ribosomal RNA genes", Nucleic Acids Research, (2007); **35**(9):3100–3108. Epub 20070422. doi: https://doi.org/10.1093/nar/gkm160. PubMed PMID: 17452365; PMCID: PMC1888812.
Cited 6266x.

155. *Coenye T.*, Drevinek P., Mahenthiralingam E., Shah S. A., Gill R. T., Vandamme P., **Ussery D. W.**, "Identification of putative noncoding RNA genes in the *Burkholderia cenocepacia* J2315 genome", FEMS Microbiology Letters, (2007); **276**(1):83–92. doi: https://doi.org/10.1111/j.1574-6968.2007.00916.x. PubMed PMID: 17937666.
Cited 49x

156. Arvas M., Kivioja T., Mitchell A., Saloheimo M., **Ussery D.**, Penttila M., Oliver S., "Comparison of protein coding gene contents of the fungal phyla *Pezizomycotina* and *Saccharomycotina*", BMC Genomics. (2007); **8**:325. Epub 20070917. doi: https://doi.org/10.1186/1471-2164-8-325. PubMed PMID: 17868481; PMCID: PMC2045113.
Cited 62x

157. *Worning P., Jensen L. J., Hallin P. F., Staerfeldt H. H.*, **Ussery D. W.**, "Origin of replication in circular prokaryotic chromosomes", Environmental Microbiology, (2006); **8**(2):353–361. doi: https://doi.org/10.1111/j.1462-2920.2005.00917.x. PubMed PMID: 164230211.
Cover image.
Cited 138x



158. **Willenbrock H.*, *Petersen A.*, *Sekse C.*, *Kiil K.*, Wasteson Y., **Ussery D. W.**, "Design of a seven-genome *Escherichia coli* microarray for comparative genomic profiling", Journal of Bacteriology, (2006); **188**(22):7713–7721. Epub 20060908. doi: https://doi.org/10.1128/JB.01043-06. PubMed PMID: 16963574; PMCID: PMC1636325.
Cited 37x

159. Read T., **Ussery D. W.**, "Opening the pan-genomics box", Current Opinion in Microbiology, (2006); **9**:496-498. doi: https://doi.org/10.1016/j.mib.2006.08.010.

Cited 30x

160.*Willenbrock H., *Friis C.,* Juncker A. S.*, **Ussery D. W.**, "An environmental signature for 323 microbial genomes based on codon adaptation indices", Genome Biology, (2006); **7**(12):R114. doi: https://doi.org/10.1186/gb-2006-7-12-r114. PubMed PMID: 17156429; PMCID: PMC1794427.
Cited 78x

161. **Ussery D. W.**, "Leaner and meaner genomes in *Escherichia coli*", Genome Biology, (2006); **7**(10):237. Epub 20061024. doi: https://doi.org/10.1186/gb-2006-7-10-237. PubMed PMID: 17076878; PMCID: PMC1794563.

162. Stanke F., Becker T., Cuppens H., Kumar V., Cassiman J. J., Jansen S., Radojkovic D., Siebert B., Yarden J., **Ussery D. W.**, Wienker T. F., Tummler B., "The TNFalpha receptor TNFRSF1A and genes encoding the amiloride-sensitive sodium channel ENaC as modulators in cystic fibrosis", Human Genetics, (2006); **119**(3):331–343. Epub 20060204. doi: https://doi.org/10.1007/s00439-006-0140-2. PubMed PMID: 16463024.
Cited 61x

163. Reen F. J., Almagro-Moreno S., **Ussery D.**, Boyd E. F., "The genomic code: inferring *Vibrionaceae* niche specialization", Nature Reviews Microbiology, (2006); **4**(9):697–704. Epub 20060807. doi: https://doi.org/10.1038/nrmicro1476. PubMed PMID: 16894340.
Cited 177x

164. *Champ P. C., *Binnewies T. T.*, Nielsen N., *Zinman G., *Kiil K., *Wu H., *Bohlin J.*, **Ussery D. W.**, "Genome update: purine strand bias in 280 bacterial genomes", Microbiology (Reading). (2006); **152**(Pt 3):579–583. doi: https://doi.org/10.1099/mic.0.28637-0. PubMed PMID: 16514138.

165.*Binnewies T. T.*, Motro Y., *Hallin P. F.*, Lund O., Dunn D., La T., Hampson D. J., Bellgard M., Wassenaar T. M., **Ussery D. W.**, "Ten years of bacterial genome sequencing: comparative-genomics-based discoveries", Functional & Integrative Genomics, (2006); **6**(3):165–185. Epub 20060512. doi: https://doi.org/10.1007/s10142-006-0027-2. PubMed PMID: 16773396.
Cited 270x

166. *Bendtsen J. D., *Binnewies T. T., *Hallin P. F.*, Sicheritz-Ponten T., **Ussery D. W.**, "Genome update: prediction of secreted proteins in 225 bacterial proteomes", Microbiology (Reading); (2005) **151**(Pt 6):1725–1727. doi: https://doi.org/10.1099/mic.0.28029-0. PubMed PMID: 15941981.
Cited 12x

167. *Willenbrock H., *Binnewies T. T., *Hallin P. F.*, **Ussery D. W.**, "Genome update: 2D clustering of bacterial genomes", Microbiology (Reading), (2005); **151**(Pt 2):333–336. doi: https://doi.org/10.1099/mic.0.27811-0. PubMed PMID: 15699184.

168. **Ussery D. W.**, *de Lichtenberg U., Jensen L. J.*, "Crystal ball. Systems biology: in the broadest sense of the word", Environmental Microbiology, (2005); **7**(4):482–483. doi: https://doi.org/10.1111/j.1462-2920.2005.803_12.x. PubMed PMID: 15816924.

169. Oguiza J. A., **Kiil K.*, **Ussery D. W.**, "Extracytoplasmic function sigma factors in *Pseudomonas syringae*", Trends Microbiology, (2005); **13**(12):565–568. Epub 20051028. doi: https://doi.org/10.1016/j.tim.2005.10.005. PubMed PMID: 16257528.
Cited 32x

170. **Kill K.*, **Binnewies T. T.*, Sicheritz-Ponten T., **Willenbrock H.*, **Hallin P. F.*, Wassenaar T. M., **Ussery D. W.**, "Genome update: sigma factors in 240 bacterial genomes", Microbiology (Reading), (2005); **151**(Pt 10):3147–3150. doi: https://doi.org/10.1099/mic.0.28339-0. PubMed PMID: 1620789.
Cited 46x

171. **Kiil K.*, Ferchaud J. B., David C., **Binnewies T. T.*, **Wu H.*, Sicheritz-Ponten T., **Willenbrock H.*, **Ussery D. W.**, "Genome update: distribution of two-component transduction systems in 250 bacterial genomes", Microbiology (Reading), (2005); **151**(Pt 11):3447–3452. doi: https://doi.org/10.1099/mic.0.28423-0. PubMed PMID: 16272367.
Cited 36x

172. **Hallin P. F.*, Nielsen N., Devine K. M., **Binnewies T. T.*, **Willenbrock H.*, **Ussery D. W.**, "Genome update: base skews in 200+ bacterial chromosomes", Microbiology (Reading), (2005); **151**(Pt 3):633–637. doi: https://doi.org/10.1099/mic.0.27889-0. PubMed PMID: 15758208.

173. **Binnewies T. T.*, **Hallin P. F.*, **Staerfeldt H. H.*, **Ussery D. W.**, "Genome Update: proteome comparisons", Microbiology (Reading), (2005); **151**(Pt 1):1–4. doi: https://doi.org/10.1099/mic.0.27760-0. PubMed PMID: 15632419.
Cited 32x

174. **Binnewies T. T.*, **Bendtsen J. D.*, **Hallin P. F.*, Nielsen N., Wassenaar T. M., Pedersen M. B., Klemm P., **Ussery D. W.**, "Genome Update: Protein secretion systems in 225 bacterial genomes", Microbiology (Reading), (2005); **151**(Pt 4):1013–1016. doi: https://doi.org/10.1099/mic.0.27966-0. PubMed PMID: 15817770.

175. **Bendtsen J. D.*, **Binnewies T. T.*, **Hallin P. F.*, **Ussery D. W.**, "Genome update: prediction of membrane proteins in prokaryotic genomes", Microbiology (Reading), (2005); **151**(Pt 7):2119–2121. doi: https://doi.org/10.1099/mic.0.28181-0. PubMed PMID: 16000701.

176. **Willenbrock H.*, **Ussery D. W.**, "Chromatin architecture and gene expression in *Escherichia coli*, Genome Biology, (2004); **5**(12):252. Epub 20041201. doi: https://doi.org/10.1186/gb-2004-5-12-252. PubMed PMID: 15575978; PMCID: PMC545790.
Cited 60x

177. **Ussery D. W.**, Tindbaek N., **Hallin P. F.*, "Genome update: promoter profiles", Microbiology (Reading), (2004); **150**(Pt 9):2791–2793. doi: https://doi.org/10.1099/mic.0.27504-0. PubMed PMID: 15347738.

178. **Ussery D. W.**, Jensen M. S., Poulsen T. R., **Hallin P. F.*, "Genome update: alignment of bacterial chromosomes", Microbiology (Reading), (2004); **150**(Pt 8):2491–2493. doi: https://doi.org/10.1099/mic.0.27416-0. PubMed PMID: 15289544.

179. **Ussery D. W.**, **Hallin P. F., *Lagesen K.*, Wassenaar T. M., "Genome update: tRNAs in sequenced microbial genomes", Microbiology (Reading). (2004); **150**(Pt 6):1603–1606. doi: https://doi.org/10.1099/mic.0.27260-0. PubMed PMID: 15184546.

180. **Ussery D. W.**, **Hallin P. F., *Lagesen K., *Coenye T.*, "Genome update: rRNAs in sequenced microbial genomes", Microbiology (Reading). (2004); **150**(Pt 5):1113–1115. doi: https://doi.org/10.1099/mic.0.27173-0. PubMed PMID: 15133066.

181. **Ussery D. W.**, **Hallin P. F.*, "Genome update: Length distributions of sequenced prokaryotic genomes", Microbiology (Reading). (2004); **150**(Pt 3):513–516. doi: https://doi.org/10.1099/mic.0.27032-0. PubMed PMID: 14993295.
Cited 19x

182. **Ussery D. W.**, **Hallin P. F.*, "Genome Update: AT content in sequenced prokaryotic genomes", Microbiology (Reading). (2004); **150**(Pt 4):749–752. doi: https://doi.org/10.1099/mic.0.27103-0. PubMed PMID: 15073284.
Cited 22x

183. **Ussery D. W.**, **Hallin P. F.*, "Genome Update: annotation quality in sequenced microbial genomes", Microbiology (Reading). (2004); **150**(Pt 7):2015–2017. doi: https://doi.org/10.1099/mic.0.27338-0. PubMed PMID: 15256543.
Cited 33x

184. **Ussery D. W.**, **Binnewies T. T., Gouveia-Oliveira R., Jarmer H., *Hallin P. F.*, "Genome update: DNA repeats in bacterial genomes", Microbiology (Reading), (2004); **150**(Pt 11):3519–3521. doi: https://doi.org/10.1099/mic.0.27628-0. PubMed PMID: 15528640.
Cited 41x

185. **Ussery D. W.**, "Genome update: 161 prokaryotic genomes sequenced, and counting", Microbiology (Reading), (2004); **150**(Pt 2):261–263. doi: https://doi.org/10.1099/mic.0.26984-0. PubMed PMID: 14766901.

186. Nosek J., Novotna M., Hlavatovicova Z., **Ussery D. W.**, Fajkus J., Tomaska L., "Complete DNA sequence of the linear mitochondrial genome of the pathogenic yeast *Candida parapsilosis*", Molecular Genetics and Genomics, (2004); **272**(2):173–180. Epub 20040729. doi: https://doi.org/10.1007/s00438-004-1046-0. PubMed PMID: 15449175.

187. Hardy K. J., **Ussery D. W**., Oppenheim B. A., Hawkey P. M., "Distribution and characterization of staphylococcal interspersed repeat units (SIRUs) and potential use for strain differentiation", Microbiology (Reading). (2004); **150**(Pt 12):4045–4052. doi: https://doi.org/10.1099/mic.0.27413-0. PubMed PMID: 15583157.
Cited 60x

188. **Hallin P. F.*, **Ussery D. W**., "CBS Genome Atlas Database: a dynamic storage for bioinformatic results and sequence data", Bioinformatics, (2004); 20(18):3682–3686. Epub 20040715. doi: https://doi.org/10.1093/bioinformatics/bth423. PubMed PMID: 15256401.
Cited 117x

189. **Hallin P. F., *Coenye T., *Binnewies T. T., Jarmer H., *Staerfeldt H. H.*, **Ussery D. W**., "Genome update: correlation of bacterial genomic properties", Microbiology (Reading). (2004); **150**(Pt 12):3899–3903. doi: https://doi.org/10.1099/mic.0.27720-0. PubMed PMID: 15583141.

190. **Hallin P. F., *Binnewies T. T.*, **Ussery D. W**., "Genome update: chromosome atlases", Microbiology (Reading). (2004); **150**(Pt 10):3091–3093. doi: https://doi.org/10.1099/mic.0.27582-0. PubMed PMID: 15470087.

191. Barnard F. M., Loughlin M. F., Fainberg H. P., Messenger M. P., **Ussery D. W**., Williams P., Jenks P. J., "Global regulation of virulence and the stress response by CsrA in the highly adapted human gastric pathogen *Helicobacter pylori*", Molecular Microbiology, (2004); **51**(1):15–32. doi: https://doi.org/10.1046/j.1365-2958.2003.03788.x. PubMed PMID: 14651608.
Cited 157x

192. Tu ZC., Ussery D. W., Pride D. T., Blaser M. J., "Genomic Characteristics of the *Campylobacter fetus* sap island", Genome Letters, (2003); **2**:34-40. doi: https://doi.org/10.1166/gl.2003.000.

193.**van Noort V., *Worning P.*, **Ussery D. W.**, Rosche W. A., Sinden R. R., "Strand misalignments lead to quasipalindrome correction", Trends in Genetics, (2003); **19**(7):365–369. doi: https://doi.org/10.1016/s0168-9525(03)00136-7. PubMed PMID: 12850440.
Cited 38x

194. **Petersen L.*, Larsen T. S., **Ussery D. W**., On S. L., Krogh A., "RpoD promoters in *Campylobacter jejuni* exhibit a strong periodic signal instead of a -35 box", Journal of Molecular Biology, (2003); **326**(5):1361–1372. doi: https://doi.org/10.1016/s0022-2836(03)00034-2. PubMed PMID: 12595250.

195. Molbak L., Tett A., **Ussery D. W**., Wall K., Turner S., Bailey M., Field D., "The plasmid genome database", Microbiology (Reading), (2003); **149**(Pt 11):3043–3045. doi: https://

doi.org/10.1099/mic.0.C0123-0. PubMed PMID: 14600215.
Cited 27x

196. Langkjaer R. B., Casaregola S., **Ussery D. W.**, Gaillardin C., Piskur J., "Sequence analysis of three mitochondrial DNA molecules reveals interesting differences among *Saccharomyces* yeasts", Nucleic Acids Research, (2003); **31**(12):3081–3091. doi: https://doi.org/10.1093/nar/gkg423. PubMed PMID: 12799436; PMCID: PMC162263.
Cited 49x

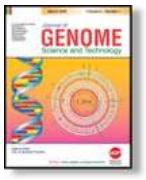
197. **Jensen L. J.*, **Ussery D. W.**, Brunak S., "Functionality of system components: conservation of protein function in protein feature space", Genome Research, (2003); **13**(11):2444–2449. Epub 20031014. doi: https://doi.org/10.1101/gr.1190803. PubMed PMID: 14559779; PMCID: PMC403763.
Cited 59x

198. **Jensen L. J.*, **Skovgaard M.*, Sicheritz-Ponten T., Jorgensen M. K., Lundegaard C., Pedersen C. C., Petersen N., **Ussery D**., "Analysis of two large functionally uncharacterized regions in the *Methanopyrus kandleri* AV19 genome", BMC Genomics, (2003); **4**(1):12. Epub 20030402. doi: https://doi.org/10.1186/1471-2164-4-12. PubMed PMID: 12697059; PMCID: PMC156604.
Cited 12x

199. Cases I., **Ussery D. W.**, de Lorenzo V., "The sigma54 regulon (sigmulon) of *Pseudomonas putida*", Environmental Microbiology, (2003); **5**(12):1281–1293. doi: https://doi.org/10.1111/j.1462-2920.2003.00528.x. PubMed PMID: 14641574.
Cited 102x

200. Weinel C., **Ussery D. W.**, Ohlson H., Sicheritz-Ponten T., Kiewitz C., Tümmler B., "Comparative Genomics of *Pseudomonas aeruginosa* PAO1 and *Pseudomonas putida* KT2440: Orthologs, Codon Usage, REP Elements, and Oligonucleotide Motif Signatures", Genome Letters, **1**:365-369, (2002). doi: https://doi.org/10.1166/gl.2002.021.
Cited 16x

201. Petersen L., On S.L.W., **Ussery D.**, "Visualisation and Significance of DNA Structural Motifs in the Campylobacter jejuni genome", Genome Letters, 1:16-25, (2002). doi: https://doi.org/10.1166/gl.2002.004.
Cover image.
Cited 103x



202.Wood V., Gwilliam R., Rajandream M. A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E. J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L.,

Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M. A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R. G., Tivey A., Walsh S., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S., Gabel C., Fuchs M., Dusterhoft A., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T. M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S. M., Lucas M., Rochet M., Gaillardin C., Tallada V. A., Garzon A., Thode G., Daga R. R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J. L., Moreno S., Armstrong J., Forsburg S. L., Cerutti L., Lowe T., McCombie W. R., Paulsen I., Potashkin J., Shpakovski G. V., **Ussery D.**, Barrell B. G., Nurse P., "The genome sequence of *Schizosaccharomyces pombe*", Nature, (2002); **415**(6874):871–880. doi: https://doi.org/10.1038/nature724. PubMed PMID: 11859360.
Cited 2223x.

203. **Ussery D.**, Soumpasis D. M., Brunak S., **Staerfeldt H. H., *Worning P.*, Krogh A., "Bias of purine stretches in sequenced chromosomes", Computers & Chemistry, (2002); **26**(5):531–541. doi: https://doi.org/10.1016/s0097-8485(02)00013-x. PubMed PMID: 12144181.
Cited 39x

204. Schembri M. A., **Ussery D. W.**, Workman C., Hasman H., Klemm P., "DNA microarray analysis of fim mutations in *Escherichia coli*", Molecular Genetics and Genomics, (2002); **267**(6):721–729. Epub 20020621. doi: https://doi.org/10.1007/s00438-002-0705-2. PubMed PMID: 12207220.
Cited 67x

205. Phylactides M., Rowntree R., Nuthall H., **Ussery D.**, Wheeler A., Harris A., "Evaluation of potential regulatory elements identified as DNase I hypersensitive sites in the CFTR gene", European Journal of Biochemistry, (2002); **269**(2):553–559. doi: https://doi.org/10.1046/j.0014-2956.2001.02679.x. PubMed PMID: 11856314.
Cited 39x

206. Petersen R. F., Langkjaer R. B., Hvidtfeldt J., Gartner J., Palmen W., **Ussery D. W.**, Piskur J., "Inheritance and organisation of the mitochondrial genome differ between two *Saccharomyces* yeasts", Journal of Molecular Biology, (2002); **318**(3):627–636. doi: https://doi.org/10.1016/S0022-2836(02)00037-2. PubMed PMID: 12054811.
Cited 53x

207. Amar P., Ballet P., Barlovatz-Meimon G., Benecke A., Bernot G., Bouligand Y., Bourguine P., Delaplace F., Delosme J. M., Demarty M., Fishov I., Fourmentin-Guilbert J., Fralick J., Giavitto J. L., Gleyse B., Godin C., Incitti R., Kepes F., Lange C., Le Sceller L., Loutellier C., Michel O., Molina F., Monnier C., Natowicz R., Norris V., Orange N., Pollard H., Raine D., Ripoll C., Rouviere-Yaniv J., Saier M., Jr., Soler P., Tambourin P., Thellier M.,

Tracqui P., **Ussery D.**, Vincent J. C., Vannier J. P., Wiggins P., Zemirline A., "Hyperstructures, genome analysis and I-cells", Acta Biotheoretica, (2002); **50**(4):357–373. doi: https://doi.org/10.1023/a:1022629004589. PubMed PMID: 12675536.

208. **Ussery D.**, *Larsen T. S., *Wilkes K. T., *Friis C., *Worning P.*, Krogh A., Brunak S., "Genome organisation and chromatin structure in *Escherichia coli*", Biochimie, (2001); **83**(2):201–212. doi: https://doi.org/10.1016/s0300-9084(00)01225-6. PubMed PMID: 11278070.
Cover image.
Cited 109x

209. *Skovgaard M., *Jensen L. J.*, Brunak S., **Ussery D.**, Krogh A., "On the total number of genes and their length distribution in complete microbial genomes", Trends in Genetics, (2001); **17**(8):425–428. doi: https://doi.org/10.1016/s0168-9525(01)02372-1. PubMed PMID: 11485798.
Cited 254x

210. *Worning P., *Jensen L. J.*, Nelson K. E., Brunak S., **Ussery D. W.**, "Structural analysis of DNA sequence: evidence for lateral gene transfer in *Thermotoga maritima*", Nucleic Acids Research, (2000); **28**(3):706–709. doi: https://doi.org/10.1093/nar/28.3.706. PubMed PMID: 10637321; PMCID: PMC102551.
Cited 112x

211. Thornhill R. H., **Ussery D. W.**, "A classification of possible routes of Darwinian evolution", J Theor Biol. (2000); **203**(2):111–116. doi: https://doi.org/10.1006/jtbi.2000.1070. PubMed PMID: 10704296.
Cited 65x

212. *Pedersen A. G., *Jensen L. J.*, Brunak S., *Staerfeldt H. H.*, **Ussery D. W.**, "A DNA structural atlas for *Escherichia coli*", Journal of Molecular Biology, (2000); **299**(4):907–930. doi: https://doi.org/10.1006/jmbi.2000.3787. PubMed PMID: 10843847.
Cover image.
Cited 273x

213. *Friis C., *Jensen L. J.*, **Ussery D. W.**, "Visualization of pathogenicity regions in bacteria", Genetica, (2000); **108**(1):47–51. doi: https://doi.org/10.1023/a:1004091626474. PubMed PMID: 11145420.
Cited 14x

214. **Ussery D. W.**, Higgins C. F., Bolshoy A., "Environmental influences on DNA curvature", Journal of Biomolecular Structure and Dynamics, (1999); **16**(4):811–823. doi: https://doi.org/10.1080/07391102.1999.10508294. PubMed PMID: 10217451.
Cited 39x

215. **Jensen L. J., *Friis C.*, **Ussery D. W.**, "Three views of microbial genomes", Research in Microbiology, (1999); **150**(9-10):773–777. doi: https://doi.org/10.1016/s0923-2508(99)00116-3. PubMed PMID: 10673014.
Cover image.
Cited 102x

216. Jordi B. J., Fielder A. E., Burns C. M., Hinton J. C., Dover N., **Ussery D. W.**, Higgins C. F., "DNA binding is not sufficient for H-NS-mediated repression of proU expression", Journal of Biological Chemistry, (1997); **272**(18):12083–12090. doi: https://doi.org/10.1074/jbc.272.18.12083. PubMed PMID: 9115277.
Cited 78x

217. Potaman V. N., **Ussery D. W.**, Sinden R. R., "Formation of a combined H-DNA/open TATA box structure in the promoter sequence of the human Na,K-ATPase alpha2 gene", Journal of Biological Chemistry, (1996); **271**(23):13441–13447. doi: https://doi.org/10.1074/jbc.271.23.13441. PubMed PMID: 8662935.
Cited 33x

218. **Ussery D. W.**, Hinton J. C., Jordi B. J., Granum P. E., Seirafi A., Stephen R. J., Tupper A. E., Berridge G., Sidebotham J. M., Higgins C. F., "The chromatin-associated protein H-NS", Biochimie, (1994); **76**(10-11):968–980. doi: https://doi.org/10.1016/0300-9084(94)90022-1. PubMed PMID: 7748941.
Cited 146x

219. Tupper A. E., Owen-Hughes T. A., **Ussery D. W.**, Santos D. S., Ferguson D. J., Sidebotham J. M., Hinton J. C., Higgins C. F., "The chromatin-associated protein H-NS alters DNA topology *in vitro*", The EMBO Journal, (1994); **13**(1):258–268. doi: https://doi.org/10.1002/j.1460-2075.1994.tb06256.x. PubMed PMID: 8306968; PMCID: PMC394800.
Cited 279x

220. **Ussery D. W.**, Sinden R. R., "Environmental influences on the *in vivo* level of intramolecular triplex DNA in *Escherichia coli*", Biochemistry, (1993); **32**(24):6206–6213. doi: https://doi.org/10.1021/bi00075a013. PubMed PMID: 8512930.
Cited 49x

221. **Ussery D. W.**, Hoepfner R. W., Sinden R. R., "Probing DNA structure with psoralen *in vitro*", Methods in Enzymology, (1992); **212**:242–262. doi: https://doi.org/10.1016/0076-6879(92)12015-i. PubMed PMID: 1325599.
Cited 38x

222. Sinden R. R., **Ussery D. W.**, "Analysis of DNA structure in vivo using psoralen photobinding: measurement of supercoiling, topological domains, and DNA-protein interactions", Methods in Enzymology, (1992); **212**:319–335. doi: https://doi.org/

10.1016/0076-6879(92)12020-q. PubMed PMID: 1518453.
Cited 32x

223. Zheng G., **Ussery D. W.**, Sinden R. R., "Estimation of superhelical density *in vivo* from analysis of the level of cruciforms existing in living cells", Journal of Molecular Biology, (1991); **221**(1):122–129. doi: https://doi.org/10.1016/0022-2836(91)80209-D. PubMed PMID: 1920400.

224. Katz J. E., Wells S., **Ussery D.,** Bustamante C., Maestre M. F., "Design and construction of a circular intensity differential scattering instrument". Reviews of Scientific Instruments, (1984); **55**(10):1574-1579. https://doi.org/10.1063/1.1137612.

13. REFEREED CONFERENCE PUBLICATIONS

REFEREED CONFERENCE PUBLICATIONS

225. Oksana Lukjancenko and **David W. Ussery**, (2010). "Design of an Enterobacteriaceae Pan-genome Microarray Chip", In: Computational Systems Biology and Bioinformatics. International Conference on Computational Systems-Biology and Bioinformatics (CSBio 2010), Proceedings. CCIS, **115**:174-189, Springer, Heidelberg (2010). https://doi.org/10.1007/978-3-642-16750-8_15

226. Matloob Qureshi, Eva Rotenberg, Hans-Henrik Stærfeldt, Lena Hansson, and **David W. Ussery**, "The Genome Atlas Resource", In: Computational Systems Biology and Bioinformatics. International Conference on Computational Systems-Biology and Bioinformatics (CSBio 2010), Proceedings. CCIS, **115**: 149-158, Springer, Heidelberg (2010). https://doi.org/10.1007/978-3-642-16750-8_13.

227. **David W. Ussery**, Jakob Bondo, Jimmy Hoffmann Hansen, Paiman Khorsand-Jamal, Anne Egholm Pedersen, Maria Seier Petersen, Pernille Nielsen, Peter Hallin, "A DNA-centric view of *Clostridium* genomes", In: Diagnosis, epidemiology and antibiotic resistance of the genus Clostridium, (Duchesnes C., Mainil J, Pelkonen S. and Menozzi MG, editors), Proceedings of the meeting, Presses de la Faculté de Médecine Vétérinaire de l'Université de Liège, pages 60-66, (2004).

228. David W. Ussery, Clare Harrington, Peter Hallin, and Stephen On, "Comparative Genomics of Five epsilon-Protobacterial Genomes", Proceedings of the 13th Annual Conference on Campylobacter, Helicobacter, and Related Organisms (2003).

14. PRESENTATIONS

Oral Presentations at OSU **July, 2025 - present**

1. "When Names Lie: Taxonomic Turbulence and Pangenome Diversity in the Enterobacteriaceae", talk for the **One Health Pangenome25** conference: THE MICROBIAL PANGENOME IN ONE HEALTH, Valencia, Spain 🇪🇸, 4 December, 2025
2. "INTERACT: Past, Present, and Future", talk for the **2025 INTERACT symposium**, Stillwater, Oklahoma, 23 October, 2025
3. "A Genomic Epidemiology Approach to One-Health", opening talk for the "Integrative Approaches to Zoonotic and Environmental Disease Control: Focus on Rural Communities" session for the **2025 INTERACT symposium**, Stillwater, Oklahoma, 23 October, 2025
4. "HIDDEN PATTERNS IN PROTEINS: How Pfam Domains Uncover Function Beyond BLAST", talk for the Bioinformatics workshop for the **2025 INTERACT symposium**, 22 October, 2025
5. "BIG PROBLEMS & BIG DATA IN BIOLOGY: Genomics and the Flow of Biological Information", talk for the **second discussion group on the future of Computational Biology at Oklahoma State University**, Room 130K of the HBRC building, 11 August, 2025
6. "THE MUSIC OF LIFE: Genomics and the Flow of Biological Information", Talk for the **Stowers Institute for Medical Research**, Kansas City, Missouri, on 9 July, 2025

Oral Presentations before joining OSU in 2025 (talks in 23 countries, 5 continents) **1998 - 2025**

1. "The Music of Life: An Introduction to Bioinformatics", Talk for **West Virginia University Cancer Institute;** Wednesday, 16 April, 2025
2. "Benchmarking High-throughput computing of viral genomes", talk for the **Third OAK Supercomputing Conference**, Wichita, Kansas 23 May, 2024
3. "Using Chat-GPT in teaching bioinformatics", talk for the **ARA "Project Scope" Seminar Series** 29 May, 2024
4. "Using Chat-GPT in teaching bioinformatics", invited talk for the first session of the **Artificial Intelligence Monthly Teleconference Series**, 4 April, 2024
5. "What Can We Learn from a Million Salmonella Genomes?", talk for the **2023 OAK Supercomputing Fall Conference** Little Rock, Arkansas 25 October, 2023
6. "Genomic Epidemiology of *E. coli*", invited talk for the **Donaghey College of Science, Technology, Engineering, and Mathematics Colloquium Series**, University of Arkansas at Little Rock, 8 September, 2023.
7. "Big Data Management: Examples from the Data Curation & Life Cycle thrust", talk for the **Arkansas NSF EPSCoR grant site visit** (RII Track-1: Data Analytics that are Robust and Trusted (DART); NSF "reverse site visit", Little Rock, Arkansas, 18 September, 2023.

8. "Who's Afraid of the Monkeypox virus?", invited talk for the **30th International Point-of-Care Diagnostics for Global Health & Biodefense** virtual conference, 8 June, 2023

9. "Big Data in Genomic Research for Big Questions, with Examples from COVID-19 and Other Zoonoses", **1rst Oak Supercomputing Conference**, Stillwater, Oklahoma, 6 April, 2023

10. "Microbiome changes with age", **23rd Annual UAMS Geriatrics and Long-Term Care Conference**; 15 September, 2022

11. "When Boring is Good: Limited Mutational Repertoire across millions of SARS-CoV-2 genomes", invited talk for the **29th International Biodetection Technologies Meeting**, virtual conference, 29 June, 2022

12. "Population Genomics of *E. coli*", talk for **Metagenomics Forum, Evolutionary Genomics Group, Universidad Miguel Hernandez, Alincante, Spain** 🇪🇸; 20 January, 2022

13. "What can we learn from 4.2 million Covid-19 genomes?", **13th International Conference on Information Technology and Electrical Engineering (ICITEE 2021)**, Bangkok, Thailand 🇹🇭, 14 October, 2021

14. "An Introduction to the Human Gut Microbiome, and how it changes with age", talk for the **UAMS Geriatrics and Long-Term Care Conference**; Little Rock, Arkansas, Thursday, 16 September, 2021

15. "When Boring is Good: Limited Mutational Repertoire across millions of SARS-CoV-2 genomes", invited talk for the **28th International Biodetection Technologies** (Virtual meeting), 18 July, 2021

16. "SARS-CoV-2 "VoC's in Arkansas -or- Stone Soup in Arkansas", Invited **Arkansas Research Alliance Project Scope** talk, 17 February, 2021

17. "Big Data Comes to Biology: Portable Genome Sequencing", workshop at the **Little Rock TechFest**, 10 October, 2019; Little Rock, Arkansas, USA.

18. "Building Standardized Dendograms for Viruses", invited talk for **National Institute on Standards (NIST) workshop on Standards for Next-Generation Sequence Detection of Viruses** on 19 September, 2019; Gaithersburg, MD, USA.

19. "Real-time, full length genome sequencing of DNA and RNA viruses", talk for **BioDefense World Summit**, on 18 June, 2019; Bethesda, Maryland, USA

20. "Rapid Sequencing of RNA and DNA Viromes from Clinical Isolates", talk for **Ouachita Baptist University,** biophysics seminar class, OBU, on 14 March, 2019, Arkansas, USA.

21. "Big Data from Clinical Genome Sequencing", talk at the **2018 AAHC Research Meeting, with the theme "Big Data Advances in Biomedical Science"**, 29 November, 2018, at the Liaison Capitol Hill Hotel in Washington, DC., USA.

22. "High-throughput comparison of genomes", talk at **St. Louis University**, St. Louis, Missouri, USA (19 September, 2018).

23. chaired opening session at "BioDefense 2018" on "**BIODETECTION TECHNOLOGIES: BIOTHREAT AND PATHOGEN DETECTION**"; gave talk on "Rapid Sequencing of RNA and DNA Viromes", Bethesda, Maryland, USA, 27 June, 2018

24. "What can Genome Quality Scores for a hundred thousand bacterial genomes tell us about standards for metagenomics?", invited talk for **2017 SIMB Annual Meeting and Exhibition**, Tuesday, 1 August, 2017, Denver, Colorado, USA.

25. chaired morning session and gave talk at the **AR-BIC conferenc**e, in Little Rock (on 21 April, 2017). "What is Life? Five-hundred Functional Domains found in all genomes across the Tree of Life", Little Rock, Arkansas, USA.

26. Lectures for **INBRE workshop** on comparative genomics, for high-school and university undergraduates and graduate students, on 19-21 March, 2017, UAMS, Little Rock, Arkansas, USA.

27. Lectures for Comparative Genomics course workshop on 22 and 23 February, 2017, at the **University of Tennessee Medical School**, in Memphis, Tennessee, USA, on using 3rd generation sequencing technology for sequencing viral genomes.

28. "What is Life? Conserved Protein Functional Domains across 100,000 Bacterial Genomes", Seminar for **UAMS Dept. Pharmacology & Toxicology,** UAMS, Little Rock, Arkansas, USA, 2 November, 2016.

29. "What is Bioinformatics? Sequences as information", invited talk at the **Arkansas Life Science Summit**, Conway, Arkansas, USA, 19 October, 2016.

30. "Microbial Communities - What can high-throughput genomics teach us about evolution?", invited lecture for **Department of BioMedical Informatics Research & Application Seminar Series**, University of Arkansas for Medical Sciences, Little Rock, Arkansas, USA, 15 September, 2016

31. "Microbial Communities - Bacterial Pan- and Core-Genomes", invited lecture on **Comparative Genomics, SiMPC Conference**, Sirirai Hospital, Mahidol University, Bangkok, Thailand 🇹🇭, 23 August, 2016.

32. "Third Generation Sequencing for Rapid Biosurviellence", invited talk at the **BioDefense World Summit**, Baltimore, Maryland, USA, 30 June, 2016.

33. "Zika virus comparative genomics", talk at **National Center for Toxicology Research (NCTR)**, Pine Bluff, Arkansas, USA, 24 June, 2016.

34. "Who Are We? Defining Microbial Ecosystems", invited talk **DTRA [Defense Threat Reduction Agency]**, Washington, D.C., USA, 4 May, 2016.

35. "Roughly 500 functional domains conserved in 70,000 bacterial genomes", lecture at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway 🇳🇴, 22 April, 2016.

36. "Microbial Communities: Bacterial Pan- and Core-genomes", lecture at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway 🇳🇴, 21 April, 2016.

37. "Comparative Genomics: Introduction to DNA Atlases", lecture at **St. Olav's Hospital, The Norwegian Technical University (NTNU),** Trondheim, Norway 🇳🇴, 20 April, 2016.

38. "Genome Quality Scores", lecture at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway 🇳🇴, 19 April, 2016.

39. "Third Generation Sequencing for Rapid Biosurviellence", lecture at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway 🇳🇴, 18 April, 2016.

40. "Introduction to Microbial Genomics - Alignments", Lecture at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway 🇳🇴, 17 April, 2016.

41. "Genome-Based taxonomy of *Vibrios*", Guest lecture for 'Compuational -omics' course at **University of Tennessee**, Knoxville, USA, 18 February, 2015.

42. "Comparative Genomics: Introduction to DNA Atlases", Guest lecture at **The University of Tennessee,** Knoxville, USA, 2 September, 2015.

43. "Introduction to Genomics: Sequences as Biological Information", Guest lecture for **Science and Faith workshop**, Gordon College, USA, 17 June, 2015.

44. "Regulation of Gene Expression in Bacterial Genomes", Guest professor talk at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway, 19 May, 2015.

45. "Genome Sequences for Rapid Biosurviellence", Guest professor talk at **St. Olav's Hospital, The Norwegian Technical University (NTNU)**, Trondheim, Norway 🇳🇴, 20 November, 2014.

46. "Third Generation Sequencing for Rapid Biosurviellence", Keynote talk for the **CoZEE Zoonoses Network Autumn Conference** on "The role of high-throughput sequencing in surveillance, diagnostics and tracking zoonotic bacteria", Dundee, Scotland 🏴, 11 November, 2014.

47. "Defining *Pseudomonas* species - with special emphasis on the *Pseudomonas fluorescens* clade", talk for the **Plant Microbe Interfaces group, Oak Ridge National Labs,** Oak Ridge, Tennessee, USA, 10 September, 2014.

48. "*Ruminiclostridium thermocellu*m genomics", lecture at **Dartmouth College**, New Hampshire, USA, 31 July, 2014.

49. "Sequences as Biological Information", set of three lectures in course "Science and Faith: A Course for Pastors", held at **Gordon College, Boston, MA**, USA, 28-30 July, 2014.

50. "Comparative Genomics", 3-week course taught at DTU, in the Center for Biological Sequence Analysis, Department of Systems Biology, The Technical University of Denmark 🇩🇰, 4-26 June, 2014.

51. "Using Genomes to Estimate Community Structures", talk for the **Plant Microbe Interfaces group, Oak Ridge National Labs, Oak Ridge**, Tennessee, USA, 28 May, 2014.

52. "Detecting and Identifying New Outbreaks during Real-time Monitoring with 3rd Generation Genomic Sequencing", invited talk for **the head of U.S. Biosurviellence Program**, at the Pentagon, Washington, D.C., USA, 9 May, 2014.

53. "Comparative Genomics -or- 'Big Data' Comes to Biology", talk for the **BioEnergy Sciences Center group, Oak Ridge National Labs**, Oak Ridge, Tennessee, USA, 1 April, 2014.

54. "Sigma Factors across a Thousand *E. coli* genomes", invited talk for the **University of Cincinnati, College of Medicine**, Cincinnati, Ohio, USA, 27 November, 2013.

55. "OTUs - Can we do better than 16S rRNA?", talk for the **Plant Microbe Interfaces group, Oak Ridge National Labs**, Oak Ridge, Tennessee, USA, 6 November, 2013.

56. "Towards an Integrated Systems Biology for BESC", group talk for the **BioEnergy Center, Oak Ridge National Labs**, USA, 5 November, 2013.

57. "Data Management Strategy for BESC", talk for **DOE annual review of the BioEnergy Center, Oak Ridge National Labs,** Oak Ridge, Tennessee, USA, 24 October, 2013.

58. Morning lectures (three days) for the "**Sixth International Course: Computational genomics**", CNSRT, Rabat, Morocco" 🇲🇦, 1-5 April, 2013.

59. Morning lectures (four days) for "Comparative Bacterial Genomics Workshop", held at **Dhulikhel Hospital, Kavrepalanchok District, Nepal** 🇳🇵 , 18-22 March, 2013.

60. "Bacterial Pan- and Core-genomes - A Skeptics View", invited talk for **NCBI Genome Annotation Workshop,** Bethesda, Maryland, USA, 4 March, 2013.

61. "Comparing Thousands of Bacterial Genomes, using high-throughput methods", invited talk at **Oak Ridge National Labs**, Oak Ridge, Tennessee, USA, 21 February, 2013.

62."Reasons to be Skeptical of Big Data", **CBS group talk**, Lyngby Denmark 🇩🇰, 4 February, 2013.

63. "From Genome Sequence to Taxonomy - A Skeptic's View", invited talk for the **University of New Mexico College of Medicine**, Albuquerque, New Mexico, USA, 7 January, 2013.

64. "Methods to Compare Bacterial Genomes, with emphasis on AT content", invited talk for **Los Alamos National Laboratory**, Los Alamos, New Mexico, USA, 4 January, 2013.

65. "Bayesian prediction of bacterial growth temperature range, based on genome sequences", talk for **InCOB2012 meeting, Bangkok**, Thailand 🇹🇭, 4 October, 2012.

66. "CMGenomics.net – Comparison of Microbial Genomes for High-throughput Monitoring and Epidemiology", talk for the **16th Annual PulseNet Update Meeting**, Atlanta, Georgia, USA, 29 August, 2012.

67. "Genome Sequence to Taxonomy: Diversity in the Human Gut Microbiome", talk for the **15th Conf. in Genomics & Proteomics of Human Pathogens**, HPA, Collindale, England 🇬🇧, 22 June, 2012.

68. "Methods to Calculate Bacterial Pan-genomes: Benchmarks, Progress and Pitfalls to Avoid", talk for the **ASM 112th General Meeting**, 18 June, 2012, San Francisco, California, USA.

69. "Comparison of hundreds of *Escherichia coli* genomes", talk for the **5th IECA conference Riviera Maya, Mexico** 🇲🇽, 6 December, 2011

70. "Comparison of 105 Vibrio genomes", talk for the **Vibrio2011 conference, Santiago de Compostela, Spain** 🇪🇸, 3 November, 2011.

71. "Veillonella: Half-way between Gram positives and Gram negatives", talk for the **Norwegian University of Science and Technology (NTNU),** Norway 🇳🇴, April, 2011.

72. "Standardization of Descriptions for Core- and Pan-genomes", talk at the **11th Genomics Standards Consortium,** Wellcome Trust Sanger Center, Cambridge, England 🇬🇧, 5 April, 2011.

73. "An Inordinate Fondness for Bacteria", invited talk at the **BioLogos workshop, Harvard Club, New York City**, USA, 10 November, 2010.

74. "The minimal set of conserved proteins across a thousand bacterial genomes", invited keynote talk at the **First International Conference on Computational Systems-Biology and Bioinformatics (CSBio2010)**, Bangkok, Thailand 🇹🇭, on Friday, 5 November, 2010.

75. "Using REAL Biology (evolution) to Design Synthetic Life", invited talk at the **Exploratory Round Table Conference of 2010 - Synthetic Biology, in Shanghai, China** 🇨🇳, 19 October, 2010.

76. "The core set of conserved proteins in more than a thousand bacterial genomes", invited talk at the **Comparative Genomics and Metagenomics, Impacts on Health and Environment Workshop in Granada, Spain** 🇪🇸, 8 October, 2010.

77. "The minimal set of conserved proteins across a thousand bacterial genomes", invited talk at **IECA Functional Genomics Mini-symposium, Purdue University**, West Lafayette, Indiana, USA, 17 April, 2010.

78. "On the Origins of a *Vibrio* species", invited talk on 10 November, 2009, at **The Biotechnology Centre of Oslo**, Norway 🇳🇴. http://www.biotek.uio.no/news/2009/guestlecture_du.html.

79. "Bacterial pangenomics - or - Using pan-genome microarrays for rapid, high-throughput typing", **talk for course on molecular typing, Hvidovre Hospital,** Denmark 🇩🇰,10 September, 2009.

80. "Comparative Pan-Genomics of *Escherichia coli* (and Friends)", invited talk at **the European Bionformatics Institute (EBI) and Sanger Center, Hinxton, England** 🇬🇧, 27 August, 2009.

81."*Pseudomonas* Pangenomics", invited opening talk for **Pseudomonas 2009 meeting, XII International Conference, in Hannover, Germany** 🇩🇪, 14 August, 2009.

82. "Full genome sequence of *Mycobacterium avium* subsp. paratuberculosis Ejlskov2007", invited talk for **PAF group, Copenhagen, Denmark** 🇩🇰, 18 June, 2009. https://orbit.dtu.dk/en/publications/full-genome-sequence-of-a-danish-isolate-of-mycobacterium-avium-s/

83. "Bacterial Pangenome Microarrays", invited external talk for **MedVetNet WP30** (fifth meeting), Utrecht, The Netherlands 🇳🇱, 7 May, 2009.

84. "Bacterial Comparative Pangenomics", invited talk for the **Joint Centre for Bioinformatics in Oslo**, Norway 🇳🇴, 25 March, 2009.

85. "Bacterial Comparative Pangenomics", invited keynote talk **Microbiology & Molecular Genetics dept., Michigan State University**, USA, 16 March, 2009.

86. "*Burkholderia* Pan-genomics", invited keynote talk at the **Annual Conference of the Association for General and Applied Microbiology (VAAM)**, Bochum, Germany 🇩🇪, 9 March, 2009.

87. "*E. coli* fuzzy pan-genomics -or- How to compare Hundreds of *E. coli* genomes", invited keynote talk at **Ulleval Universitetssykehus, Oslo**, Norway 🇳🇴, 10 December, 2008.

88. "*E. coli* pangenomics - How to compare hundreds of *E. coli* genomes", invited keynote talk at 3rd International *E. coli* Alliance meeting, Cambridge, England 🇬🇧, 24-28 September, 2008.

89. "Discovering natural groups in *Vibrio*", invited talk at **XII International Congress of Bacteriology and Applied Microbiology (IUMS),** section on Prokaryote systematics - is it relevant to modern science?, Istanbul, Turkey 🇹🇷, 8 August, 2008.

90. Morning lectures at the **2nd Workshop on Comparative Microbial Genomics, Bangkok**, Thailand 🇹🇭, 2-6 June, 2008.

91. "*Burkholderia* Pan-genomics", invited talk at the **Max Planck Institut fur Terrestrial Microbiology, Marburg, Germany** 🇩🇪, 26 May, 2008.

92. "On the Origins of Bacterial Species", invited talk at the **Center for Environmental Systems Microbiology, Georgia Tech**, USA, 17 March, 2008.

93. "Introduction to Bacterial PanGenomics", invited talk at **Medizinischen Hochschule Hannover,** Germany 🇩🇪, 30 January, 2008.

94. "Where does *Vibrio cholera* come from?", invited talk at **University of Copenhagen Microbiology dept., Denmark** 🇩🇰, 20 January, 2008.

95. "On the Origins of a Bacterial Species", invited Keynote talk at the **Vibrio2007 meeting, Paris**, France 🇫🇷, 29 November, 2007.

96. "Minimal genomes in bacterial Genera", invited talk at the **European Conference on Synthetic Biology: Design, Programming and Optimisation of Biological Systems**, Hotel Eden Roc, Sant Feliu de Guixols, Spain 🇪🇸, 26 November 2007.

97. "Bacterial PanGenomics", invited talk at the **Florida Institute of Technology**, Melbourne, Florida, USA, 5 November, 2007.

98. "Pangenomics of 'Bioterrorism Bacteria' -or- How to Compare and Analyse Hundreds of Bacterial Genome Sequences from the Same Organism", invited talk for the **BioDefense conference, Medizinische B-Schutz-Tagung, Munich, Germany** 🇩🇪, 17 Oktober, 2007.

99. "Development of an *E. coli* pan-genome microarray", invited talk for **NimbleGen, Reykjavik, Iceland** 🇮🇸, 29 August, 2007.

100. "Evolutionary Fossils in Bacterial Genomes", invited talk for the **Biology Department, Emory University,** USA, 20 August, 2007.

101. "*Campylobacter* Pangenomics", invited talk for **5th Symposium on Food Microbiology**, LO skolen, Helsingør, Denmark 🇩🇰, 23 May, 2007.

102. "Evolutionary Fossils in Bacterial Genomes", invited talk for the **Workshop on Microbial Evolution, held at DTU**, Denmark 🇩🇰, 15 May, 2007.

103. "Sequencing and Analysis of the *Escherichia coli* Oslo O103 strain", invited talk at **NVH, Oslo**, Norway 🇳🇴,15 January, 2007.

104. "Opening the pan-genomics box for *E. coli*", invited talk at the **"Genomics of pathogenic *Escherichia coli*: European and Japanese perspectives" meeting, INRA**, 147 rue de l'Université, Paris, France 🇫🇷, 29 September, 2006.

105. "New -omics approaches and bioinformatics", invited talk at the **"International Specialized Symposium on Yeasts (ISSY25) Systems Biology of Yeasts - From Models to Applications"**, Helsinki, Finland 🇫🇮, 28-21 June, 2006.

106. "Comparison of 20 *E. coli* genomes", invited talk for the **Norwegian National Molecular Microbiology meeting, Oslo**, Norway 🇳🇴, 17 June, 2006.

107. "A Brief History of *Escherichia coli*", invited talk at the **Norwegian Veterinary Hospital, in Oslo**, Norway 🇳🇴, 25 May, 2006.

108. "Comparison of 20 *E. coli* genomes", invited talk at the Stockholm Bioinformatics Center, Sweden 🇸🇪, 17 May, 2006.

109. "10 Years of Sequencing Bacterial Genomes", invited group talk, I**nformatics and Mathematical Modeling, DTU**, Denmark 🇩🇰, 26 April, 2006.

110. "Comparison of Bacterial Genomes", invited talk at **UMB, Ås, Norway** 🇳🇴, 20 April, 2006.

111. "Methods to Compare Bacterial Genomes", invited talk **CMBN, Universitet i Oslo**, Norway 🇳🇴, 29 marts, 2006.

112. "20 Methods to Compare Bacterial Genomes", invited talk at the **European Science Foundation - Japanese Society for the Promotion of Science Workshop on Functional Genomics, Tokyo, Japan** 🇯🇵, 8 March, 2006.

113. "20 Methods to Compare Bacterial Genomes", invited talk at **Trinity College, Dublin, Ireland** 🇮🇪, 24 January, 2006.

114. "*Aspergillus niger* genomic properties", invited talk for the **Workshop for the A. niger Nature Biotech manuscript**, Noordwijkerhout, The Netherlands 🇳🇱, 12 January, 2006.

115. "Structural Atlases of Microbial Genomes", invited talk for the **Nordic Bioinformatics Network Symposium, Stockholm**, Sweden 🇸🇪, 6 December, 2005.

116. "Towards a 'Systems Microbiology' of *Escherichia coli*", invited talk in **Bremen, Germany** 🇩🇪, 21 November, 2005.

117. "10 Methods to Compare Fungal Genomes", invited talk for **EUROFUNGBASE meeting, Sevilla, Spain** 🇪🇸, 17 November, 2005.

118. "YSBN Databases", invited talk for **YSBN Kick-off meeting, Bordeaux, France** 🇫🇷, 11 November, 2005.

119. "Bioinformatic Tools to Compare *Vibrio* Genomes", invited talk for the **Vibrio2005 meeting, Ghent, Belgium** 🇧🇪, 8 November, 2005.

120. "Chromatin structure and gene expression in *Escherichia coli*", invited talk for the **'Geometry of the Genome' meeting**, Leicester University, England 🇬🇧, 23 September, 2005.

121. "The GenomeAtlas Database: 20 Methods to Compare Bacterial Genomes", invited talk for the **eGenomics meeting, Cambridge**, England 🇬🇧, 7 September, 2005.

122. "Systems Microbiology of *Salmonella entericia*", invited talk for **Dept. of Cancer Research and Molecular Medicine, Norwegian University of Science and Technology,** Trondheim, Norway 🇳🇴, 2 June, 2005.

123. "Three Levels of Gene Regulation in Bacterial Genomes ", invited talk for **ESF Workshop on Transcription Networks: A Global View,** Madrid, Spain 🇪🇸, 27 May, 2005.

124. "CBS Microbial Genome Database", invited talk for **Eurofung database project meeting**, Manchester, England 🇬🇧, 23 May, 2005.

125. "Comparative Genomics of Food Pathogens", invited talk for **3rd Symposium on Food Microbiology, Gl. Avernæs, Ebberup, Fyn**, Denmark 🇩🇰, 17 May, 2005.

126. "Towards a systems biology of *Salmonella*", invited talk for **Systems Biology meeting, the University East Anglia, England** 🇬🇧, 6 May, 2005.

127. "Chromatin and Gene Expression in *E. coli* ", invited talk for **The Epigenomics Project, Genopole Evry, France** 🇫🇷, 28 January, 2005.

128. "Prediction of pathogenicity networks in bacterial proteomes", invited talk for **The Norwegian Biochemical Society winter meeting in Tromsø, Norway** 🇳🇴, 15 January, 2005.

129. "DNA Chromatin and Gene Expression", tutorial at **the Norwegian Veterinary Institute, Oslo,** Norway 🇳🇴, 5 December, 2004.

130. "Bioinformatics of Fungal Genomes -or- Bioinformatics of 18 genomes in 18 minutes", invited talk for **Eurofung meeting, Wageningen, The Netherlands** 🇳🇱, 19 November, 2004.

131. "Comparative Genomics of Bacterial Oral Pathogens", invited talk for the **Bioinformatics & Exploiting Genomic Information Oral Microbiology & Immunology Group symposium, Bristol,** England 🇬🇧, 11 November, 2004.

132. "Prediction of pathogenicity networks in bacterial proteomes", invited talk at the **College Veterinary Medicine, Oklahoma State University**, Stillwater, Oklahoma, USA, 21 Oktober, 2004.

133. "Classification of pathogenic proteins in bacterial proteomes", invited talk for **Norsk forening for mikrobiologi Høstmøtet, Oslo**, Norway 🇳🇴, 13 Oktober, 2004.

134. "Prediction of pathogenicity networks in bacterial proteomes", invited talk for **Tierärztliche Hochschule in Hannover**, Germany 🇩🇪, 23 September, 2004.

135. "Comparison of 150 Bacterial Genomes", invited talk for **Rikshospitalet University Hospital, Oslo**, Norway 🇳🇴, 21 June, 2004.

136. "Visualisation of sequenced Yeast Genomes - Or, an introduction to DNA Chromosome Atlases", invited talk for **EUROFUNG workshop, WICC, Wageningen**, The Netherlands 🇳🇱, 25 February, 2004.

137. "Leading strand Oligomer-bias in Bacterial Genomes - Including a discussion of the *Alkanivorax borkumensis* genome", invited talk for **Meeting of the Task Force Genome Linguistics at the Max Planck Institute in Bremen,** Germany 🇩🇪, 16 February, 2004.

138. "Comparative Genomics of five *Clostridium* species", invited talk for workshop on **DIAGNOSIS, EPIDEMIOLOGY AND ANTIBIOTIC RESISTANCE OF THE GENUS *CLOSTRIDIUM***, Parma, Italy 🇮🇹, 17 October, 2003.

139. "Prediction of Highly Expressed Genes in Prokaryotic Genomes - A DNA-centric perspective", invited talk for a special session of the **SGM meeting (Exploiting Genomes: Bases to Megabases in 50 years), University of Manchester**, England 🇬🇧, 8 September, 2003.

140. "DNA Atlases for *Campylobacter, Helicobacter*, and Related Organisms", KEYNOTE opening talk for **CHRO2003 (*Campylobacter, Helicobacter,* and Related Organisms), Aarhus**, Denmark 🇩🇰, 6 September, 2003.

141. "Genome Atlases for the Study of Evolutionary Systems", invited talk for the **European Science Foundation / LESC workshop on Horizontal Gene Transfer, St. Catherine's College, Oxford,** England 🇬🇧, 13 June, 2003.

142. "Visualisation of DNA Structural Information", invited talk for the **Institute of Biosciences and Technology, Texas A & M University, Houston, Texas,** USA,13 June, 2003.

143. "Visualisation of DNA Structural Information in Sequenced Plasmids", invited talk at **CEH-Oxford, Oxford**, England, 28 May, 2003.

144. "DNA Atlases for Visualisation of Positional Information within Bacterial Genomes", invited talk for **5th Annual Conference on Functional Genomics, in Göteborg, Sweden**, August 29 - 30 (2002).

145. "Bioinformatics of *Pseudomonas* genomes.", invited Bioinformatics lecture for the **summer school course on *Pseudomonas*, Gesellschaft für Biotechnologische Forschung, in Braunschweig**, Germany (26 August, 2002).

146. "Bioinformatics of *Helicobacter pylori* - A DNA-centric view", talk for the **5th International Workshop on Pathogenesis and Host Response in *Helicobacter* Infections, LO Skolen, Helsingnor**, Denmark, 4-7 July, 2002

147. "Bioinformatics of Bacterial Genomes", talk for meeting of the **Task Force for Microbial Genome Linguistics, as part of The Competence Network: Genome Research on Bacteria relevant for Environmental Protection, Agriculture and Biotechnology, Meeting at the Medizinische Hochschule, Hannover,** Germany, 24 May, 2002.

148. "Gene Finding in Three-Dimensions", invited lecture for at **Informatik og teknik i jordbruget, Fuglsøcentret, Denmark**, 1 March, 2002.

149. "Bacterial Chromatin, Genome Organisation and Gene Expression in *E. coli*", invited lectures at Wesleyan University department of Molecular Biology, Middleton, Connecticut, USA, 11 December, 2001.

150. "Bioinformatics of Microbial Genomes", two lectures for the **GBB/Groningen Genomics Center MASTERCLASS on Microbial Genomics, at the Biological Center, Haren, The Netherlands**, 21-23 November, 2001.

151. "Genome Organisation in prokaryotic and eukaryotic chromosomes", invited talk at the **Sanger Centre, Hinxton,** England, 25 October, 2001.

152. "Genome Organisation, chromatin structure, and gene expression in bacteria", invited talk at the **Veterinary Laboratories Agency, Weybridge, England**, 24 October, 2001.

153. "DNA Atlases for *Helicobacter* genomes", invited talk at the **Sir William Dunn School of Pathology, Oxford University**, England, 22 October, 2001.

154. "DNA chip Analysis of Gene Expression in *E. coli*", invited talk at **The Nordic GeneChip Users Meeting, Lund University**, Sweden, 2 October, 2001.

155. "Chromatin Structure and Gene Expression in *E. coli*", invited plenary talk for the **28th Congreso de la Sociedad Espanola de Microbiologia, University of Alicante,** Spain, 18 September, 2001.

156. "Bioinformatics of *E. coli* genomes", talk for the **Protein Design Group, CNB-CSIC, Cantoblanco, Madrid,** Spain 🇪🇸, 14 September, 2001.

157. "DNA Chip Atlases for Analysis of Gene Expression", invited talk for the **4th Annual Affymetrix User's Group Meeting,** 9-10 May, 2001, in Cannes, France 🇫🇷.

158. "Genome Organization and Chromatin Structure in *Escherichia coli*", talk at the **Albert B. Alkek Institute of Biosciences and Technology, Texas A&M University System, Health Science Center, Houston,** Texas, USA, 1 February, 2001.

159. "DNA Structural Atlases for Eukaryotic Chromosomes", invited plenary talk at the **ASM & TIGR Conference on Microbial Genomes, Monterey, California**, USA, 31 January, 2001.

160. "Visualisation of Whole Genome Expression in *Escherichia coli*", **Departmental Seminar at the Microelectronics Center (MIC), Danish Technical University, Kgs. Lyngby**, Denmark 🇩🇰, 19 January, 2001.

161. "Affymetrix DNA Chip analysis of the *Escherichia coli* Genome", informal talk for the Affymetrix User's group, **Department of Biotechnology, Danish Technical University,** Kgs. Lyngby, Denmark 🇩🇰, 5 January, 2001.

162. "Bacterial Pathogenicity and DNA Structures", talk for the Department of Biotechnology's annual January meeting, **Danish Technical University, Kgs. Lyngby,** Denmark 🇩🇰, 2 January, 2001.

163. "DNA Structural Atlases", invited talk at the **Department of Microbiology, Danish Vetinary Laboratory, Copenhagen**, Denmark 🇩🇰, 5 October, 2000.

164. "DNA Atlases for Chromosomes from All Five Kingdoms of Life", talk at the **Joint Stockholm/Copenhagen Bioinformatics Meeting, Stockholm,** Sweden 🇸🇪, 24 September, 2000.

165. "DNA Structural Atlases", Departmental Seminar at the **Microbiology Dept., Danish Technical University, Kgs. Lyngby,** Denmark 🇩🇰, 14 September, 2000.

166. "12 Different Views of *Escherichia coli* p0157", invited talk at the **Dept. of Microbiology, Danish Veterinary Laboratory, Copenhagen,** Denmark 🇩🇰, 11 September, 2000.

167. "DNA Structures in Whole Genomes", invited talk at the **EMBO Workshop on Cell Cycle and Nucleoid Organisation in Bacteria**, 2-6 September, 2000, held on the Island of Texel, The Netherlands 🇳🇱.

168. "Presentation and discussion of perspectives of biosequence analysis in biology research.", invited talk as part of the **Dina Research School Workshop on Biosekvensanalyse, Koldbaekgaard Landboskole, Skejby, Denmark** 🇩🇰, 7 April 2000.

169. "DNA structural periodicities in complete genomes: Evolutionary Genomic Signatures", invited talk at the **Dept. of Evolutionary Biology, Copenhagen University,** Denmark 🇩🇰, 10 December, 1999.

170. "A DNA Structural Atlas for *E. coli*", invited talk at the *E. coli* Genetics group, **University of Wisconsin, Madison, Wisconsin**, USA, 23 November, 1999.

171. "A DNA Structural Atlas for *E. coli"*, invited talk at the Department of Molecular Biology, Odense University, Denmark 🇩🇰, 29 October, 1999.

172. "Prediction of Gene Expression in *E. coli*", invited talk at the Department of Pharmacology, Microbiology and Food Hygiene, The Norwegian School of Veterinary Science, Oslo, Norway 🇳🇴, 16 September, 1999.

173. "Identification of Bacterial Promoter Sequences", invited talk at Microbial Genomes III: Sequencing, Functional Characterization and Comparative Genomics", in Chantilly, Virginia, USA. on 1 Feb., 1999.

174. "Gene Finding in 3D", invited talk at 2nd Annual TIGR conference on "Comparative Microbial Genomics", in Reston, Virginia, USA. (Oct. 31 to Nov. 3, 1998).

Poster Presentations before joining OSU in 2025 **1998 - 2023**

1. David W. Ussery, "Using AI in Education" poster for the **14th Annual Teach the Teacher: Developing and Sustaining Professional Identity Symposium** at the University of Arkansas for Medical Sciences, presented on Friday, May 5, 2023.

2. Visanu Wanchai, Arvind Ramanathan, Intawat Nookaew, David Foutch, Preecha Pratumcharoenpol, Se-Ran Jun, Trudy Wassenaar, Mike Leuze, and David W. Ussery, "What is Life? A set of 500 conserved functional domains", Poster for **UAMS Showcase of Medical Discoveries: Biomedical Informatics Research,** Sept. 21, 2016, UAMS, Little Rock, Arkansas, USA.

3. Intawat Nookaew, Visanu Wanchai, Preecha Pratumcharoenpol, Mike Leuze, Se-Ran Jun, and David Ussery, "Microbiomics: linking human gut microbiome with human health and disease", Poster for **UAMS Showcase of Medical Discoveries: Biomedical Informatics Research**, Sept. 21, 2016, UAMS, Little Rock, Arkansas, USA.

4. Se-Ran Jun, Skylar Connor, Duah Hamza Alkam, Intawat Nookaew, and David W Ussery, "Comparative Genomic Evidence of Zika Virus Epidemiology", P**oster for UAMS Showcase of Medical Discoveries: Biomedical Informatics Research**, Sept. 21, 2016, UAMS, Little Rock, Arkansas, USA.

5. David Ussery, Se-Ran Jun, Collin M. Timm, W. Nathan Cude, Tse-Yuan Lu, Miriam Land, Intawat Nookaew, Christopher W. Schadt, Gerald Tuskan, Mitchel J. Doktycz, Dale A. Pelletier, "Defining the functional diversity of the *Populus* root microbiome", poster for the **JGI (Joint Genomes Institute) meeting, 23-25 March, 2015, Walnut Creek**, California, USA.

6. Deborah A. Weighill, Gerald A. Tuskan, David W. Ussery, Dan A. Jacobson, "Correlotypes: Discovering complex, heterogenous genotypes in the *Populus* pan-genome responsible for phenotypes and macrobiotic associations", **DOE Genomic Science Contractors-Grantees Meeting XIII/USDA-DOE Plant Feedstock Genomics for Bioenergy**, 23-25 February, 2015, Tyson's Corner, Virginia, USA.

7. Intawat Nookaew, Daniel G. Olson, Mirko Basen, Manesh Shah, Visanu Wanchai, Cong Trinh, Philip D. Hyatt, Steve D. Brown, Miriam L. Land, Michael R Leuze, Robert L. Hettich, Robert M. Kelly, Mike Adams, Lee Lynd, David W. Ussery, and Paul Gilna, "Integration of Multi-Omic Data for Advanced Consolidated Bioprocesses", **DOE Genomic Science Contractors-Grantees Meeting XIII/USDA-DOE Plant Feedstock Genomics for Bioenergy**, 23-25 February, 2015, Tyson's Corner, Virginia, USA.

8. Se-Ran Jun, Sanjeev Dahal, Suresh Poudel, Visanu Wanchai, Tse-Yuan Lu, Miriam Land, Intawat Nookaew, Chris W. Schadt, Collin M. Timm, Tatiana V. Kapinets, Daniel A. Jacobson, Trudy M. Wassenaar, Dale A. Pelletier, and David W. Ussery, "Plant-Microbe Interfaces: Comparative Genomics of Populus rhizosphere microbiomes", **DOE Genomic Science Contractors-Grantees Meeting XIII/USDA-DOE Plant Feedstock Genomics for Bioenergy**, 23-25 February, 2015, Tyson's Corner, Virginia, USA.

9. Marie Skovgaard, Lars Juhl Jensen, Thomas Sicheritz-Ponten and David W. Ussery, "Functionally uncharacterized genes in prokarytic genomes - junk or treasure?", poster and talk for **Bioinformatics2003 conference,** 22-24 May, 2003, in Helsinki, Finland.

10. Vera van Noort, Haakan Ohlson, Peter Hallin, Merete K. Jørgensen, Anders Gorm Pedersen, Lars Juhl Jensen, and David W. Ussery, "Promoter Binding Sites for Sigma Factors", poster for **TIGR's 14th International Genome Sequencing & Analysis Conference**, 2-5 October, 2002, in Boston, MA, USA.

11. Peder Worning, Lars Juhl Jensen, Hans Henrik Stærfeldt, and David W. Ussery, "Origin of Replication in Circular Bacterial Genomes and Plasmids", poster for **Bioinformatics2002 conference,** Bergen, Norway, 4-7 April, 2002.

12. Vera van Noort, David Ussery, Thomas Schou Larsen, and Marie Skovgaard, "Re-Annotation of the E. coli genome", poster for the **Third Georgia Tech-Emory International Conference on Bioinformatics,** 15-18 November, 2001, Atlanta, Georgia, USA.

13. T. Sicheritz-Ponten, J.O. Andersson, D. Ussery, A.J- Roger, J. Logsdon, R. Hirt, and T.M. Embley, "Phylogenomic Atlases for Sequenced Microbial Genomes", poster for the **Third Georgia Tech-Emory International Conference on Bioinformatics,** 15-18 November, 2001, Atlanta, Georgia, USA.

14. Lise Petersen, Stephen On, and David Ussery, "DNA atlases for the *Campylobacter jejuni* genome", poster and talk for the **11th International Workshop on Campylobacter, Helicobacter and Related Organisms**, 1-5 September, 2001, in Freiburg, Germany.

15. Vera van Noort, David Ussery, Thomas Schou Larsen, and Marie Skovgaard, "Annotation of the *E. coli* genome revisited", poster for the **9th International Conference on Intelligent Systems for Molecular Biology**, 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

16. Marie Skovgaard, Lars Juhl Jensen, Søren Brunak, David Ussery, and Anders Krogh, "An estimate of the total number of genes in microbial genomes based on length distributions", poster for the **9th International Conference on Intelligent Systems for Molecular Biology**, 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

17. David W. Ussery, Dikeos Mario Soumpasis, Hans Henrik Stærfeldt, Peder Worning, and Anders Krogh, "Estimation of the Amount of A-DNA and Z-DNA in Sequenced

Chromosomes", poster for the **9th International Conference on Intelligent Systems for Molecular Biology,** 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

18.Carsten Friis, Peder Worning, Birgitte Regenberg, Chris Workman, Steen Knudsen, and David W. Ussery, "Measurement and Prediction of Gene Expression in Whole Genomes", poster for the **9th International Conference on Intelligent Systems for Molecular Biology,** 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

19.Peder Worning, Lars Juhl Jensen, Hans Henrik Stærfeldt, and David W. Ussery, "Origin of Replication in Circular Bacterial Genomes and Plasmids", poster for the **9th International Conference on Intelligent Systems for Molecular Biology**, 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

20.Christian B. Jendresen, Maiken H. Pedersen, Morten S. Thomsen, Torsten Kolind, and David Ussery, "DNA atlases for the Staphylococcus aureus genome", poster for the **9th International Conference on Intelligent Systems for Molecular Biology**, 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

21.Lise Petersen, Stephen L.W. On, and David Ussery, "DNA atlases for the Campylobacter jejuni genome", poster for the **9th International Conference on Intelligent Systems for Molecular Biology,** 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

22.David Ussery, Heidi Dvinge, Herluf Riddersholm, Nikolaj Blom, Kristoffer Rapacki, and Søren Brunak, "Genome Size Distribution in Prokaryotes, Eukaryotes, and Viruses", poster for the **9th International Conference on Intelligent Systems for Molecular Biology**, 21-25 July, 2001, at Tivoli Gardens, Copenhagen, Denmark.

23.Peder Worning, Lars Juhl Jensen, Hans Henrik Stærfeldt, and David W. Ussery, "Origin of Replication in Circular Bacterial Genomes and Plasmids", poster for the **BIOINFORMATICS 2001 Meeting**, 29 March - 1 April, 2001, at the First Resort Billingehus Hotel and Conference Centre, Skövde, Sweden.

24.Carsten Friis, Peder Worning, Birgitte Regenberg, Chris Workman, Steen Knudsen, and David W. Ussery, "Measurement and Prediction of Gene Expression in Whole Genomes", poster for the **BIOINFORMATICS 2001 Meeting**, 29 March - 1 April, 2001, at the First Resort Billingehus Hotel and Conference Centre, Skövde, Sweden.

25.Anders Gorm Pedersen, Lars Juhl Jensen, Hans Henrik Stærfeldt, Søren Brunak, and David W. Ussery, "DNA Structural Atlases for Complete Genomes", poster at the **EMBO Workshop on Cell Cycle and Nucleoid Organisation in Bacteria**, 2-6 September, 2000, held on the Island of Texel, The Netherlands.

26.Anders Gorm Pedersen, Lars Juhl Jensen, Carsten Friis, Hans Henrik Stærfeldt, Søren Brunak, and David W. Ussery, "A DNA Structural Atlas for *E. coli*", poster for the **8th International Conference on Intelligent Systems for Molecular Biology**, 19-23 August, 2000, at the Price Center, UC San Diego, La Jolla, California, USA.

27.David W. Ussery, Lars Juhl Jensen, Richard R. Sinden, and Peder Worning, "Analysis of DNA Repeats in Complete Genomes", poster for **18th International Congress of Biochemistry and Molecular Biology - "BEYOND THE GENOME: Understanding and Exploiting Molecules and Cells in the 3rd Millennium",** 16-20 July, 2000, in Birmingham, England.

28.Carsten Friis, Lars J. Jensen, and David W. Ussery, "Localisation of DNA Repeats in complete chromosomes", poster for **Bioinformatics 2000 conference**, 27-30 April, 2000, at the Hotel Marienlyst in Elsinore, Denmark.

29.Peder Worning, Lars Juhl Jensen, Karen E. Nelson, Søren Brunak, and David W. Ussery, "Structural analysis of DNA sequence: Evidence for lateral gene transfer in *Thermotoga maritima*", poster for B**ioinformatics 2000** conference, 27-30 April, 2000, at the Hotel Marienlyst in Elsinore, Denmark.

30.R.F. Petersen, J. Hvidtfeldt, R.B. Langkjaer, C. Groth, W. Palmen, D. Ussery, and J. Piskur, "Structure and Genetic Stability of the *Saccharomyces castelli* Mitochondrial Genome", Poster for the **Genomes 2000: International Conference on Microbial and Model Genomes**, 11-15 April, 2000, Paris, France.

31.David W. Ussery, Anders Gorm Pedersen, Lars Juhl Jensen, Carsten Friis, Hans Henrik Stærfeldt, and Søren Brunak"A DNA Structural Atlas for *E. coli*", electronic poster for the **Third Annual Conference On Computational Genomics**, 18-21 November, 1999, at the Renaissance Harborplace Hotel Baltimore, MD.

32.Peder Worning, Lars Juhl Jensen, Karen E. Nelson, Søren Brunak, and David W. Ussery, "Structural analysis of DNA sequence: Evidence for lateral gene transfer in *Thermotoga maritima"*, electronic poster for the **Third Annual Conference On Computational Genomics,** 18-21 November, 1999, at the Renaissance Harborplace Hotel Baltimore, MD, USA.

33.Carsten Friis, Lars Juhl Jensen, and David W. Ussery, "Three Views of Microbial Genomes", poster for the **7th Annual Conference on Small Genomes**, 13-17 November, 1999, at The Doubletree Hotel, Arlington, Virginia, USA. Sponsored by the U. S. Department of Energy, The Office of Naval Research, and the National Science Foundation.

34.Peder Worning, Lars Juhl Jensen, Karen E. Nelson, Søren Brunak, and David W. Ussery, "Structural analysis of DNA sequence: Evidence for lateral gene transfer in *Thermotoga maritim*a ", poster for the **7th Annual Conference on Small Genomes**, 13-17 November, 1999, at The Doubletree Hotel, Arlington, Virginia, USA. Sponsored by the U. S. Department of Energy, The Office of Naval Research, and the National Science Foundation.

35.Peder Worning, Lars Juhl Jensen, Karen E. Nelson, Søren Brunak, and David W. Ussery, "Structural analysis of DNA sequence: Evidence for lateral gene transfer in *Thermotoga maritima*", poster for the annual **meeting of the Danish Society for Biochemistry and Molecular Biology,** 3-5 October, 1999; Helsingnør, Denmark.

36.David W. Ussery, Anders Gorm Pedersen, Lars Juhl Jensen, Hans Henrik Stærfeldt, and Peder Worning, "A DNA Structural Atlas for *E. coli*", Poster at **Bioinformatics '99 meeting in Lund, Sweden**, 15-18 April, 1999.

37.Lars Juhl Jensen, Anders Gorm Pedersen, Hans Henrik Stærfeldt, Søren Brunak and David W. Ussery, "A DNA structural atlas of promoters in microbial genomes", Poster at **Microbial Genomes III: Sequencing, Functional Characterization and Comparative Genomics,** in Chantilly, Virginia, USA., Jan. 29 - 1 Feb., 1999.

38.David W. Ussery, Anders Gorm Pedersen, Alex Bolshoy, Hans Henrik Stærfeldt and Søren Brunak, "A DNA structural atlas of promoters in microbial genomes" Poster for the **2nd**

Annual TIGR conference on "Comparative Microbial Genomics", in Reston, Virginia, USA (Oct. 31 to Nov. 3, 1998).

15. REPORTS & OTHER OUTPUTS (including NON-REFEREED PUBLICATIONS)

229. *Jing Jin*, Yasir Rahmatallah, Horacio Gomez-Acevedo, Yong-Moon Mark Park, **David W. Ussery**, Ebrahim Jakoet, and Mohammed S. Orloff, "Data from: A Tracts of Homozygosity Approach Identifies Methylation-Regulated CSMD1 Expression Targets in Non - Small Cell Lung Cancers Related to Smoking Behavior", American Association for Cancer Research Collection, **34**(12):2247-2258, (2025). posted online on 12 December, 2025. doi: https://doi.org/10.1158/1538-7445.AM2025-1923

230. **David Ussery** and Ake Vastermark, "Lost in taxonomy: Why bacterial type strains are the anchor we need", Open Access Government, posted on 5 December, 2025. doi: https://www.openaccessgovernment.org/article/lost-in-taxonomy-why-bacterial-type-strains-are-the-anchor-we-need/202149/

231. **David Ussery** and Pratul Agarwal, "What can we learn from millions of viral genome sequences?", Open Access Government, posted on 26 September, 2025. doi: https://doi.org/10.56367/OAG-048-11845.

232. **David Ussery** and Aakash Bhattacharyya, "Using machine learning to predict the severity of salmonella infection", Open Access Government, posted on 25 July, 2025. doi: https://doi.org/10.56367/OAG-047-11845.

233. **David Ussery** and *Brian Delavan*, "Bioinformatics into TB surveillance: A new approach to an ancient foe", Open Access Government, posted on 18 February, 2025. doi: https://doi.org/10.56367/OAG-046-11845.

234. Mayumi Nakagawa, Teresa Evans, Milan Bimali, Hannah Coleman, Jasmine Crane, Nadia Darwish, Jennifer L. Faulkner, Amy Jones, Haley Kelly, Benjamin J. Lieblong, Yong-Chen Lu, Keanna Marsh, Intawat Nookaew, Charles M. Quick, **David Ussery**, Michael Robeson, Sumit Shah, Takeo Shibata, Heather R. Williams, William Greenfield, "A Randomized Double-Blind Phase 2 Clinical Trial Treating Cervical Intraepithelial Neoplasia 2/3 with PepCan or Candida", medRxiv, posted on 19 January, 2025. doi: https://doi.org/10.1101/2025.01.18.25320725.

235. Mayumi Nakagawa, Teresa Evans, Milan Bimali, Hannah Coleman, Jasmine Crane, Nadia Darwish, Yong-Chen Lu, Intawat Nookaew, Keanna Marsh, Michael Scott Robeson, Takeo Shibata, David Ussery, and William Greenfield, Immune responses in a phase 2 clinical trial of peptide-based therapeutic human papillomavirus vaccine, PepCan, versus Candida adjuvant alone in treating cervical intraepithelial neoplasia 2/3,

J Clin Oncol 42, 2634(2024) DOI: 10.1200/JCO.2024.42.16_suppl.2634 https://ascopubs.org/jco/abstracts-breast-cancer-24

236. **David Ussery**, "*E. coli* genomes, big data, and messy biology", Open Access Government, posted on 8 November, 2024. doi: https://doi.org/10.56367/OAG-045-11822.

237. **Sangam Kandel*, Susanna L. Hartzell, Ashton K. Ingold, Grace A. Turner, Joshua L. Kennedy, **David W. Ussery**, "Genomic Surveillance of SARS-CoV-2 Using Long-Range PCR Primers", bioRxiv, Posted July 11, 2023. doi: https://doi.org/10.1101/2023.07.10.548464

238. Mayumi Nakagawa, Teresa Evans, Hannah Coleman, Jasmine Crane, Nadia Darwish, Jennifer L. Faulkner, Amy Jones, Haley Kelly, Benjamin Lieblong, Yong-Chen Lu, Intawat Nookaew, Yang Ou, Charles Matthew Quick, David Ussery, Michael Scott Robeson, Sumit Shah, Takeo Shibata, Horace Spencer, Heather Williams, and William Greenfield, A peptide-based human papillomavirus therapeutic vaccine, PepCan, or Candida adjuvant alone in treatment of cervical intraepithelial neoplasia 2/3 (CIN2/3), J Clin Oncol 41, 5538(2023) DOI: https://doi.org/10.1200/JCO.2023.41.16_suppl.5538.

239. *Dina Elsaye*d, Cody Ashby, Christopher P Wardell, Frits Rhee, **David W Ussery,** Fenghuang Zhan, Michael A Bauer, "Identification of novel long noncoding RNA with distinct expression patterns in different subtypes of multiple myeloma", Research Square, posted 18 Aug, 2022. https://doi.org/10.21203/rs.3.rs-1954260/v1. This is a preprint; it has not been peer reviewed by a journal.

240. **Kaleb Z Abram, Zulema Udaondo, *Carissa Bleker, *Visanu Wanchai*, Trudy M Wassenaar, Michael S Robeson, **David W Ussery**, "What can we learn from over 100,000 Escherichia coli genomes?", bioRxiv, posted 15 January, 2020. doi: https://doi.org/10.1101/708131. Cited 11x

241. Piroon Jejaroenpun, Thidathip Wongsurawat, Annick DeLoose, **David Ussery**, Intawat Nookaew, J D Day, and Analiz Rodriguez, "Transcriptome-Wide Analysis Using Nanopore Third Generation Sequencing in a Rat Glioblastoma Model: Proof Of Principle", Neuro Oncol., 21(Suppl 6): vi101 (2019). https://doi.org/10.1093/neuonc/noz175.420. PMCID: PMC6847510.

242. Thidathip Wongsurawat, Piroon Jejaroenpun, Annick DeLoose, **David Ussery**, *Duah Alkam*, J D Day, Intawat Nookaew, and Analiz Rodriguez, "Rapid Simultaneous IDH Mutation and MGMT Methylation Status Assessment in Glioma Patients Using Crispr-Cas9-Targeted Nanopore Sequencing", Neuro-Oncology, **21**(Suppl 6): vi143–vi144 (2019). https://doi.org/10.1093/neuonc/noz175.601. PMCID: PMC6847173.

243. Rudolf I Amann, Shakuntala Baichoo, Benjamin J Blencowe, Peer Bork, Mark Borodovsky, Cath Brooksbank, Patrick SG Chain, Rita R Colwell, Daniele G Daffonchio, Antoine Danchin, Victor de Lorenzo, Pieter C Dorrestein, Robert D Finn, Claire M Fraser,

Jack A Gilbert, Steven J Hallam, Philip Hugenholtz, John PA Ioannidis, Janet K Jansson, Jihyun F Kim, Hans-Peter Klenk, Martin G Klotz, Rob Knight, Konstantinos T Konstantinidis, Nikos C Kyrpides, Christopher E Mason, Alice C McHardy, Folker Meyer, Christos A Ouzounis, Aristides AN Patrinos, Mircea Podar, Katherine S Pollard, Jacques Ravel, Alejandro Reyes Muñoz, Richard J Roberts, Ramon Rosselló-Móra, Susanna-Assunta Sansone, Patrick D Schloss, Lynn M Schriml, João C Setubal, Rotem Sorek, Rick L Stevens, James M Tiedje, Adrian Turjanski, Gene W Tyson, **David W Ussery**, George M Weinstock, Owen White, William B Whitman, Ioannis Xenarios, "Consent insufficient for data release—Response", Science, **364** (6439):446. https://doi.org/10.1126/science.aax7509. (2019).

244. *Katrina Schlum*, Se-Ran Jun, *Zulema Udaondo*, **David Ussery**, Scott J Emrich, "Improved bacteria population structure analysis on thousands of genomes using unsupervised methods", bioRxiv, Posted April 09, 2019. doi: https://doi.org/10.1101/599944.

245. Rudolf I Amann, Shakuntala Baichoo, Benjamin J Blencowe, Peer Bork, Mark Borodovsky, Cath Brooksbank, Patrick SG Chain, Rita R Colwell, Daniele G Daffonchio, Antoine Danchin, Victor de Lorenzo, Pieter C Dorrestein, Robert D Finn, Claire M Fraser, Jack A Gilbert, Steven J Hallam, Philip Hugenholtz, John PA Ioannidis, Janet K Jansson, Jihyun F Kim, Hans-Peter Klenk, Martin G Klotz, Rob Knight, Konstantinos T Konstantinidis, Nikos C Kyrpides, Christopher E Mason, Alice C McHardy, Folker Meyer, Christos A Ouzounis, Aristides AN Patrinos, Mircea Podar, Katherine S Pollard, Jacques Ravel, Alejandro Reyes Muñoz, Richard J Roberts, Ramon Rosselló-Móra, Susanna-Assunta Sansone, Patrick D Schloss, Lynn M Schriml, João C Setubal, Rotem Sorek, Rick L Stevens, James M Tiedje, Adrian Turjanski, Gene W Tyson, David W Ussery, George M Weinstock, Owen White, William B Whitman, Ioannis Xenarios, "Toward unrestricted use of public genomic data", Science, **363**(6425):350-352 (2019). Epub 2019/01/27. https://doi.org/10.1126/science.aaw1280. PubMed PMID: 30679363.

246. Thidathip Wongsurawat, Piroon Jenjaroenpun, Trudy M. Wassenaar, *Taylor D Wadley, Visanu Wanchai*, Nisreen S. Akel, Aime T. Franco, Michael L. Jennings, **David W. Ussery**, Intawat Nookaew, "Decoding the Epitranscriptional Landscape from Native RNA Sequences", BioRxiv, Posted December 17, 2018; https://doi.org/10.1101/487819.

247. Thidathip Wongsurawat, Piroon Jenjaroenpun, Mariah K. Taylor, Jasper Lee, Aline Lavado Tolardo, Jothi Parvathareddy, *Sangam Kandel, Taylor D*. Wadley, Bualan Kaewnapan, Niracha Athipanyasilp, Andrew Skidmore, Donghoon Chung, Chutikarn Chaimayo, Michael Whitt, Wannee Kantakamalakul, Ruengpung Sutthent, Navin Horthongkham, **David W. Usser**y, Colleen B. Jonsson, Intawat Nookaew, "Rapid Sequencing of Multiple RNA Viruses in their Native Form", BioRxiv, Posted November 29, 2018. doi: https://doi.org/10.1101/482471.

248. Scott Federhen, Ramon Rossello-Mora, Hans-Peter Klenk, Brian J Tindall, Konstantinos T Konstantinidis, William B Whitman, Daniel Brown, David Labeda, **David Ussery**, George M Garrity, Rita R Colwell, Nur Hasan, Joerg Graf, Aidan Parte, Pablo Yarza, Brittany Goldberg, Heike Sichtig, Ilene Karsch-Mizrachi, Karen Clark, Richard McVeigh,

Kim D Pruitt, Tatiana Tatusova, Robert Falk, Seán Turner, Thomas Madden, Paul Kitts, Avi Kimchi, William Klimke, Richa Agarwala, Michael DiCuccio, James Ostell, "Meeting report: GenBank microbial genomic taxonomy workshop (12–13 May, 2015)", Standards in Genomic Sciences, **11**:1 (2016). https://doi.org/10.1186/s40793-016-0134-1. Cited 85x

249. Scott A Beatson, Nouri L Ben Zakour, Makrina Totsika, Brian M Forde, Rebecca E Watts, Amanda N Mabbett, Jan M Szubert, Sohinee Sarkar, Minh-Duy Phan, Kate M Peters, Nicola K Petty, Nabil-Fareed Alikhan, Mitchell J Sullivan, Jayde A Gawthorne, Mitchell Stanton-Cook, Nguyen Thi Khanh Nhu, Teik Min Chong, Wai-Fong Yin, Kok-Gan Chan, Viktoria Hancock, **David W Ussery**, Glen C Ulett, Mark A Schembri, BA McCormick, "Data for Molecular analysis of asymptomatic Bacteriuria *Escherichia coli* strain VR50 reveals adaptation to the urinary tract by gene acquisition" [Dataset], Published May 2015 by the University of Warwick, Warwick Medical School http://wrap.warwick.ac.uk/96020.

250. **David W. Ussery**, "What is the minimal genome?", Journal of Cosmology, **16**:7013-7016, (2011). https://thejournalofcosmology.com/indexVol16CONTENTS.htm.

251. Lundegaard, C., Aagaard, C., **Ussery, D.**, Andersen, P. L., & Jungersen, G. (2011). "Rational Discovery of T Helper Epitopes Specific for Bovine Infections with *Mycobacterium avium* ssp paratuberculosis", Scandinavian Journal of Immunology, **73**(4), 392-393. https://doi.org/10.1111/j.1365-3083.2011.02516.x.

252. **David W. Ussery**, "One Small Step for Bacteria, or One Giant Leap for Mankind?", Journal of Cosmology, **8**:3 (2010) https://thejournalofcosmology.com/ArtificialLife100.html.

253. *Vesth, T. C., Lagesen, K., Otto, S. J.*, & **Ussery, D. W.**, "Functions of Giant proteins in Bacterial genomes", (2009); poster published in: BMC Evolutionary Biology, **9**(258), 19860885.

254. Ussery, D. W., & Tümmler, B. (2003). Special Issue on *Campylobacter* and *Helicobacter* Genomics. *Genome Letters*, *2*(1-2), 1-1.
Cover image.

255. **David W. Ussery**, "Signal Peptide Cleavage Site Prediction", GenomeBiology, **1**:3-5, (2000). https://doi.org/10.1186/gb-2000-1-3-reports2054.

256. **David W. Ussery**, "Bioinformatics2000 Meeting Report", GenomeBiology, **1**:1-2, (2000). https://doi.org/10.1186/gb-2000-1-3-reports4014.

257. Richard Thornhill, and **David W. Ussery**, "A Classification of Possible Routes in Darwinian Evolution", Journal of Theoretical Biology, **202**:111-116, (2000). https://doi.org/10.1006/jtbi.2000.1070. PubMed PMID: 10704296

258. **David W. Ussery** and Richard R. Sinden, "Environmental Influences On Triplex DNA Formation *In Vivo*", The FASEB Journal, **6**:A219-A219. 9650 Rockville Pike, Bethesda, MD 20814-3998: Federation Amer Soc Exp Biol, 1992.

Other Creative Products

Video links 2017 - present

"Data Curation and SARS-CoV-2: population genomics of 2.5 million genomes",
DART Webinar, on 28 July, 2021
https://dartproject.org/dart-webinar-2021-jul-28/

Discovery Economics column "Unlocking Genomics"
https://arkansasvoices4research.com/discovery-economics

ARA Project Scope talk - 17 February, 2021
https://aralliance.org/video/ara-project-scope-with-david-ussery/

UALR/UAMS IMBRE Genomics Workshop - part 1 "What Is Biological Information?"
https://www.youtube.com/watch?v=fO0W4BIOUfo
22 March, 2021

UALR/UAMS IMBRE Genomics Workshop - part 2 "Sequence Alignments"
https://www.youtube.com/watch?v=jpRbtYGivS4
22 March, 2021

UALR/UAMS IMBRE Genomics Workshop - part 3 "Introduction to R-BioTools"
https://www.youtube.com/watch?v=5-jgQJMEcfs
22 March, 2021

UALR/UAMS IMBRE Genomics Workshop - Part 4 "Comparing Genomes"
https://www.youtube.com/watch?v=eo_-0VcfWf0
23 March 2021

UALR/UAMS IMBRE Genomics Workshop - part 5 "Introduction to Atlases"
https://www.youtube.com/watch?v=ohma7fXIL5Q
23 March, 2021

UALR/UAMS IMBRE Genomics Workshop - part 6 "Comparing Proteomes"
https://www.youtube.com/watch?v=VJbeR6ssF-w
23 March, 2021

UALR/UAMS IMBRE Genomics Workshop - part 7 "Viral Genomics"
https://www.youtube.com/watch?v=xHa1oVvY6a4
24 March, 2021

UALR/UAMS IMBRE Genomics Workshop - part 8 "The Human Genome Project"
https://www.youtube.com/watch?v=S3jXMWyEAyY

24 March, 2021

Covid-19 projects at ArC-GEM - September, 2020
https://www.youtube.com/watch?v=wuql-ZaUV_s

Tip - Glioma methylation - July, 2020
https://www.youtube.com/watch?v=gk-bXlU4gxk

"Gut Brain Interactions" ARA talk, July, 2020
https://www.youtube.com/watch?v=mOJnh48iqsM

Duah - talk for Oxford Nanopore conference - February, 2020
https://www.youtube.com/watch?v=BR63q_dj21M

Summer Undergraduate Research Fellowship (SURF) program

2018 Harding College rotation student (Ana Swearingen)
https://www.youtube.com/watch?v=IRTdK0kl9v4
July, 2018

2017 Harding College rotation student (Connor Purvis)
https://www.youtube.com/watch?v=CC11Jlydqrc

June, 2017

Mumps sequencing - with Tip, Skylar, Piroon
https://www.youtube.com/watch?v=ttOB_Cr6Bas
July, 2017

Arkansas Research Alliance 2017 Fellows Announcement
https://www.youtube.com/watch?v=B6PUcB-QVYA
August, 2017

Tip's video on 'elephant DNA':
https://www.youtube.com/watch?v=E5Kge3ZpQP4&feature=youtu.be
September, 2017

16. BOOK REVIEWS

259. **David Ussery**, "C.S. Lewis Philosopher — Who Changed My Life. Notes on the Margins of The Magician's Twin", Filozoficzne Aspekty Genezy, (2025), **21**(2). https://doi.org/10.53763/fag.2024.21.2.240

260. **David W. Ussery**, "The best books on the history of heredity and DNA", published on 8 April, 2024, by Shepherd Books, https://shepherd.com/best-books/the-history-of-heredity-and-dna

261. **David W. Ussery**, "Natural genetic engineering: intelligence & design in evolution?", Microbial Informatics and Experimentation, **1**:11 (2011). Published online, 31 October, 2011. https://doi.org/10.1186/2042-5783-1-11 PMCID: PMC3372291

262. **David W. Ussery**, "The Skeptical Biochemist: Is There an Edge to Evolution?", Review for BioLogos, October, 2010. https://biologos.org/articles/is-there-an-edge-to-evolution

263. **David W. Ussery**, "An Inordinate Fondness for Bacteria", a review of Stephen Meyer's "SIGNATURE IN THE CELL - DNA and the Evidence for Intelligent Design", Reports of the NCSE, **30**:59-60. (December, 2009). https://ncse.ngo/rncse. Link to pdf of the review: https://ussery.org/2010_Meyer_review_NCSE.pdf

264. **David W. Ussery**, "The Purpose-Driven iPod", a review of David Bartholomew's "God, Chance, and Purpose: Can God have it both ways?", Christian Century, (23 September, 2008, pages 11-12). https://www.christiancentury.org/article/2008-09/purpose-driven-ipod

265. **David W. Ussery**, "The Stealth Creationists", Skeptic, **8**:72-74, (2001). https://link.gale.com/apps/doc/A76495418/AONE?u=nm_p_oweb&sid=bookmark-AONE&xid=8812121c. (accessed June 4, 2022).

266. **David W. Ussery**, "A Biochemist's Response to 'The Biochemical Challenge to Evolution'", a review of Michael Behe's "DARWIN's BLACK BOX: The Biochemical Challenge to Evolution", Bios, **70**:40-45, (1999). https://ussery.org/Review_of_Michael_Behe__DarwinsBlackBox.pdf
Cited 24x

17. INTELLECTUAL PROPERTY

INTELLECTUAL PROPERTY

Patents and Technology Transfer

Charles Parker, George Garrity, **David Ussery**, **Visanu Wanchai*, and Intawat Nookaew. "Method for Identification and Characterization of Prokaryotes Using Whole Genome DNA Sequence Data." US Provisional Patent Application No. 62/232,925. Filed September 25, 2015. Washington, DC: U.S. Patent and Trademark Office.

18. RESEARCH FUNDING HISTORY

RESEARCH FUNDING HISTORY

Grants and Contract Awards at OSU 2025 - present

Current funding at OSU (pending, January, 2026):

Waiting for confirmation of transfer of PI:
NIH R01 GM148886 Grant Title: Biophysical Model of Enzyme Catalysis: Conformational Substates, Solvent Coupling and Energy Networks
[$1,110,275] 2023 - 2028

Waiting for McCasland Foundation Professorship in Physiological Sciences, DVM, OSU - January 2026

Previous funding (total of ~$51,163,951, where I was **PI or Co-I**) 2001- 2025

Arkansas Research Alliance (ARA) Fellow 2016 - 2025
[$500,000 towards UAMS start-up funds]

Helen G. Adams and ARA Chair in Biomedical Informatics 2017 - 2025
[$1 million endowment - from ARA and the Helen G. Adams Foundation]

NSF OIA-1946391 Jennifer Fowler / Jack Cothren (PIs) 2020 - 2025
"RII Track-1: Data Analytics that are Robust and Trusted (DART): From Smart Curation to Socially Aware Decision Making"
Role: Co-Lead for Data Curation and Life Cycle thrust and PI for UAMS grad. students
[$24,000,000 in total for 5 years; ~$300,000 per year for UAMS graduate students]

NIH T32 GM106999 Paul Prather (PI) 2023 - 2028
"Systems Pharmacology and Toxicology Training Program"
Role: Member of the Training Faculty
[$873,220]

NIH INBRE Jonathan Stubblefield & David Ussery (co-PIs) 2024 - 2025
"Benchmarking Genomic Comparison Tools Across Different Organisms" (INBRE Collaborative Research Grant)
Role: Co-PI
[$52,726]

ABI grant supplement Wen Zhang and Dave Ussery (PIs) 2024-2025
"Long-Range PCR Sequencing in Wastewater Surveillance of Disease Outbreak"
Role: Co-PI
[$17,450]

ABI grant supplement Chris Nelson and Dave Ussery (PIs) 2023-2024
"A versatile long-read sequencing method for analysis of DNA-editing therapies"
Role: Co-PI
[$17,450]

NIH UL1 TR003107-01 Laura P. James (PI) 2019 - 2024
"Expanding Translational Research in Arkansas"
Role: Other personnel; I was funded as a 10% FTE for Covid-19 work, for 1 year (2020).
[$24,200,000]

NIH T32 GM106999 Paul Prather (PI) 2018 - 2023
"Systems Pharmacology and Toxicology Training Program"
Role: Member of the Training Faculty
[$740,000]

ARA 239/G1-53307-01, Arkansas Research Alliance Ussery, David (PI) 2021 - 2022
"Genomic Epidemiology of SARS-CoV-2 in Arkansas"
Role: PI
[$50,000]

UAMS VCRI equipment grant Ussery, David (PI) 2021
"Oxford Nanopore GridION machine for high-throughput sequencing "
Role: PI
[$51,105]

NIH P20 Administrative supplement Josh Kennedy (PI) July, 2021 - June, 2021
"Sequencing and Analysis of SARS-CoV-2 Variants in Arkansas"
Role: Co-Investigator

[$765,000]

NIH / NGMS P20 GM121293-01, NIH/NGMS Alan Tackett (PI) 2017 – 2022
"Center for Translational Pediatric Research"
Role: Co-Investigator
[$11,500,000]

ARA Impact Grant (Dave Ussery, PI) 2020 - 2021
"Rapid Biosurviellence for Covid-19"
Role: PI
[$37,000]

NIH ISPCTN pilot award from RFA-OD-19-026 Onarecker, Timothy (PI) 2019 - 2020
"Rapid Genomic Sequencing of Pneumococcal Meningitis Isolates"
Role: co-mentor.
[$25,000]

ARA Impact Grant (Dave Ussery, PI) 2019 - 2020
"Identification of Staphylococcus aureus Genes that Contribute to the Pathogenesis of Osteomyelitis"
Role: PI
[$75,000]

ARA Impact Grant (Dave Ussery, PI) 2019 - 2020
"Sleep Apnea Gut Microbiome"
Role: PI
[$25,000]

DOE internal funding, ORNL Jeremy Archileta (PI) 2015 - 2016
"Accumulative Linking and Analysis of Scientific Results: A New Data-Infrastructure Paradigm to Enable Data-Driven Discoveries"(AspenGrove LDRD - part of the DOE 'exascale' initiative)
Role: Co-investigator.
[$720,000]

Industry Ph.D. grant from the Danish Research Council Dave Ussery (PI) 2012 - 2015
"Comprehensive Proteomics of Streptococcus thermophilus in Industrial Dairy Products"
Role: PI
[DKK 2.5 million (~ $500,000 U.S.)]

Danish Council for Strategic Research Frank M. Aarestrup (PI) 2010 - 2015
"Center for genomic epidemiology"
Role: Co-Investigator
[DKK 35 million (~$7 million U.S.)]

Danish Council for Strategic Research Hanne Ingmer (PI) 2008 - 2012
"Biocide resistance; an emerging threat to public health?"
Role: Co-Investigator
[DKK 45 million (~$9 million U.S.)]

EU consortium Dave Ussery (PI) 2008
"MedVetNet: Campylobacter jejuni microarrays"
Role: PI
[€240,000 (~$292,000)]

DTU infrastructure Søren Brunak, Zoltan Szallasi, Chris Workman, & Dave Ussery, co-PIs 2007
"Custom DNA Microarray Platform for Integrative Systems Biology"
Role: Co-PI
[DKK 30 million (~$6 million U.S.)]

Danish FNU Dave Ussery (PI) 2007 - 2009
"Comparative Genomics of Campylobacter jejuni"
Role: PI
[DKK 3 million (~$600,000)]

Danish FNU Søren Molin (PI) 2007 - 2009
"Host-parasite relationships and evolution of microbial persistent infections"
Role: Co-Investigator
[DKK 3 million (~$600,000)]

Danish Research Council Gregers Jungersen (PI) 2007
"Pathogens in the Food Chain"
Role: PI for Bacterial Genomics thrust
[DKK 20 million (~$4 million)]

Norwegian Vet. Institute Yngvild Wasteson (PI) 2006 - 2007
"Genome sequencing and characterization of the E. coli O103 outbreak strain"
Role: Co-Investigator
[NOK 360,000 (~$73,000)]

Danish Galethea III Nikolaj Blom (PI) 2005 - 2008
"DNA of the Polar Seas"
Role: Co-Investigator
[DKK 2 million (~$400,000)]

EU Coordination Action grant [35 partners from 17 countries] 2005 - 2008
"EUROFUNG - European Fungal Genomics DataBase"
Role: member of the scientific steering committee (Cees van den Hondel, Leiden University; Steve Oliver, University of Manchester; and David Ussery, CBS/DTU)
[€500,000 (~$608,000)]

Danish SJVF Hanne Ingmer and Dave Ussery (PIs) 2005 - 2007
"The biology of Campylobacter jejuni during colonization of the chicken gut"
Role: Co-PI
[DKK 3 million (~$600,000)]

Danish IVC application to STVF Søren Brunak, PI 2004 - 2007
"Systemic Genomics in Medicine and Biotechnology"
Role: Co-Investigator

[DKK 10 million (~$2 million)]

Norwegian EMBIO Torbjørn Rognes (PI) 2004 - 2006
"Discovery of genome maintenance genes and non-coding RNA genes by microbial transcriptome analysis"
Role: Co-Investigator
[NOK 150,000 (~$30,000)]

Norwegian Research council Yngvild Wasteson (PI) 2002 - 2005
"The effect of stress on genetic recombination and pathogenicity of Shiga toxin-encoding bacteriophages"
Role: Co-Investigator
[NOK 3 million (~$600,000)]

BMBF, German government Burkhard Tuemmler (PI) 2002 - 2005
"The competence network: Genome Research with Bacteria relevant for Environmental Protection, Agriculture and Biotechnology."
Role: Co-Investigator
[€487,000 (~$592,000)]

Danish STVF Dave Ussery (PI) 2001 - 2003
"Comparative genetics of Camplyobacter jejuni: A bioinformatics-mediated approach"
Role: Co-Investigator
[DKK 1.6 million (~$320,000)]

19. PRACTICE OF PROFESSIONAL SKILLS

a. Clinical responsibilities, contribution to clinical service and other professional practice:

None at OSU (yet!).

Grand Rounds and other Clinical Presentations at UAMS **2017 - 2024**

"AI-Assisted Genome Studies Are Riddled with Errors", talk for the **University of Arkansas for Medical Sciences** Clinical Informatics Journal Club, 21 November, 2024.

Who's Afraid of the Monkeypox virus?, invited talk for the **University of Arkansas for Medical Sciences Faculty Excellence Series**, Sponsored by the UAMS Academic Senate; Wednesday, 9 November, 2022

"Rapid Detection of Anti-Microbial-Resistant ESKAPE Pathogens from Clinical Isolates Using High-Throughput Sequencing", invited talk for the **Arkansas American Society for Clinical Laboratory Science Spring Conference,** Baptist Health College, Little Rock, Arkansas; Friday, 8 April, 2022.

"Genomic Epidemiology in Arkansas", Arkansas Department of Health **Grand Rounds**, 3 November, 2022.

"Healthy Gut, Healthy Heart? The microbiome & cardiovascular health", UAMS Department of Internal Medicine **Grand Rounds**, October, 2018.

"Community profiles in atherosclerotic plaques from UAMS patients", UAMS **Grand Rounds**, 30 November, 2017.

"Genomic Epidemiology of the Mumps Outbreak in NW Arkansas", NWA Internal Medicine **Grand Rounds**, 27 March, 2017.

b. American College of Veterinary Internal Medicine (ACVIM)-related responsibilities:

None.

c. Scientific reviews and related activities:

U.S. and European Grant Review Panels	**2013 - 2025**
NIAID Technologies for Cancer Research Special Emphasis Panel (R33 and R61)	July, 2025
UKRI Funding Service BBSRC-NSF 24/25 Oxford / MIT collaboration	July, 2025
NIAID New Innovators Awards (DP2)	April, 2025
UAMS NIH K-12 applications (3x)	March, 2025
ESF (European Science Foundation) Belgium post-doctoral application.	Feb., 2025
FWF ASTRA Austrian Science Awards application	Jan., 2025
UKRI Funding Service	Dec., 2024
U.S. National STEM (Science Fair)	Nov., 2024
NIH Centers for Research in Emerging Infectious Diseases (CREID) Network (U01)	Oct., 2024
UKRI Funding Service	June, 2024
UAMS Internal Grant Applications	April, 2024
NIAID New Innovators Awards (DP2)	March, 2024
UAMS NIH K-12 applications (3x)	March, 2024
Belgian Fundamental Research grant (FWO)	March, 2024
UAMS Internal Grant Applications	Nov., 2023
UAMS NIH K-12 applications (3x)	April, 2023

NIAID New Innovators Awards (DP2)	March, 2023
UAMS Internal Grant Applications	March, 2023
ESF (European Science Foundation) post-doctoral applications (4x).	Feb., 2023
Canadian Poultry Research Council	Oct., 2022
UAMS Internal Grant Applications	Oct., 2022
UAMS Internal Grant Applications	May, 2022
UAMS Internal Grant Applications	Nov., 2021
NCI R01 and R21 grants review panel	Oct., 2021
UAMS Internal Grant Applications	Nov., 2020
I-SITE ULNE (France)	Sept., 2020
NIAID Emerging Infectious Diseases Research Centers (U01)	Nov., 2019
NIAID System Biology: The Next generation for Infectious Diseases (U19) chair.	July, 2017
NIAID Rapid Assessment of Zika Virus (ZIKV) Complications (R21)	April, 2017
BBSCR (UK)	March, 2017
AERES (France) 2 grants	March, 2014
NIAID Genomic Centers for Infectious Diseases (U19)	Nov., 2013

20. PRACTICE OF PROFESSIONAL SKILLS

ADMINISTRATIVE SERVICE

Committee Assignments and Administrative Services at UAMS	**2017 - 2025**
Chair, DBMI Tenure and Promotion Committee	2017 - 2022
Member, DBMI Tenure and Promotion Committee	2017 - 2025
Member, UAMS Graduate Council	2018 - 2024
Member, UAMS College of Medicine Research Council	2019 - 2025
Chair of Search Committee for DBMI Vice-Chair of Clinical Informatics	2019
UAMS Senator, “Member at large”	2021 - 2023

21. PROFESSIONAL OR ASSOCIATION OFFICES AND COMMITTEE ACTIVITY OUTSIDE OSU

Editorial Board Appointments

Associate Editor, Frontiers in Bioinformatics	2024 - present
Associate Editor, Frontiers in Microbiology	2019 - present
Associate Editor, Associate Editor, Molecular Genetics and Genomics	2005 - present
Associate Editor, BMC Genomics	2013 - 2018
Associate Editor, Microbiology (UK)	1998 - 2012

22. PUBLIC AND COMMUNITY CONTRIBUTIONS

Professional Community Activities 2013 - 2024

Interview for Discover Economics magazine on "CREATING ARKANSAS' NEXT GENERATION OF RESEARCHERS", May, 2024.
https://armoneyandpolitics.com/creating-arkansas-next-generation-of-researchers/

Interview for Discovery Economics magazine on "Unlocking Genomics", January, 2021.
https://arkansasvoices4research.com/discovery-economics

"Science Cafe" panel discussion at the Whole Hog Cafe in Little Rock, on "Indwelling Gut Bacteria and You", followed by a radio interview, on 23 May, 2017.
http://ualrpublicradio.org/post/science-cafe-role-microbiome-bacteria-and-human-body

Talk for the Copenhagen 'Skeptics in the Pub', on the Human Genome Project, on 8 July, 2013.
https://www.facebook.com/CopenhagenSkeptics/

23. OTHER ACTIVITIES

I enjoy photography, especially taking landscape pictures as I travel and of sunrises / sunsets at home, and going for long hikes. I also love music and enjoy singing in choirs.