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Introduces the rapidly evolving field of genome plasticity, presents the latest

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research findings, and explores the relevance of these findings to infection and infection control. Compiles and analyzes current investigations on the genome fluidity of pathogenic microbes.

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Jorg Hacker ...

Genome plasticity and
infectious diseases.

[Jörg Hacker; Ulrich
Dobrindt; Reinhard
Kurth;] --

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Comprehensive examination of the current understanding of pathogen adaptation and microevolution.

Introduces the rapidly evolving field of genome plasticity, presents the latest research findings, ...

Genome plasticity and infectious diseases
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Impact of genome
plasticity on adaptation
of Escherichia coli
during urinary bladder
colonization / Ulrich
Dobrindt, Jaroslaw
Zdziarski, Jörg Hacker
--Genotypic changes in
enterohemorrhagic
Escherichia coli during
human infection /
Alexander Mellmann,
Martina Bielaszewska,
and Helge Karch

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--Genomic fluidity of
the human gastric
pathogen *Helicobacter
pylori* / Niyaz Ahmed
[and others] --Genome
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staphylococci / Wilma
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This book introduces the rapidly evolving field of genome plasticity, presents the latest research findings, and explores the relevance of these findings to infection and infection control. It explores bacteria, viruses, fungi, and parasites from the aspect of host genome plasticity and its impact on infection.

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**TDS - Genome
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Genome Plasticity in Health and Disease provides a fully up-to-date overview on genome plasticity and its role in human physiology and disease. Following an introduction to the field, a diverse range of

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chapters cover genomic and epigenomic analysis and the use of model organisms and genomic databases in studies.

**Genome Plasticity in
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agr-Defective
Staphylococcus aureus
during Clinical
Infection. ... Department

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of Medicine, Division of
Infectious Diseases,
Icahn School of
Medicine at Mount
Sinai, New York City,
... suggests that much of
the genetic complexity
of agr-defective strains
results from prolonged
infection or therapy-
induced stress.
However, in ...

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**agr-Defective
Staphylococcus aureus**

...

Genome Plasticity of
Herpesviruses:
Conservative yet
Flexible, p 248-266. In
Hacker J, Dobrindt U,
Kurth R (ed), Genome
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Washington, DC. doi: 1
0.1128/9781555817213.
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ASMscience | Genome Plasticity of Her

Whole-genome
sequence analysis of the
XDR *V. cholerae*
isolates revealed the
presence of multiple
resistance traits against
each class of
antimicrobial scaffold .
?-Lactams are the most
widely used broad-
spectrum antibiotics,

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and resistance to β -lactams is a serious threat for infectious disease management, surgery, and organ transplantation.

Genomic plasticity associated with antimicrobial ...

Evolutionary selection of viruses capable of infecting a wide range of hosts has been a key

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hypothesis underpinning disease emergence theory 7,21, and we provide evidence for the importance of viral host plasticity as a synergistic trait aiding mechanisms of disease transmission, particularly at the high-risk human-animal interfaces reported here.

Spillover and

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**pandemic properties of
zoonotic viruses with**

...

The completed or ongoing genome projects will provide enormous opportunities for the discovery of novel vaccines and drug targets against human pathogens as well as the improvement of diagnosis and discovery of infectious agents and

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the development of new strategies for invertebrate vector control.

**Genetics and
Evolution of Infectious
Diseases |
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Infectious diseases remain a global threat contributing to excess morbidity and death annually, with the

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persistent potential for destabilizing pandemics. Improved understanding of the pathogenesis of bacteria, viruses, fungi, and parasites, along with rapid diagnosis and treatment of human infections, is essential for improving infectious disease outcomes worldwide.

CRISPR-Cas Biology

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**and Its Application to
Infectious Diseases**

Genome Plasticity and
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(2012) Germ Proof
Your Kids: The
Complete Guide to
Protecting Your Family
from Infections (2008)
Global Health 101 - 4th
Ed. (2021) Handbook of
Tuberculosis: Clinics,
Diagnostics, Therapy,
and Epidemiology

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(2008) HIV and the
Pathogenesis of AIDS -
3rd Ed. (2007)

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Diseases and
Department of
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Tropical Diseases, and
Institute for Human
Infections and ...

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**Evolution of Genome
Size and Complexity in
the Rhabdoviridae**

The Bioinformatics
Resource Centers
(BRCs) for Infectious
Diseases program was
initiated in 2004 with
the main objective of
providing public access
to computational
platforms and analysis
tools that enable

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collecting, archiving,
updating, and
integrating a variety of
genomics and related
research data relevant to
infectious diseases, and
pathogens and their
interaction with hosts

**Bioinformatics
Resource Centers |
NIH: National
Institute ...**

The Laboratory of
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Immune System
Biology (LISB) is
focused on the basic
genetics, molecular
biology, and cell
biology of the immune
system, as well as on
human disease informed
by these more basic
studies. How
dysregulation of the
immune system results
in immunodeficiencies,
autoimmunity,

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inflammation, allergy,
chronic infections, and
lymphoproliferative
diseases and what
strategies might be ...

**Laboratory of Immune
System Biology | NIH:
National ...**

Recently, the genome
plasticity of EBOV in
Vero cells was
demonstrated by several
studies [15, 16], and

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such plasticity may influence several aspects of filovirus research, since Vero or Vero-derived cells have been used as the standard cell lines for propagation of EBOV stocks. Mutations arising during virus propagations may alter the phenotype of the virus from the original wild-type virus.

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**Improved Reverse
Genetics System to
Overcome Cell-Type ...**

Background: Shiga
toxin-producing
Escherichia coli
O157:H7 is a foodborne
pathogen that causes
severe human diseases
including hemolytic
uremic syndrome
(HUS). The virulence
factor that mediates

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HUS, Shiga toxin (Stx), is encoded within the genome of a lambdoid prophage. Although draft sequences are publicly available for a large number of E. coli O157:H7 strains, the high sequence similarity ...

**Escherichia coli
O157:H7 strains
harbor at least three ...**

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We characterized 170 complete genome assemblies from clinical *Bordetella pertussis* isolates representing geographic and temporal diversity in the United States. These data capture genotypic shifts, including increased pertactin deficiency, occurring amid the current pertussis disease

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resurgence and provide a foundation for needed research to direct future public health control strategies.

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