

# Contig: A New Open-Access Forum for Genetics, Genomics, and Breeding

*Introducing Contig: scope, standards, and an invitation to the global genetics community.*

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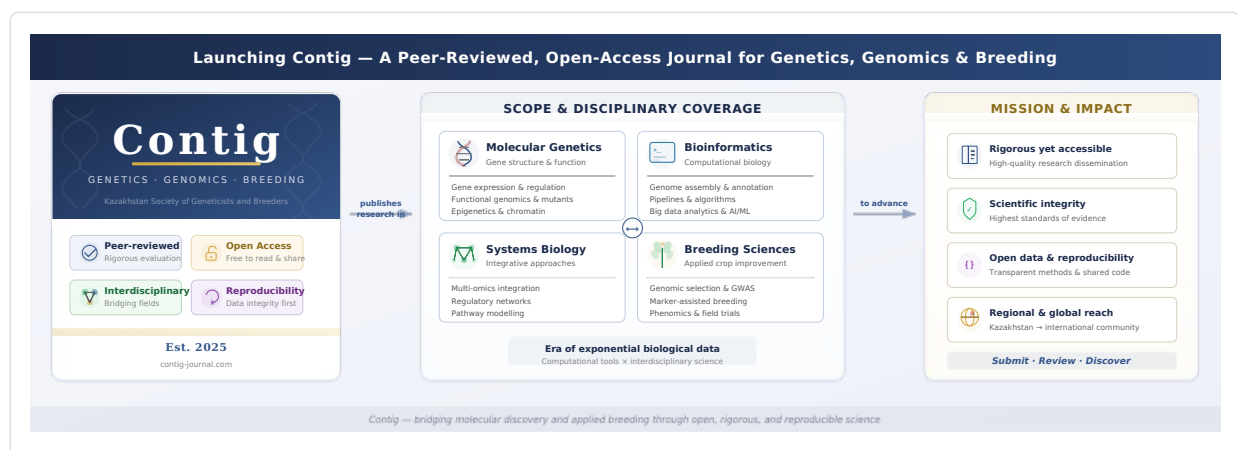
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## Abstract

It is with great enthusiasm that we launched Contig, a peer-reviewed, open-access journal dedicated to advancing the fields of genetics, genomics, and breeding. Published by the Kazakhstan Society of Geneticists and Breeders, Contig aims to provide a rigorous, yet accessible platform for disseminating high-quality research that spans molecular genetics, bioinformatics, systems biology, and applied breeding sciences. In an era defined by the exponential growth in biological data and computational tools, there is an urgent need for journals that embrace interdisciplinary approaches while maintaining the highest standards of scientific integrity and reproducibility.

## Graphical Abstract



## Mission and Vision

Contig was founded on the principle that scientific progress thrives on the open exchange of ideas and transparent reporting. Our mission is to publish original research, innovative methods, and comprehensive reviews that advance our understanding of living systems, from molecular mechanisms to population-level dynamics. We are particularly committed to fostering research that addresses the

dynamic and complex nature of biological systems, with a special emphasis on systems biology, synthetic biology, and systems medicine.

Modern genetics and genomics require integration across traditional disciplinary boundaries. To investigate gene regulatory networks, engineer novel biological systems, or develop climate-resilient crop varieties, researchers must navigate vast datasets, sophisticated computational methods, and complex experimental designs. Contig provides a home for such integrative work, welcoming manuscripts that combine experimental rigour with computational innovation.

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### **Scope and Topics**

The scope of Contig is intentionally broad, reflecting the interconnected nature of modern biological science. We have published work on molecular genetics and functional genomics, bioinformatics and algorithm development, artificial intelligence and machine learning applications, biotechnology and biomedical engineering, computational biology and mathematical modeling, evolutionary and ecological genomics, gene regulation and epigenetics, quantitative imaging and phenotyping, metabolomics and systems-level metabolism, microbiome and metagenomic studies, network biology and multi-omics integration, protein science and proteomics, synthetic biology and engineered systems, systems genetics and personalized medicine, as well as plant and animal breeding, quantitative genetics, and population, medical, and conservation genomics.

This expansive scope reflects our belief that the most impactful discoveries often emerge at a disciplinary interface. We encourage submissions that bridge basic and applied research, connect computational predictions with experimental validation, or integrate insights from model organisms with translational applications in medicine, agriculture, and conservation.

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### **Editorial Standards and Priorities**

Contig prioritize scientific novelty, broad biological significance, and clear mechanistic insights. We value research that not only reports new findings but also provides a deeper understanding of the underlying principles. Our editorial decisions are guided by the assessment of experimental design, statistical rigor, reproducibility, and potential impact on the field.

Reproducibility and transparency are cornerstones of editorial philosophy. We require authors to provide detailed methods, share code and data where feasible, and clearly document analytical pipelines. For computational studies, we encouraged the deposition of scripts and workflows in public repositories. For the experimental work, we asked for a comprehensive reporting of reagents, protocols, and statistical approaches. We believe that open science practices not only strengthen individual publications but also accelerate scientific progress by enabling others to build upon published work.

In addition to full-length research articles, Contig welcomes reports describing new methods, software tools, databases, and other resources to advance the technical capabilities of the community. We recognize that methodological innovations are as valuable as conceptual breakthroughs and deserve rigorous peer review and wide dissemination.

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### **Peer Review and Transfer Options**

We are committed to a fair, constructive, and timely peer review. All submissions underwent rigorous evaluation by experts in the relevant fields, with editorial oversight to ensure a balanced assessment. To reduce redundant peer review and accelerate publication, Contig welcomes manuscripts accompanied by authoritative referee reports from Review Commons and other journals. Such submissions may be assessed with a reduced need for additional reviews, where feasible, allowing us to leverage existing evaluations while maintaining our editorial standards.

This approach recognizes that peer review is a collective scientific endeavours. By accepting and

building on prior reviews, we aim to streamline the publication process without compromising quality, ultimately benefiting authors and readers alike.

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### **Open Access and Global Reach**

As an open-access journal, Contig ensures that all published research is freely available to readers worldwide, thereby removing barriers to knowledge access. We believe that scientific findings, particularly those addressing global challenges in health, agriculture, and biodiversity, should be accessible to researchers, practitioners, policymakers, and the public regardless of institutional affiliation or geographic location. This commitment to openness aligns with evolving expectations in research funding and publishing ethics and positions Contig as a platform for truly global scientific collaboration.

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### **Multilingual Publishing and Living Documents**

In recognition of the global nature of scientific research and the importance of linguistic accessibility, Contig adopts an innovative approach to publication by simultaneously releasing articles in three languages. This multilingual framework ensures that research findings reach broader audiences across different linguistic communities, facilitating knowledge exchange and collaboration among researchers who may prefer to read scientific literature in their native language. By removing language barriers, we aim to democratize access to cutting-edge research and foster truly inclusive scientific dialogue.

All articles published in Contig are presented as dynamic HTML documents rather than static PDF files. This web-based format offers several advantages: enhanced readability across devices, integrated multimedia content, direct linking to references and data repositories, and improved accessibility for readers using assistive technologies. Moreover, HTML publication enables more sophisticated presentation of complex data, interactive figures, and embedded code, providing readers with richer engagement with published research.

Perhaps most importantly, the HTML format allows Contig to implement a "living document" model. Unlike traditional print-based publishing, where errors or ambiguities remain frozen in the published record, our platform permits post-publication corrections and clarifications. Authors may request modifications to their published articles to correct errors, clarify methodology, update citations, or add supplementary information. All such changes are subject to editorial review and approval to maintain scientific integrity and prevent misuse.

When post-publication modifications are made, we maintain full transparency through version control. Each revision is clearly documented with a timestamp, description of changes, and rationale. Readers can access the complete revision history, ensuring accountability while allowing the scientific record to evolve and improve over time. This approach acknowledges that scientific understanding is iterative and that published work may benefit from refinement as new insights emerge or methodological details require elaboration.

We believe this combination of multilingual accessibility and dynamic, correctable HTML publication represents a forward-looking model for scientific communication - one that prioritizes accuracy, transparency, and global reach while embracing the possibilities of digital technology.

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### **An Invitation to the Community**

We invited researchers from around the world to submit this work to Contig. The development of new algorithms for genome assembly, engineering synthetic biological circuits, mapping quantitative trait loci in crop species, or integrating multi-omics data to understand disease mechanisms, Contig offers a rigorous and supportive venue for future research. We are particularly eager to hear from early career scientists, researchers in emerging scientific communities, and those working at the intersection of

disciplines.

The launch of Contig presents an opportunity to shape a new publishing forum that reflects the values and priorities of the contemporary genetics and genomics community. We welcome feedback, suggestions, and engagement as we build this journal together. Through collaborative effort and a shared commitment to scientific excellence, we aim to make Contig a valued resource for advancing knowledge and addressing the pressing biological questions of our time.

We look forward to receiving your submissions and fostering a vibrant scientific community around Contig.

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