

## Genome Sequence of the Antibiotic-Resistant Pathogen *Elizabethkingia miricola* DSM 14571 Isolated from a Russian Space Station

*Elizabethkingia miricola* DSM 14571 was isolated from condensation water aboard a Russian space station and cultured on cysteine-lactose-electrolyte-deficient medium agar before genome sequencing, which revealed 4,064 predicted genes including virulence and resistance-associated elements.

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Genome of *Elizabethkingia miricola* DSM 14571

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### Abstract

*Elizabethkingia miricola* DSM 14571 is a Gram-negative opportunistic and antibiotic-resistant human pathogen isolated from a Russian space station. The genome contains 4,064 genes, including virulence factors and secondary metabolic clusters. This research could offer further insight into pathogenicity, environmental resilience, resistance mechanisms, and zoonotic risks.

### Announcement

#### *First section (introduction and rationale)*

*Elizabethkingia miricola* DSM 14571 is a Gram-negative, rod-shaped bacterium isolated from condensation on the Russian space station in 2003 (1). Astronauts used sterile swabs to sample the condensation water and cultured the bacteria on cysteine-lactose-electrolyte-deficient medium agar (2). *E. miricola* is primarily an opportunistic human pathogen associated with immunocompromised individuals, and has been isolated from other organisms, including amphibians (3). Sequencing its genome is necessary for understanding its pathogenicity, mechanisms of antibiotic resistance, and virulence factors, as well as insight into its ecological role and genetic potential (4). These findings will enhance our understanding of antibiotic-resistant pathogens and opportunistic pathogenicity, which will remain global health threats (5)

Overall, the sequencing of this genome is part of a broader study led by the Joint Genome Institute to explore microbial diversity and its functional implications in public health and environmental microbiology.

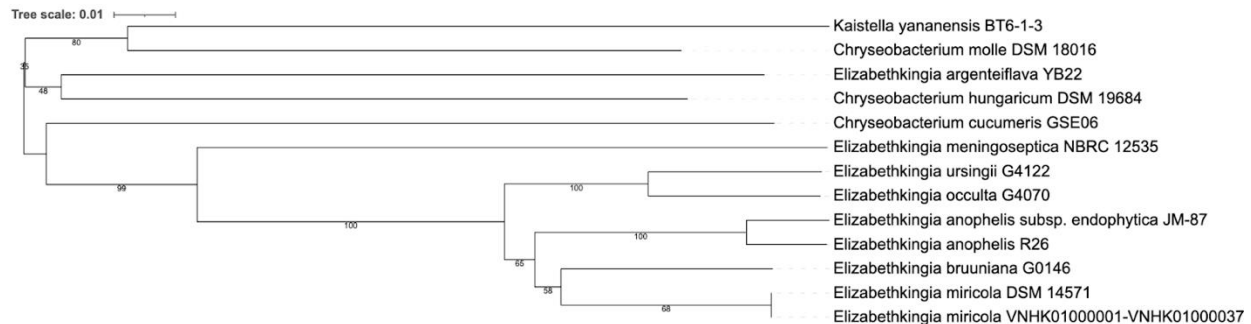
#### *Second section (methods and related outcomes)*

Details on organism growth and DNA isolation to be provided by DSMZ. The draft genome was sequenced at the DOE Joint Genome Institute (JGI) using Illumina technology (6). A standard Illumina shotgun library was prepared and sequenced on the Illumina HiSeq 2000 platform, generating 8,984,416 reads with a total output of 1,347.7 Mb. The raw Illumina sequence data was processed using DUK, a program developed at JGI, to remove known Illumina sequencing and library preparation artifacts (7). The sequencing depth was 270X, with a read length of 2×150 bp. Genome assembly was performed using Velvet (version 1.2.07), with the default settings applied (8). The final genome assembly was deemed 100% complete, with a contamination level of 0.35% (9). Annotation was conducted using the standard JGI Microbial Genome Annotation Pipeline (10).

#### *Final section (results)*

| Feature                     | Finding |
|-----------------------------|---------|
| Genome Length (bp)          | 4295221 |
| No. of scaffolds            | 37      |
| Scaffold N50 (bp)           | 303726  |
| Average fold coverage (x)   | 598     |
| GC content (%)              | 35.81   |
| No. of genes                | 4064    |
| No. of protein-coding genes | 4006    |
| No. of rRNA genes           | 6       |

|                   |    |
|-------------------|----|
| No. of tRNA genes | 46 |
|-------------------|----|



**Figure 1. Whole-genome-based phylogenetic classification of *Elizabethkingia miricola* DSM 14571.** The genome BLAST distance phylogeny (GBDP) tree was generated with the Type Strain Genome Server (TYGS [8]; accessed 15 March 2025). Tree inferred with FastME 2.1.6.1 [7] from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula  $d_5$ . The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 75.3 %. The tree was rooted at the midpoint [8].

Virulence factors that were found in the area of the genome include: carbamoyl phosphate synthase (Pyrimidine biosynthesis-Nutritional/Metabolic factor), endopeptidase Clp ATP-binding chain C (Stress survival), urease beta subunit UreB (Stress survival), urea amidohydrolase (Adherence), Hsp60 60K heat shock protein HtpB (Adherence), chaperonin GroEL (Adherence), botulinum neurotoxin (Exotoxin), and type 8 capsular polysaccharide synthesis protein Cap8D (Capsule-Immune modulation) (11). Analysis using the Comprehensive Antibiotic Resistance Database (CARD) (12) identified the presence of blaB-26 and GOB-32, both metallo- $\beta$ -lactamase genes associated with resistance to carbapenems, penicillin-class beta-lactams, and cephalosporins. Types of secondary metabolite clusters that were detected include: Non-alpha poly-amino acids like e-Polylysin, Class I lanthipeptides like nisin (most similar known cluster is pinensins), RRE-element containing cluster, NRPS-independent, lucA/lucC-like siderophores (most similar cluster is fulvivirgamide A2/fulvivirgamide B2/fulvivirgamide B3/fulvivirgamide B4) (13).

## Data availability statement

The whole genome shotgun sequence has been deposited in GenBank under the accession number [VNHK01000000](#). The raw reads have been deposited in the NCBI SRA under the accession number [SRX6767152](#). Additional data can be explored or downloaded from the JGI Integrated Microbial Genomes with Microbiomes (IMG/M) portal using the taxon ID 2593339301.

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# References

1. Lin J-N, Lai C-H, Yang C-H, Huang Y-H. 2019. *Elizabethkingia* Infections in Humans: From Genomics to Clinics. *Microorganisms* 7:295.
2. Kawamura Y, Li Y, Liu H, Huang X, Li Z, Ezaki T. 2001. Bacterial Population in Russian Space Station “Mir.” *Microbiology and Immunology* 45:819–828.
3. Soler-Iborte E, Rivera-Izquierdo M, Valero-Ubierna C. 2024. Opportunistic *Elizabethkingia miricola* Infections in Intensive Care Unit, Spain. *Emerg Infect Dis* 30.
4. Badawi K, Deskins S, Catherman K, Lastinger A. 2022. Out of this world: *Elizabethkingia miricola* complicated urinary tract infection in a patient with associated pubic symphysis osteomyelitis and pyomyositis. *IDCases* 29:e01573.
5. Qi P-Q, Zeng Y-J, Peng W, Kuai J. 2024. Lung imaging characteristics in a patient infected with *Elizabethkingia miricola* following cerebral hemorrhage surgery: A case report. *World J Clin Cases* 12:169–175.
6. Bennett S. 2004. Solexa Ltd. pgs 5:433–438
7. Aizenberg-Gershtein Y, Izhaki I, Lapidus A, Copeland A, Reddy T, Huntemann M, Pillay M, Markowitz V, Göker M, Woyke T, Klenk H-P, Kyrpides NC, Halpern M. 2016. High quality permanent draft genome sequence of *Phaseolibacter flectens* ATCC 12775T, a plant pathogen of French bean pods. *Stand in Genomic Sci* 11:4.
8. Zerbino DR, Birney E. 2008. Velvet: Algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res* 18:821–829.
9. Chklovski A, Parks DH, Woodcroft BJ, Tyson GW. 2024. Author Correction: CheckM2: a rapid, scalable and accurate tool for assessing microbial genome quality using machine learning. *Nat Methods* 21:735–735.

10. Huntemann M, Ivanova NN, Mavromatis K, Tripp HJ, Paez-Espino D, Palaniappan K, Szeto E, Pillay M, Chen I-MA, Pati A, Nielsen T, Markowitz VM, Kyrpides NC. 2015. The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). *Stand in Genomic Sci* 10:86.
11. Liu, B., Zheng, D., Zhou, S., Chen, L., & Yang, J. (2022). VFDB 2022: a general classification scheme for bacterial virulence factors. *Nucleic acids research*, 50(D1), D912-D917.
12. Alcock BP, Huynh W, Chalil R, Smith KW, Raphenya AR, Wlodarski MA, Edalatmand A, Petkau A, Syed SA, Tsang KK, Baker SJC, Dave M, McCarthy MC, Mukiri KM, Nasir JA, Golbon B, Imtiaz H, Jiang X, Kaur K, Kwong M, Liang ZC, Niu KC, Shan P, Yang JYJ, Gray KL, Hoad GR, Jia B, Bhando T, Carfrae LA, Farha MA, French S, Gordzevich R, Rachwalski K, Tu MM, Bordeleau E, Dooley D, Griffiths E, Zubyk HL, Brown ED, Maguire F, Beiko RG, Hsiao WWL, Brinkman FSL, Van Domselaar G, McArthur AG. 2023. CARD 2023: expanded curation, support for machine learning, and resistome prediction at the Comprehensive Antibiotic Resistance Database. *Nucleic Acids Research* 51:D690–D699.
13. Blin, K., Shaw, S., Augustijn, H. E., Reitz, Z. L., Biermann, F., Alanjary, M., ... & Weber, T. (2023). antiSMASH 7.0: new and improved predictions for detection, regulation, chemical structures and visualisation. *Nucleic acids research*, 51(W1), W46-W50.