

# <sup>1</sup> CGView.js: a JavaScript package for visualizing small genomes

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DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

## Software

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Submitted: 04 September 2025 <sup>13</sup>

Published: unpublished

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## <sup>5</sup> Summary

<sup>6</sup> Genome maps are routinely generated as a way of understanding or conveying the functional properties and sequence characteristics of organisms. CGView.js is a JavaScript-based viewer designed for microbial and organellar genomes, as well as plasmids. Inspired by the original <sup>9</sup> Java-based CGView ([Stothard & Wishart, 2005](#)), it generates high-quality interactive maps <sup>10</sup> that can easily be embedded in web pages. Its comprehensive API supports map manipulation <sup>11</sup> and integration with third-party tools, making it suitable for developers building bioinformatics <sup>12</sup> platforms.

## <sup>13</sup> Statement of need

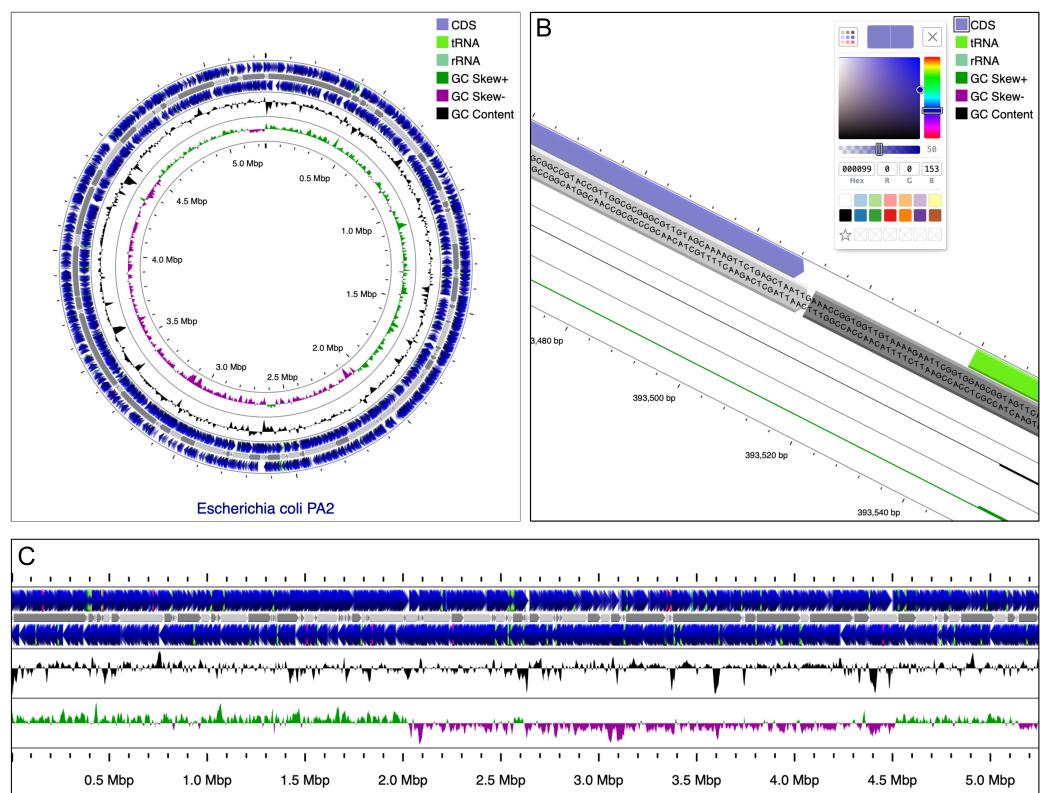
<sup>14</sup> Microbial and organellar genomics frequently require circular maps and fast navigation between scales. CGView.js addresses this need by providing circular and linear map layouts with <sup>15</sup> nucleotide-level detail, accessible through an embeddable component suited to web applications. <sup>16</sup> [Figure 1](#) shows examples of CGView.js circular and linear layouts, plus a zoomed view that <sup>17</sup> displays base-pair detail.

## <sup>19</sup> State of the field

<sup>20</sup> Several JavaScript-based genome browsers, including JBrowse ([Diesch et al., 2023](#)), igv.js <sup>21</sup> ([Robinson et al., 2022](#)), and pileup.js ([Vanderkam et al., 2016](#)), are widely used for general <sup>22</sup> genomics visualization. However, few support the circular maps that are often preferred for <sup>23</sup> microbial and organellar genomes, and none provide the rapid and smooth zooming to the <sup>24</sup> DNA sequence level available in CGView.js. CGView.js complements these tools by focusing <sup>25</sup> on circular visualization and tight integration into web pipelines rather than operating as a <sup>26</sup> standalone browser.

## <sup>27</sup> Software design

<sup>28</sup> CGView.js is an embeddable interactive map component, intended to be tightly integrated <sup>29</sup> into and managed by surrounding web applications. The API exposes common actions on map <sup>30</sup> components such as features, tracks, contigs, legends, and labels. A standard set of actions is <sup>31</sup> provided (read, add, remove, update, reorder). All actions (except “read”) trigger events that <sup>32</sup> can be used as hooks for callbacks. For example, the features-add event passes the added <sup>33</sup> features to a callback, enabling host tools to react dynamically.



**Figure 1:** CGView.js maps of the *Escherichia coli* PA2 genome (GenBank accession: GCF\_000335355.2) displaying sequence features and base composition plots. (A) Circular view of the genome. (B) Circular view zoomed to the base pair level, with the legend color picker shown in the top-right corner. (C) Linear view of the same genome.

34 Maps are rendered using the HTML canvas rather than SVG, which significantly improves  
 35 performance when displaying thousands of features. During animations such as zooming or  
 36 panning, the number of visible features is temporarily reduced to maintain responsiveness.  
 37 Once the animation completes, the map is redrawn at full detail.

38 CGView.js uses web workers to create GC skew, GC content, and ORF tracks based on the  
 39 provided genome sequence. Web workers generate these tracks in background threads without  
 40 blocking the user interface, allowing users to continue moving, zooming, or interacting with  
 41 the map. These processes communicate with the main thread to provide visual feedback in the  
 42 form of a growing progress track. When the worker is finished, the progress track is replaced  
 43 with the new plot or set of features.

44 The performance of CGView.js depends on the capabilities of the host system. No internal  
 45 limits are set on genome size or the number of features that can be displayed. However, large  
 46 genomes (e.g. more than 10 million base pairs) and large numbers of features (e.g. millions)  
 47 can result in slower map rendering and navigation. For this reason, we recommend using  
 48 CGView.js primarily for microbial and organellar genomes.

49 CGView.js maps can be quickly generated for sequences in GenBank, EMBL, and FASTA  
 50 formats using the companion CGParse.js package (<https://github.com/sciguy/cgview-parse>).  
 51 Features described in GenBank and EMBL files are automatically converted into CGView.js  
 52 features for display on the map. CGParse.js can also convert GFF3, GTF, BED, CSV,  
 53 and TSV files into CGView.js map features, allowing results from a variety of other sources  
 54 (e.g. third-party analysis tools) to be easily visualized.

55 Configuration and interchange rely on a lightweight CGView JSON format that stores genome

56 information and display settings. Maps can be imported from and exported to this format  
57 for sharing and archiving. Publication-ready output is supported through PNG export up to  
58 16,000 × 16,000 pixels and SVG export for downstream vector editing.

## 59 Research impact statement

60 Since its release in 2021, CGView.js has been integrated into multiple online bioinformatics  
61 platforms and web servers, including Proksee (Grant et al., 2023), PHATEST (Wishart, Han,  
62 et al., 2023), PlasMapper 3.0 (Wishart, Ren, et al., 2023), MOBHunter (Rojas-Villalobos et  
63 al., 2025), PLSDB (Molano et al., 2024), BASys2 (Poelzer et al., 2025), and HLRMDB (Zhai et  
64 al., 2025). In Proksee, hundreds of CGView.js maps are downloaded daily, indicating active  
65 external use.

66 The project website (<https://js.cgview.ca>) provides detailed documentation, examples, and  
67 tutorials that generate interactive maps directly from the shown code, supporting reproducibility  
68 and community uptake. Users who prefer a graphical interface can use Proksee (Grant et al.,  
69 2023), which renders maps with CGView.js and exposes many viewer settings through a GUI.

## 70 Conclusion

71 CGView.js enables the generation of high-quality interactive and static genome maps for  
72 microbial and organellar genomes. Its embeddable JavaScript design and comprehensive API  
73 make it suitable for integration into web-based platforms that visualize genomic annotations or  
74 pipeline outputs.

## 75 AI usage disclosure

76 Generative AI (ChatGPT) was used occasionally for issue triage, small code suggestions, and  
77 copy editing of documentation and this manuscript. All AI-assisted code and text were reviewed  
78 and verified by the authors. No figures or data were generated by AI.

## 79 Acknowledgements

80 This work was funded by Genome Alberta and Genome Canada.

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