

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

## COV2HTML

RRID:SCR\_002886

Type: Tool

### Proper Citation

COV2HTML (RRID:SCR\_002886)

### Resource Information

**URL:** <http://mmonot.eu/COV2HTML/connexion.php>

**Proper Citation:** COV2HTML (RRID:SCR\_002886)

**Description:** An interactive web interface addressed to biologists, allowing both coverage visualization and analysis of NGS alignments performed on prokaryotic organisms (bacteria and phages). Its strength is to make NGS analysis without software installation, login or long training period.

**Abbreviations:** COV2HTML

**Resource Type:** service resource, production service resource, analysis service resource, data analysis service

**Keywords:** next generation sequencing

**Availability:** Free, Available for download, Freely available

**Resource Name:** COV2HTML

**Resource ID:** SCR\_002886

**Alternate IDs:** OMICS\_01302

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260731T042643+0000

### Ratings and Alerts

No rating or validation information has been found for COV2HTML.

No alerts have been found for COV2HTML.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 9 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Boudry P, et al. (2021) Identification of RNAs bound by Hfq reveals widespread RNA partners and a sporulation regulator in the human pathogen *Clostridioides difficile*. *RNA biology*, 18(11), 1931.

Sekulovic O, et al. (2019) Expanding the repertoire of conservative site-specific recombination in *Clostridioides difficile*. *Anaerobe*, 60, 102073.

Blasdel BG, et al. (2017) Comparative transcriptomics analyses reveal the conservation of an ancestral infectious strategy in two bacteriophage genera. *The ISME journal*, 11(9), 1988.

Collery MM, et al. (2017) What's a SNP between friends: The influence of single nucleotide polymorphisms on virulence and phenotypes of *Clostridium difficile* strain 630 and derivatives. *Virulence*, 8(6), 767.

Namouchi A, et al. (2016) The *Mycobacterium tuberculosis* transcriptional landscape under genotoxic stress. *BMC genomics*, 17(1), 791.

Chevallereau A, et al. (2016) Next-Generation "-omics" Approaches Reveal a Massive Alteration of Host RNA Metabolism during Bacteriophage Infection of *Pseudomonas aeruginosa*. *PLoS genetics*, 12(7), e1006134.

Lévi-Meyrueis C, et al. (2014) Expanding the RpoS/σ<sup>S</sup>-network by RNA sequencing and identification of σ<sup>S</sup>-controlled small RNAs in *Salmonella*. *PloS one*, 9(5), e96918.

Saujet L, et al. (2013) Genome-wide analysis of cell type-specific gene transcription during spore formation in *Clostridium difficile*. *PLoS genetics*, 9(10), e1003756.

Soutourina OA, et al. (2013) Genome-wide identification of regulatory RNAs in the human pathogen *Clostridium difficile*. *PLoS genetics*, 9(5), e1003493.