

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 15, 2026

CRISPy-web

RRID:SCR_017970

Type: Tool

Proper Citation

CRISPy-web (RRID:SCR_017970)

Resource Information

URL: <https://crispy.secondarymetabolites.org>

Proper Citation: CRISPy-web (RRID:SCR_017970)

Description: Web tool to design sgRNAs for CRISPR applications. Web tool based on CRISPy to design sgRNAs for any user-provided microbial genome. Implemented as standalone web application for Cas9 target prediction.

Synonyms: single guide RNA desing

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:29062934](#)

Keywords: Design, sgRNA, CRISP, microbial, genome, Cas9, target, prediction, data, guide, single, editing, bio.tools

Funding: Novo Nordisk Foundation

Availability: Free, Freely available

Resource Name: CRISPy-web

Resource ID: SCR_017970

Alternate IDs: biotools:crispy

Alternate URLs: <https://bio.tools/crispy>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260912T195855+0000

Ratings and Alerts

No rating or validation information has been found for CRISPy-web.

No alerts have been found for CRISPy-web.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Popelá?ová B, et al. (2026) Mind the Porins: Differential Effects of Porin Knockouts and Overexpression on Glucose and Xylose Uptake and Utilization in *Pseudomonas putida*. *Microbial biotechnology*, 19(7), e70406.

Will PM, et al. (2026) Design and validation of an inducible and curable EvolvR system for directed evolution in *Corynebacterium glutamicum*. *Frontiers in bioengineering and biotechnology*, 14, 1827071.

Wilcken S, et al. (2025) The TetR-like regulator Sco4385 and Crp-like regulator Sco3571 modulate heterologous production of antibiotics in *Streptomyces coelicolor* M512. *Applied and environmental microbiology*, 91(5), e0231524.

Saraswat P, et al. (2025) Unlocking the potential of CRISPR tools and databases for precision genome editing. *Frontiers in plant science*, 16, 1563711.

Pipes BL, et al. (2025) Generation and validation of a versatile inducible multiplex CRISPRi system to examine bacterial regulation in the *Euprymna-Vibrio fischeri* symbiosis. *Archives of microbiology*, 207(7), 147.

Yan H, et al. (2025) A rational multi-target combination strategy for synergistic improvement of non-ribosomal peptide production. *Nature communications*, 16(1), 1883.

Sun Y, et al. (2025) Application of multiple genomic-editing technologies in *Streptomyces fungicidicus* for improved enduracidin yield. *Synthetic and systems biotechnology*, 10(2), 564.

Orsi E, et al. (2025) Computation-aided designs enable developing auxotrophic metabolic sensors for wide-range glyoxylate and glycolate detection. *Nature communications*, 16(1), 2168.

Wu Y, et al. (2025) Optimizing genome editing efficiency in *Streptomyces fradiae* via a CRISPR/Cas9n-mediated editing system. *Applied and environmental microbiology*, 91(2), e0195324.

Yang M, et al. (2024) Enhancement of acyl-CoA precursor supply for increased avermectin B1a production by engineering meilingmycin polyketide synthase and key

primary metabolic pathway genes. *Microbial biotechnology*, 17(5), e14470.

Li X, et al. (2024) Metabolic engineering of *Streptomyces roseosporus* for increased production of clinically important antibiotic daptomycin. *Microbial biotechnology*, 17(11), e70038.

Lei Y, et al. (2024) Transcriptionally induced nucleoid-associated protein-like *ccr1* in combined-culture serves as a global effector of *Streptomyces* secondary metabolism. *Frontiers in microbiology*, 15, 1422977.

Krusenstjerna AC, et al. (2024) DnaA modulates the gene expression and morphology of the Lyme disease spirochete. *bioRxiv : the preprint server for biology*.

Zhang Y, et al. (2024) Simultaneous multiplex genome loci editing of *Halomonas bluephagenesis* using an engineered CRISPR-guided base editor. *Synthetic and systems biotechnology*, 9(3), 586.

Liu X, et al. (2023) Identification of multiple regulatory genes involved in TGase production in *Streptomyces mobaraensis* DSM 40587. *Engineering microbiology*, 3(4), 100098.

McLean TC, et al. (2023) Evidence of a role for CutRS and actinorhodin in the secretion stress response in *Streptomyces coelicolor* M145. *Microbiology (Reading, England)*, 169(7).

Pankratz D, et al. (2023) An expanded CRISPR-Cas9-assisted recombineering toolkit for engineering genetically intractable *Pseudomonas aeruginosa* isolates. *Nature protocols*, 18(11), 3253.

Kim MS, et al. (2021) Cytosine Base Editor-Mediated Multiplex Genome Editing to Accelerate Discovery of Novel Antibiotics in *Bacillus subtilis* and *Paenibacillus polymyxa*. *Frontiers in microbiology*, 12, 691839.

Román-Hurtado F, et al. (2021) One Pathway, Two Cyclic Non-Ribosomal Pentapeptides: Heterologous Expression of BE-18257 Antibiotics and Pentaminomycins from *Streptomyces cacaoi* CA-170360. *Microorganisms*, 9(1).

Ntie-Kang F, et al. (2021) Computational Applications in Secondary Metabolite Discovery (CAiSMD): an online workshop. *Journal of cheminformatics*, 13(1), 64.