

DOI 10.7764/ijanr.v52i1.2592

RESEARCH NOTE

The complete plastid genome of *Strombocarpa burkartii* (Caesalpinioideae, Mimosoid clade), an endangered species from the Atacama Desert (Chile)

Roberto Contreras-Díaz^{1,4}, Felipe Carevic^{2,4} Mariana Arias-Aburto³

¹Centro Regional de Investigación y Desarrollo Sustentable de Atacama (CRIDESAT). Universidad de Atacama, Copiapó, Chile.

²Laboratorio de Ecología Vegetal, Facultad de Recursos Naturales Renovables. Universidad Arturo Prat, Campus Huayquique, Iquique, Chile.

³Máster universitario de Bioinformática y Bioestadística, Universitat Oberta de Catalunya. Barcelona, España.

⁴Núcleo Milenio de Ecología Histórica Aplicada para los Bosques Áridos (AFOREST). Santiago, Chile.

Abstract

R. Contreras-Díaz, F. Carevic, and M. Arias-Aburto. 2025. The complete plastid genome of *Strombocarpa burkartii* (Caesalpinioideae, Mimosoid clade), an endangered species from the Atacama Desert (Chile). Int. J. Agric. Nat. Resour. 55-61. In this study, we assembled the complete plastid genome of *Strombocarpa burkartii*, an endangered species inhabiting the Atacama Desert (Chile). Here, we describe the structure and phylogeny of the complete plastid genome of *S. burkartii*. The plastid genome consisted of 162,104 bp, with typical quadripartite structures: a large single copy (91,119 bp), a small single copy (18,643 bp), and two inverted repeats (26,171 bp). A complete plastid analysis of *S. burkartii* revealed 128 genes, including 83 protein-coding genes, 37 tRNA genes and 8 rRNA genes. Phylogenetic analysis of 21 complete plastid genomes confirmed the placement of *S. burkartii* within the genus *Strombocarpa* (Mimosoid clade). In the present work, we report the complete plastid genome of *S. burkartii* for the first time, which can be used for future studies on population genetics, evolution, and conservation.

Keywords: Atacama Desert; Plastome; *Prosopis*; *Strombocarpa*

Highlights

- The complete plastid genome of *S. burkartii* was assembled and annotated, revealing a total length of 162,104 bp
- The plastid genome contains 128 genes, including 83 protein-coding genes (PCGs), 8 rRNA genes, and 37 tRNA genes.
- Phylogenomic analysis revealed that *S. burkartii* forms a monophyletic clade with *S. strombulifera* and *S. tamarugo*, with strong support (BS=100).
- The genome data can be used to study

genotypes, haplotype diversity, intraspecific variation, and evolutionary pathways within the genus *Strombocarpa*.

Introduction

The genus *Prosopis* L. (Fabaceae, Caesalpinioideae, mimosoid clade) comprises approximately 57 species placed in five sections (*Anonychium*, *Prosopis*, *Strombocarpa*, *Monilicarpa* and *Algarobia*) (Burkart, 1976). The endemic *Prosopis burkartii* Muñoz species from the formerly known *Strombocarpa* section is found in the Atacama Desert, specifically the Pampa del Tamarugal (Contreras et al., 2020). The scientific names of this species and the concept of *Prosopis* established by Bentham (1875) and Burkart (1976) have only recently been deconstructed (Hughes et al., 2022) because *Prosopis* was found to be polyphyletic (Catalano et al., 2008); therefore, *P. burkartii* was renamed *Strombocarpa burkartii* (Muñoz) C.E. Hughes & G.P. Lewis. In terms of conservation status, *S. burkartii* is listed as critically endangered (MMA, 2024). *Strombocarpa burkartii* presents a shrub-like structure, intense basal branching, a tangled habit and an absence of rhizomes (Figure 1A) (Muñoz, 1971). Its fruits are bispherical and have a septate endocarp, a diagnostic characteristic of

the *Strombocarpa* section; furthermore, they are compacted and grouped in glomerulus form (Figure 1B), whereas the seeds are flattened, hard and brown (Figure 1C) (Muñoz, 1971). *Strombocarpa burkartii* has not been studied in depth in relation to other *Strombocarpa* species (Contreras-Díaz et al., 2021, 2024). Molecular genetic methods based on nuclear and organelle genomes have proven to be essential tools for plant phylogenetic, phylogeographic and genome evolution studies (Bessega et al., 2021; Catalano et al., 2008; Contreras et al., 2020); however, no information for *S. burkartii* has been available until now. We hypothesize that the plastid genome information of *S. burkartii* would reveal phylogenetic closeness, structure and genes such as those of *S. tamarugo*. For this reason, we used Next Generation Sequencing (NGS) and assembled the complete plastid genome of *S. burkartii* to determine its structure and phylogenetic relationship compared with other closely related species within the tribe *Mimoseae*, where the genus *Strombocarpa* is found.

Materials and Methods

Single fresh samples of *S. burkartii* were collected by Roberto Contreras-Díaz from near La Tirana town of Provincia del Tamarugal in Chile



Figure 1. *Strombocarpa burkartii* (Muñoz) C.E. Hughes & G.P. Lewis. Field photographs of one complete shrub (A), fruit (B) and seeds (C). The photograph was taken near La Tirana, Provincia del Tamarugal, Chile.

(GPS: 20°24'45.0"S, 69°41'29.7"W; 896 msl). The research permit for sampling was approved by CONAF (National Forestry Corporation) N° N00024/08-11-2019 (JBH/FAP/JVO) and N° N00003-2023/27-01-2023 (NOO/FAP/JVO). The samples were identified using the taxonomic criteria described by Burkart (1976). Moreover, the voucher specimens (EIF13355) were deposited in the Herbarium EIF of the Facultad de Ciencias Forestales y de la Conservación de la Naturaleza (<https://sweetgum.nybg.org/science/ih/herbarium-details/?irn=126262>), Universidad de Chile (Dr. Nicolás García; herbarium curator; ngarcia@uchile.cl).

The total DNA of *S. burkartii* was extracted using a modified CTAB method (Contreras-Díaz et al., 2021). Genomic paired-end sequencing (PE150) was performed on an Illumina NovaSeq 6000, and approximately 24 GB of clean reads were generated; sequencing was performed by Novogene Corporation, Inc. (Sacramento, CA), and library preparation was performed using the Standard 350 bp DNA library (Illumina, San Diego, CA). Trim Galore was used to filter low-quality reads and sequencing adapters. The complete plastid genome was *de novo* assembled using GetOrganelle v1.7.5 (Jin et al., 2020) with default parameters. The complete plastome was annotated using the online tool CPGAVAS2 (Shi et al., 2019), and a circular map of the plastome genome was generated using the CPGView program (Liu et al., 2023). The annotated plastid genome was submitted to the NCBI GenBank database with the assigned accession PP646452.

Phylogenetic analyses were conducted using complete plastid genome sequences of 20 species of the tribe *Mimoseae*, and one species of the tribe *Acacieae* was included as an outgroup. Thus, the complete plastid genome sequences that were used in the phylogenomic analysis included *S. burkartii* (PP646452), *Neltuma alba* (Griseb.) C.E. Hughes & G.P. Lewis (OP672364), *Neltuma chilensis* (Molina) C.E. Hughes & G.P. Lewis (OP672365), *Strombocarpa strombulifera* (Lam.) A.

Gray (OP672366), *Strombocarpa tamarugo* (Phil.) C.E. Hughes & G.P. Lewis (MW582314), *Neltuma glandulosa* (Torr.) Britton & Rose (NC_026683), *Neltuma juliflora* (Sw.) Raf. (MN104889), *Neltuma pallida* (Humb. & Bonpl. ex Willd.) C.E. Hughes & G.P. Lewis (NC_084206), *Prosopis farcta* (Banks & Sol.) J.F. Macbr. (MZ073639), *Cylicodiscus gabunensis* Harms (MZ274089), *Piptadeniastrum africanum* (Hook.f.) Brenan. (MZ274093), *Xylia xylocarpa* (Roxb.) W.Theob. (NC_057267), *Adenanthera microsperma* Teijsm. & Binn. (NC_034986), *Dichrostachys cinerea* (L.) Wight & Arn. (NC_035346), *Leucaena trichandra* (Zucc.) Urb. (NC_028733), *Parkia javanica* (Lam.) Merr. (NC_034989), *Piptadenia communis* Benth. (NC_034990), *Stryphnodendron adstringens* (Mart.) Coville (NC_044627), *Mimosa diplotricha* var. *intermis* (Adelb.) M.K. Alam & M. Yusof (OM585629), *Mimosa pigra* L. (NC_061906), and *Acacia ligulata* A.Cunn. ex Benth. (NC_045513) as outgroup species. The complete plastid genome sequences with default parameters were aligned using MAFFT software (Katoh & Standley, 2013). We used the complete alignment of the genomes (including gaps) in the analyses. The best-fitting nucleotide substitution model of sequence evolution, model TVM+G4, was determined using the Corrected Akaike Information Criterion (AICc) through Modeltest-NG v.0.1.5 on XSEDE. The maximum likelihood (ML) inference was carried out using RAxML-HPC BlackBox v.8.1.12 with 1,000 bootstrap replicates, using the CIPRES Science Gateway v3.3 (Miller et al., 2010). Nonparametric bootstrap support (BS) values were used to measure the internal nodes of the resulting trees.

Results and discussion

Genomic research with NGS technology has revolutionized the field of genomics, allowing efficient sequencing of complete plastid genomes (Satam et al., 2023). Here, we successfully assembled and annotated the plastid genome sequence of *S. burkartii*. The plastid genome of *S. burkartii*

is composed of four regions, with a total length of 162,104 bp (Figure 2). The two inverted repeat regions (IRs) contain 26,171 bp and are separated by a large single copy region (LSC) of 91,119 bp and a small single copy region (SSC) of 18,643 bp (Figure 2). Therefore, the length of the *S. burkartii* plastid sequence (162,104 bp) is greater than those of *S. strombulifera* (160,569 bp) and *S. tamarugo* (161,575 bp) (Contreras-Díaz et al., 2024). The GC content in the plastid genome of *S. burkartii* was 36%, similar to that in *S. strombulifera* (36,2%) and *S. tamarugo* (36%) (Contreras-Díaz et al., 2024). A total of 128 genes were predicted,

including 83 protein-coding genes (PCGs), eight rRNA genes, and 37 tRNA genes. Six unique PCGs (*rps12*, *rps7*, *rpl2*, *rpl23*, *ndhB*, and *ycf2*), seven unique tRNA genes (*trnA-UGC*, *trnI-GAU*, *trnL-CAA*, *trnI-CAU*, *trnN-GUU*, *trnR-UGC* and *trnV-GAC*) and four unique rRNA genes (*rrn16S*, *rrn23S*, *rrn4.5S*, and *rrn5S*) were located in the IR regions. In the complete plastome, fourteen genes (*rps16*, *rpoC1*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *ndhA*, *trnK-UUU*, *trnG-GCC*, *trnL-UAA*, *trnV-UAC*, *trnI-GAU* and *trnA-UGC*) contained one intron each, whereas two genes (*ycf3* and *clpP*) contained two introns. These results confirm that

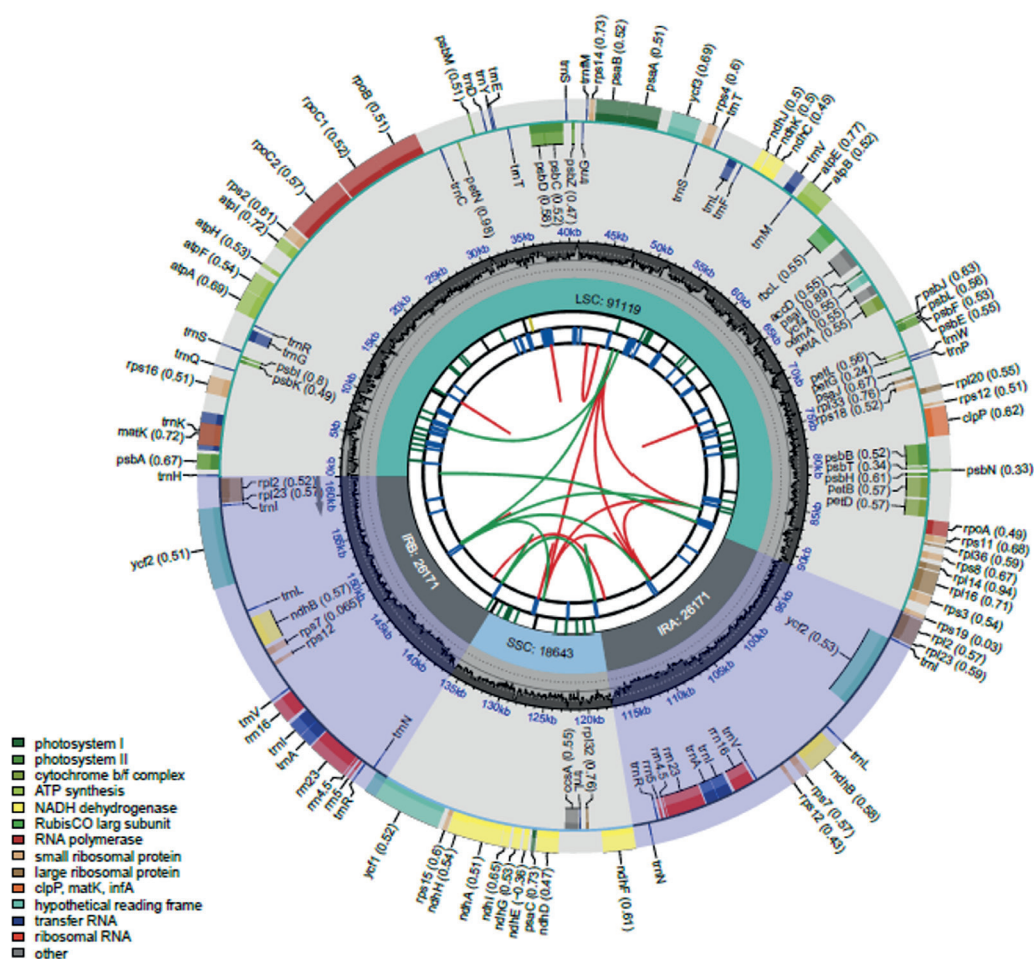


Figure 2. Circular map of the plastid genome of *Strombocarpa burkartii*. The map is comprised of six circles. The first circle represents the forward and reverse repeats indicated by red and green arcs, respectively. The second and third circles are indicated by short bars for tandem repeats and microsatellite sequences, respectively. The fourth circle shows the plastome structure (LSC, SSC, IRA, and IRB regions). The fifth circle shows the GC ratio in dark gray. Genes with different functions are color-coded on the sixth circle, and the optional codon usage bias is shown in parentheses after the gene name.

S. burkartii has the same number of genes as *S. tamarugo* and *S. strombulifera* (Contreras-Díaz et al., 2024). However, the length of the complete sequence of *S. burkartii* is ~708 bp longer than that of *S. tamarugo* because two polymorphic zones (gaps or indels) are located at positions 16,558 and 31,155 (when *S. burkartii* is aligned with *S. tamarugo*).

ML phylogenomic analysis revealed that the twenty *Mimoseae* species were segregated into eight clades, which support the genera *Prosopis*, *Strombocarpa* and *Neltuma* (BS=100) (Figure 3), as described by Contreras-Díaz et al., (2024). Within the *Neltuma* cluster, *N. alba*, *N. chilensis*, *N. juliflora*, *N. glandulosa* and *N. pallida* (BS=100) were identified, whereas the *Prosopis* cluster included only *P. farcta*. The phylogenetic tree revealed that *S. burkartii* and two *Strombocarpa*

species (*S. strombulifera* and *S. tamarugo*) formed a monophyletic clade (BS=100) (Figure 3), and the analysis strongly supported *S. burkartii* as a sister species of *S. tamarugo* (BS=100). These results were consistent with those of previous studies, indicating a clear division of the species into distinct clades (Catalano et al., 2008; Contreras et al., 2020). In fact, the old *Prosopis* L. cluster (57 species) is currently divided into six genera: *Anonychium*, *Prosopis*, *Neltuma*, *Strombocarpa*, *Xerocladia* and *Indopiptadenia* (Hughes et al., 2022). Moreover, one study revealed that *S. tamarugo* and *S. strombulifera* are involved in the formation of *S. burkartii* (Burkart, 1976; Contreras et al., 2020). Therefore, we deduced that the plastid genome of *S. burkartii* has *S. tamarugo* as its maternal parent, which was also reported by Contreras et al. (2020). This work helps to increase the evidence for *Prosopis* disintegration,

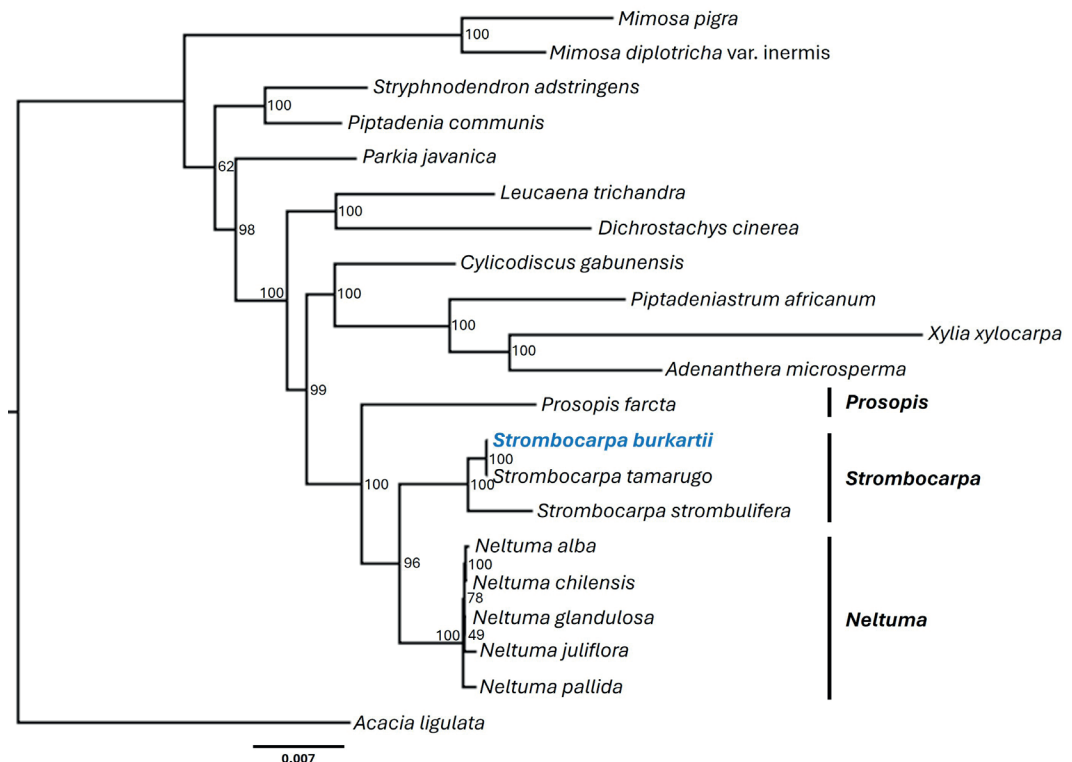


Figure 3. The maximum-likelihood tree was constructed on the basis of the twenty plastid genome sequences of *Mimoseae* species and *Acacia ligulata* as outgroup species. The bootstrap support values are placed on the nodes.

grouping *S. burkartii* with their possible parental species, *S. strombulifera* and *S. tamarugo*. Here, for the first time, we report the complete structure of the plastid genome structure and genes of endangered *S. burkartii*, which could be used to determine genotypes, haplotype diversity, intraspecific variation and evolutionary paths in the genus *Strombocarpa*.

Funding

RC thanks projects ANID-FONDECYT initiation 11230668 and DIUDA 22423 (Universidad de Atacama). RC and FC thanks AFOREST, a Millenium Nucleus supported by ANID – MI-LENIO – NCS2022_024.

References

- Bessega, C., Pometti, C., Fortunato, R., Greene, F., Santoro, C. M. & McRostie, V. (2021). Genetic studies of various *Prosopis* species (*Leguminosae*, Section *Algarobia*) co-occurring in oases of the Atacama Desert (northern Chile). *Ecology and Evolution*, 11(5), 2375-2390. <https://doi.org/10.1002/ece3.7212>
- Burkart, A. (1976). A monograph of the genus *Prosopis* (*Leguminosae* subfam. *Mimosoideae*). *Journal of the Arnold Arboretum*, 450-525. <https://www.jstor.org/stable/43781999>
- Catalano, S. A., Vilardi, J. C., Tosto, D. & Saidman, B. O. (2008). Molecular phylogeny and diversification history of *Prosopis* (*Fabaceae: Mimosoideae*). *Biological Journal of the Linnean Society*, 93(3), 621-640. <https://doi.org/10.1111/j.1095-8312.2007.00907.x>
- Contreras-Díaz, R., Carevic, F. S., van den Brink, L., Huanca-Mamani, W. & Jung, P. (2024). Structure, gene composition, divergence time and phylogeny analysis of the woody desert species *Neltuma alba*, *Neltuma chilensis* and *Strombocarpa strombulifera*. *Scientific Reports*, 14(1). <https://doi.org/10.1038/s41598-024-64287-y>
- Contreras-Díaz, R., van den Brink, L., Navarrete-Fuentes, M. J. & Arias-Aburto, M. (2021). Characterization of the complete chloroplast genome of *Prosopis tamarugo* (*Prosopis*, *Leguminosae*), an endangered endemic tree species from the Atacama Desert. *Bosque*, 42(3), 365-370. <https://doi.org/10.4067/S0717-92002021000300365>
- Contreras, R., Carevic, F. S., Porcile, V. & Arias, M. (2020). Development of ssr loci in *Prosopis tamarugo* phillipi and assessment of their transferability to species of the *Strombocarpa* section. *Forest Systems*, 29(2), 1-10. <https://doi.org/10.5424/fs/2020292-16706>
- Contreras, R., van den Brink, L., Burgos, B., González, M. & Gacitúa, S. (2020). Genetic characterization of an endangered chilean endemic species, *Prosopis burkartii* Muñoz, reveals its hybrids parentage. *Plants*, 9(6), 1-19. <https://doi.org/10.3390/plants9060744>
- Hughes, C. E., Ringelberg, J. J., Lewis, G. P. & Catalano, S. A. (2022). Disintegration of the genus *Prosopis* L. (*Leguminosae*, *Caesalpinioideae*, *mimosoid* clade). *PhytoKeys*, 205, 147-189. <https://doi.org/10.3897/PHYTOKEYS.205.75379>
- Jin, J. J., Yu, W. Bin, Yang, J. B., Song, Y., Depamphilis, C. W., Yi, T. S. & Li, D. Z. (2020). GetOrganelle: A fast and versatile toolkit for accurate de novo assembly of organelle genomes. *Genome Biology*, 21(1), 241. <https://doi.org/10.1186/s13059-020-02154-5>
- Katoh, K. & Standley, D. M. (2013). MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. *Molecular Biology and Evolution*, 30(4), 772-780. <https://doi.org/10.1093/molbev/mst010>
- Liu, S., Ni, Y., Li, J., Zhang, X., Yang, H., Chen, H. & Liu, C. (2023). CPGView: A package for visualizing detailed chloroplast genome structures. *Molecular Ecology Resources*, 23(3), 694-704. <https://doi.org/10.1111/1755-0998.13729>
- Miller, M. A., Pfeiffer, W. & Schwartz, T. (2010). Creating the CIPRES Science Gateway for inference of large phylogenetic trees. *2010 Gateway Computing Environments Workshop, GCE 2010*. <https://doi.org/10.1109/GCE.2010.5676129>
- MMA. (2024). *Prosopis burkartii* Muñoz P08, estado de conservación en Peligro Crítico. Ministerio de Medio Ambiente. <https://clasificacionespecies.mma.gob.cl/wp-content/uploads/2019/10/>

- Prosopis_burkartii_P08_propuesta.pdf
- Muñoz, P. (1971). Una nueva especie de *Prosopis* para el norte de Chile. *Bol. Mus. Nac. Hist. Nat. Chile*, 32, 363-370.
- Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., Thakare, R. P., Banday, S., Mishra, A. K., Das, G. & Malonia, S. K. (2023). Next-Generation Sequencing Technology: Current Trends and Advancements. *Biology*, 12(7), 997. <https://doi.org/10.3390/biology12070997>
- Shi, L., Chen, H., Jiang, M., Wang, L., Wu, X., Huang, L. & Liu, C. (2019). CPGAVAS2, an integrated plastome sequence annotator and analyzer. *Nucleic Acids Research*, 47(W1), W65-W73. <https://doi.org/10.1093/nar/gkz345>

