

Publicaciones

1. Escriche y col. 2001. Effect of Ozone Treatment and Storage Temperature on Physicochemical Properties of Mushrooms (*Agaricus bisporus*). <https://doi.org/10.1106/6A9R-DKEV-ADV7-Y30X>
2. Retamales y col. 2002. Development of the sexual reproductive cycle of *Xanthophyllomyces dendrorhous*. [https://doi.org/10.1016/S0167-7012\(01\)00349-9](https://doi.org/10.1016/S0167-7012(01)00349-9)
3. Muñoz y col. 2002. Vegetables Collected in the Cultivated Andean Area of Northern Chile: Total and Inorganic Arsenic Contents in Raw Vegetables. <https://doi.org/10.1021/jf011027k>
4. Ganga y Martínez. 2004. Effect of wine yeast monoculture practice on the biodiversity of non-*Saccharomyces* yeasts. <https://doi.org/10.1046/j.1365-2672.2003.02080.x>
5. Martínez y col. 2004. Genomic characterization of *Saccharomyces cerevisiae* strains isolated from wine-producing areas in South America. <https://doi.org/10.1111/j.1365-2672.2004.02255.x>
6. Combina y col. 2005. Yeasts associated to Malbec grape berries from Mendoza, Argentina. <https://doi.org/10.1111/j.1365-2672.2005.02540.x>
7. Combina y col. 2005. Dynamics of indigenous yeast populations during spontaneous fermentation of wines from Mendoza, Argentina. <https://doi.org/10.1016/j.ijfoodmicro.2004.08.017>
8. Muñoz y col. 2005. Estimation of the dietary intake of cadmium, lead, mercury, and arsenic by the population of Santiago (Chile) using a Total Diet Study. <https://doi.org/10.1016/j.fct.2005.05.006>
9. Martínez y col. 2006. Production of *Rhodotorula glutinis*: A yeast that secretes α -L-arabinofuranosidase. <https://doi.org/10.2225/vol9-issue4-fulltext-8>
10. Martínez y col. 2007. High degree of correlation between molecular polymorphism and geographic origin of wine yeast strains. <https://doi.org/10.1111/j.1365-2672.2007.03493.x>

11. Combina y col. 2008. Yeast identification in grape juice concentrates from Argentina. <https://doi.org/10.1111/j.1472-765X.2007.02291.x>
12. Godoy y col. 2008. Purification and characterization of a p-coumarate decarboxylase and a vinylphenol reductase from *Brettanomyces bruxellensis*. <https://doi.org/10.1016/j.ijfoodmicro.2008.05.011>
13. Contreras y col. 2008. Polymerase chain reaction confirmatory method for microbiological detection of *Brettanomyces bruxellensis* in wines. <https://doi.org/10.1111/j.1745-4581.2008.00137.x>
14. Niklitschek y col. 2008. Genomic organization of the structural genes controlling the astaxanthin biosynthesis pathway of *Xanthophyllomyces dendrorhous*. <http://dx.doi.org/10.4067/S0716-9760200800010001>
15. Salinas y col. 2009. Taqman real-time PCR for the detection and enumeration of *Saccharomyces cerevisiae* in wine. <https://doi.org/10.1016/j.fm.2008.12.001>
16. Godoy y col. 2009. Study of the coumarate decarboxylase and vinylphenol reductase activities of *Dekkera bruxellensis* (anamorph *Brettanomyces bruxellensis*) isolates. <https://doi.org/10.1111/j.1472-765X.2009.02556.x>
17. Cubillos y col. 2009. Self-fertilization is the main sexual reproduction mechanism in native wine yeast populations. <https://doi.org/10.1111/j.1574-6941.2008.00600.x>
18. Medina y col. 2010. Study on image analysis application for identification Quinoa seeds (*Chenopodium quinoa* Willd) geographical provenance. <https://doi.org/10.1016/j.lwt.2009.07.010>
19. Salinas y col. 2010. Genomic and phenotypic comparison between similar wine yeast strains of *Saccharomyces cerevisiae* from different geographic origins. <https://doi.org/10.1111/j.1365-2672.2010.04689.x>

20. García y col. 2010. Effects of using mixed wine yeast cultures in the production of Chardonnay wines. <https://www.redalyc.org/articulo.oa?id=213014867015>
21. Saavedra y col. 2011. Chemometric approaches for the zoning of Pinot Noir wines from the Casablanca valley, Chile. <https://doi.org/10.1016/j.foodchem.2011.01.132>
22. Ganga y col. 2011. Cinnamic acid, ethanol and temperature interaction on coumarate decarboxylase activity and the relative expression of the putative *cd* gene in *D. bruxellensis*. <https://doi.org/10.2225/vol14-issue5-fulltext-2>
23. Díaz y col. 2011. Low occurrence of patulin-producing strains of penicillium in grapes and patulin degradation during winemaking in Chile. <https://doi.org/10.5344/ajev.2011.11034>
24. Mercado y col. 2011. Biodiversity of *Saccharomyces cerevisiae* populations in Malbec vineyards from the "Zona Alta del Río Mendoza" region in Argentina. <https://doi.org/10.1016/j.ijfoodmicro.2011.09.026>
25. García y col. 2012. Development and characterization of hybrids from native wine yeasts. <https://doi.org/10.1590/S1517-83822012000200008>
26. Salinas y col. 2012. The genetic basis of natural variation in oenological traits in *Saccharomyces cerevisiae*. <https://doi.org/10.1371/journal.pone.0049640>
27. Contreras y col. 2012. Identification of genes related to nitrogen uptake in wine strains of *Saccharomyces cerevisiae*. <https://doi.org/10.1007/s11274-011-0911-3>
28. Yáñez y col. 2012. Chemometric Analysis for the Detection of Biogenic Amines in Chilean Cabernet Sauvignon Wines: A Comparative Study between Organic and Nonorganic Production. 10.1111/j.1750- <https://doi.org/3841.2012.02796.x>
29. Sangorrín y col. 2013. Molecular and physiological comparison of spoilage wine yeasts. <https://doi.org/10.1111/jam.12134>

30. Martínez y col. 2013. Gene expression of specific enological traits in wine fermentation. <https://doi.org/10.2225/vol16-issue4-fulltext-8>
31. Cubillos y col. 2013. High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <https://doi.org/10.1534/genetics.113.155515>
32. Vaca y col. 2013. Cultivable psychrotolerant yeasts associated with Antarctic marine sponges. <https://doi.org/10.1007/s11274-012-1159-2>
33. Martínez y col. 2014. The *ICY1* gene from *Saccharomyces cerevisiae* affects nitrogen consumption during alcoholic fermentation. <https://doi.org/10.1016/j.ejbt.2014.04.006>
34. Jara y col. 2014. Mapping genetic variants underlying differences in the central nitrogen metabolism in fermenter yeasts. <https://doi.org/10.1371/journal.pone.0086533>
35. Godoy y col. 2014. Identification of the *Dekkera bruxellensis* phenolic acid decarboxylase (PAD) gene responsible for wine spoilage. <https://doi.org/10.1016/j.foodcont.2014.03.041>
36. Valdés y col. 2014. Draft genome sequence and transcriptome analysis of the wine spoilage yeast *Dekkera bruxellensis* LAMAP2480 provides insights into genetic diversity, metabolism and survival. <https://doi.org/10.1111/1574-6968.12630>
37. Sturm et al. 2015. Relation between coumarate decarboxylase and vinylphenol reductase activity with regard to the production of volatile phenols by native *Dekkera bruxellensis* strains under 'wine-like' conditions. <https://doi.org/10.1016/j.ijfoodmicro.2015.04.023>
38. Coronado y col. 2015. Comparison of the behaviour of *Brettanomyces bruxellensis* strain LAMAP L2480 growing in authentic and synthetic wines. <https://doi.org/10.1007/s10482-015-0413-7>
39. Junqueira-Gonçalves y col. 2015. Isolation and characterization of phenolic compounds and anthocyanins from Murta (*Ugni molinae*)

- Turcz.) fruits. Assessment of antioxidant and antibacterial activity. <https://doi.org/10.3390/molecules20045698>
40. Salinas y col. 2016. Natural variation in non-coding regions underlying phenotypic diversity in budding yeast. <https://doi.org/10.1038/srep21849>
 41. Kessi-Pérez y col. 2016. *RIM15* antagonistic pleiotropy is responsible for differences in fermentation and stress response kinetics in budding yeast. <https://doi.org/10.1093/femsyr/fow021>
 42. Cubillos. 2016. Exploiting budding yeast natural variation for industrial processes. <https://doi.org/10.1007/s00294-016-0602-6>
 43. Palacios y col. 2016. β -Galactosidase activity in microorganisms isolated from Antarctic environments. <https://doi.org/10.1016/j.nbt.2016.06.1100>
 44. Godoy y col. 2016. Comparative transcriptome assembly and genome-guided profiling for *Brettanomyces bruxellensis* LAMAP2480 during p-coumaric acid stress. <https://doi.org/10.1038/srep34304>
 45. González y col. 2017. Survival and Growth Improvement of Palm Ruff, *Seriolella violacea*, Larvae Fed *Artemia* Nauplii Enriched with an Experimental Emulsion. <https://doi.org/10.1111/jwas.12375>
 46. Rojo y col. 2017. Incidence of osmophilic yeasts and *Zygosaccharomyces rouxii* during the production of concentrate grape juices. <https://doi.org/10.1016/j.fm.2016.11.017>
 47. Cubillos y col. 2017. Identification of Nitrogen Consumption Genetic Variants in Yeast Through QTL Mapping and Bulk Segregant RNA-Seq Analyses. <https://doi.org/10.1534/g3.117.042127>
 48. Godoy y col. 2017. Metabolism, Survival Strategies, and Biotechnological Applications of *Brettanomyces bruxellensis* LAMAP2480. <https://doi.org/10.1159/000471924>

49. Quispe y col. 2017. Genetic basis of mycotoxin susceptibility differences between budding yeast isolates. <https://doi.org/10.1038/s41598-017-09471-z>
50. Brice y col. 2018. Adaptability of the *Saccharomyces cerevisiae* yeasts to wine fermentation conditions relies on their strong ability to consume nitrogen. <https://doi.org/10.1371/journal.pone.0192383>
51. Lorca y col. 2018. Screening of native *S. cerevisiae* strains in the production of Pajarete wine: a tradition of Atacama Region, Chile. <https://doi.org/10.1080/09571264.2018.1465900>
52. Tapia y col. 2018. *GPD1* and *ADH3* Natural Variants Underlie Glycerol Yield Differences in Wine Fermentation. <https://doi.org/10.3389/fmicb.2018.01460>
53. Candia-Onfray y col. 2018. Treatment of winery wastewater by anodic oxidation using BDD electrode. <https://doi.org/10.1016/j.chemosphere.2018.04.175>
54. Salinas y col. 2018. Fungal Light-Oxygen-Voltage Domains for Optogenetic Control of Gene Expression and Flocculation in Yeast. <https://doi.org/10.1128/mBio.00626-18>
55. Kessi-Pérez y col. 2019. Indirect monitoring of TORC1 signalling pathway reveals molecular diversity among different yeast strains. <https://doi.org/10.1002/yea.3351>
56. Oporto y col. 2019. Distinct Transcriptional Changes in Response to Patulin Underlie Toxin Biosorption Differences in *Saccharomyces cerevisiae*. <https://doi.org/10.3390/toxins11070400>
57. Molinet y col. 2019. Genetic variants of TORC1 signaling pathway affect nitrogen consumption in *Saccharomyces cerevisiae* during alcoholic fermentation. <https://doi.org/10.1371/journal.pone.0220515>
58. Kessi-Pérez y col. 2019. *KAE1* Allelic Variants Affect TORC1 Activation and Fermentation Kinetics in *Saccharomyces cerevisiae*. <https://doi.org/10.3389/fmicb.2019.01686>

59. Villalobos-Cid y col. 2019. Comparison of Phylogenetic Tree Topologies for Nitrogen Associated Genes Partially Reconstruct the Evolutionary History of *Saccharomyces cerevisiae*. <https://doi.org/10.3390/microorganisms8010032>
60. Kessi-Pérez y col. 2020. Disentangling the genetic bases of *Saccharomyces cerevisiae* nitrogen consumption and adaptation to low nitrogen environments in wine fermentation. <https://doi.org/10.1186/s40659-019-0270-3>
61. Devia y col. 2020. Transcriptional Activity and Protein Levels of Horizontally Acquired Genes in Yeast Reveal Hallmarks of Adaptation to Fermentative Environments. <https://doi.org/10.3389/fgene.2020.00293>
62. Molinet y col. 2020. *GTR1* Affects Nitrogen Consumption and TORC1 Activity in *Saccharomyces cerevisiae* Under Fermentation Conditions. <https://doi.org/10.3389/fgene.2020.00519>
63. Kessi-Pérez y col. 2020. Differential Gene Expression and Allele Frequency Changes Favour Adaptation of a Heterogeneous Yeast Population to Nitrogen-Limited Fermentations. <https://doi.org/10.3389/fmicb.2020.01204>
64. Kessi-Pérez y col. 2020. Generation of a Non-Transgenic Genetically Improved Yeast Strain for Wine Production from Nitrogen-Deficient Musts. <https://doi.org/10.3390/microorganisms8081194>
65. Burgos-Díaz y col. 2021. Synthesis of New Chitosan from an Endemic Chilean Crayfish Exoskeleton (*Parastacus pugnax*): Physicochemical and Biological Properties. <https://doi.org/10.3390/polym13142304>
66. Villalobos-Cid y col. 2022. A multi-modal algorithm based on an NSGA-II scheme for phylogenetic tree inference. <https://doi.org/10.1016/j.biosystems.2022.104606>
67. Aguilera y col. 2022. Use of Cocktail of Bacteriophage for *Salmonella* Typhimurium Control in Chicken Meat. <https://doi.org/10.3390/foods11081164>

68. Kessi-Pérez y col. 2022. Yeast as a biological platform for vitamin D production: A promising alternative to help reduce vitamin D deficiency in humans. <https://doi.org/10.1002/yea.3708>
69. Rozas y col. 2022. Genetically modified organisms: adapting regulatory frameworks for evolving genome editing technologies. <https://doi.org/10.1186/s40659-022-00399-x>
70. Pinheiro y col. 2022. Food Availability in Different Food Environments Surrounding Schools in a Vulnerable Urban Area of Santiago, Chile: Exploring Socioeconomic Determinants. <https://doi.org/10.3390/foods11070901>
71. Burgos-Díaz y col. 2022. Food-grade bioactive ingredient obtained from the *Durvillaea incurvata* brown seaweed: Antibacterial activity and antioxidant activity. <https://doi.org/10.1016/j.algal.2022.102880>
72. Pizarro y col. 2023. Dietary and physical activity practices and preferences in children: An approach from school parliaments in educational public establishments. <https://doi.org/10.32641/andespediatr.v94i2.4164>
73. Kessi-Pérez y col. 2023. Single nucleotide polymorphisms associated with wine fermentation and adaptation to nitrogen limitation in wild and domesticated yeast strains. <https://doi.org/10.1186/s40659-023-00453-2>
74. Gil-Durán y col. 2023. CRISPR/Cas9-Mediated Disruption of the *pcz1* Gene and Its Impact on Growth, Development, and Penicillin Production in *Penicillium rubens*. <https://doi.org/10.3390/jof9101010>
75. Sandoval y col. 2024. Enhancing industrial swine slaughterhouse wastewater treatment: Optimization of electrocoagulation technique and operating mode. <https://doi.org/10.1016/j.jenvman.2023.119556>
76. Herrera-Muñoz y col. 2024. Assessment of contaminants of emerging concern and antibiotic resistance genes in the Mapocho River (Chile): A comprehensive study on water quality and

municipal wastewater impact.
<https://doi.org/10.1016/j.scitotenv.2024.176198>

77. Rocha y col. 2024. Phenotyping of a new yeast mapping population reveals differences in the activation of the TORC1 signalling pathway between wild and domesticated yeast strains.
<https://doi.org/10.1186/s40659-024-00563-5>
78. Figueroa y col. 2025. Optogenetic control of horizontally acquired genes prevent stuck fermentations in yeast.
<https://doi.org/10.1128/spectrum.01794-24>
79. Bastías y col. 2025. Specific Point Mutations in the *RRT5* Gene Modulate Fermentative Phenotypes of an Industrial Wine Yeast.
<https://doi.org/10.3390/fermentation11020088>
80. Kessi-Pérez y col. 2025. Genetically Improved Yeast Strains with Lower Ethanol Yield for the Wine Industry Generated Through a Two-Round Breeding Program.
<https://doi.org/10.3390/jof11020137>
81. Gómez y col. 2025. High-Throughput Indirect Monitoring of TORC1 Activation Using the pTOMAN-G Plasmid in Yeast.
<https://doi.org/10.21769/BioProtoc.5356>
82. Riquelme-Zamora y col. 2026. Identification of SNPs and Genes Associated with Quantitative Oenological Traits in *Saccharomyces cerevisiae* Using Regression and Machine Learning Models.
<https://doi.org/10.1080/03610470.2025.2595368>
83. Guerrero y col. 2026. A new set of optogenetic switches in yeast based on the BcWCL1 photoreceptor.
<https://doi.org/10.1002/yea.70021>