

Archibald Lab publications (June 2025)

199. Schoenle, A., Francis, O., **Archibald, J. M.**, Leger, M., Irisarri, I., Strassert, J. F. H., Florent, I., Yurchenko, V., Hehenberger, E., Massana, R., Burki, F., Lukeš, J., Worden, A. Z., Nitsche, F., Lara, E., de Vries, J., Eme, L., Dumack, K., Mathur, V., Hoffmeyer, T., Hall, N., del Campo, J., & Waldvogel, A.-M. 2025. Protist genomics: key to understanding eukaryotic evolution. **Trends Genet.** In press.

198. Colp, M. J. & **Archibald, J. M.** 2025. Complex and variable ploidy in *Acanthamoeba castellanii*. **Genome Biol. Evol.** Under review.

197. Tashyreva, D., Drahomíra, F., Stříbrná, E., Prokopchuk, G., Horák, A., Lukeš, J., **Archibald, J. M.**, Oatley, G., Sinclair, E., Aunin, E., Gettle, N., Santos, C., Paulini, M., McKenna, V., O'Brien, R., Niu, H., Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory Team, Wellcome Sanger Institute Scientific Operations: Sequencing Operations, Wellcome Sanger Institute Tree of Life Core Informatics Team, EBI Aquatic Symbiosis Genomics Data Portal Team, Aquatic Symbiosis Genomics Project Leadership. 2025. The genome sequences of the diplomonad protist *Fleptonema* sp. DT1601 and its bacterial endosymbiont *Ca. Syngnamydia salmonis*). **Wellcome Open Res.** 10:233.

196. Chung, D., Brask, N., Matar, S., Gallot-Lavallée, L., Pringle, E. Duguay, B., Blais, C., Slamovits, C. H., Leyland, B., Rest, J. S., Collier, J. L., McCormick, C., & **Archibald, J. M.** 2025. Persistent mirusvirus infection in the marine protist *Aurantiochytrium*. **Nature Comm.** Under revision. Research Square preprint: doi: 10.21203/rs.3.rs-5686297/v1.

195. Tashyreva, D., Drahomíra, F., Stříbrná, E., Horák, A., Lukeš, J., **Archibald, J. M.**, Oatley, G., Sinclair, E., Aunin, E., Gettle, N., Santos, C., Paulini, M., McKenna, V., O'Brien, R., Niu, H., Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory Team, Wellcome Sanger Institute Scientific Operations: Sequencing Operations, Wellcome Sanger Institute Tree of Life Core Informatics Team, EBI Aquatic Symbiosis Genomics Data Portal Team, Aquatic Symbiosis Genomics Project Leadership. 2025. The genome sequences of the diplomonad protist *Diplonema japonicum* yPF1604 and its bacterial endosymbionts *Ca. Cytomitobacter primus* and *Ca. Nesciobacter abundans*. **Wellcome Open Res.** 10:193.

194. Tashyreva, D., Drahomíra, F., Lukeš, J., **Archibald, J. M.**, Oatley, G., Sinclair, E., Aunin, E., Gettle, N., Santos, C., Paulini, M., McKenna, V., O'Brien, R., Niu, H., Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory Team, Wellcome Sanger Institute Scientific Operations: Sequencing Operations, Wellcome Sanger Institute Tree of Life Core Informatics Team, EBI Aquatic Symbiosis Genomics Data Portal Team, Aquatic Symbiosis Genomics Project Leadership. 2025. The genome sequences of the diplomonad protist *Rhynchopus euleeides* YPF1915 and its bacterial endosymbiont *Ca. Syngnamydia salmonis*. **Wellcome Open Res.** Under review.

193. Sibbald, S. J., Lawton, M., Maclean, C., Roger, A. J., & **Archibald, J. M.** 2025. Pangenome biology and evolution in harmful algal-bloom-forming pelagophytes. **Curr. Biol.** Under revision. Biorxiv pre-print doi: 10.1101/2024.10.30.620910.

192. Sganzerla-Martinez, G., Kumar, A., Kiganda-Lusamaki, E., Dutt, M., Wawina Bokalanga, T., Toloue, A. Mawete Francisca, M., Makangara-Cigolo, J. C., Kelvin, P., Adrienne, A. A., Richardson, C. D., Lokilo, E.,

Luakanda, G., Ayouba, A., Rimoin, A. W., Mukadi-Bamuleka, D., Delaporte, E., Pilarowski, G., Kindrachuk, J., Liesenborghs, L., Hensley, L. E., Subissi, L., Peeters, M., Hoff, N. A., Tshiani-Mbaya, O. Tessema, S., Muyembe Tamfum, J.-J., Ahuka-Mundeké, S., Kelvin, A. A, **Archibald, J. M.**, Mbala-Kingebeni, P., Flores-Giron, L., & Kelvin, D. J. 2025. Monkeypox virus pangenomics reveals determinants of clade Ib. Submitted. medRxiv pre-print doi: 10.1101/2024.10.31.24315917.

191. Schvarcz, C. R., Stancheva, R., Turk-Kubo, K. A., Wilson, S. T., Zehr, J. P., Edwards, K. F., Steward, G. F., **Archibald, J. M.**, Oatley, G., Sinclair, E., Aunin, E., Gettle, N., Santos, C., Paulini, M., McKenna, V., O'Brien, R., Niu, H., Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory Team, Wellcome Sanger Institute Scientific Operations: Sequencing Operations, Wellcome Sanger Institute Tree of Life Core Informatics Team, EBI Aquatic Symbiosis Genomics Data Portal Team, Aquatic Symbiosis Genomics Project Leadership. 2025. The genome sequences of the chain-forming marine diatom *Epithemia catenata* (Schvarcz, Stancheva & Steward, 2022) and its nitrogen-fixing cyanobacterial endosymbiont. **Wellcome Open Res.** Under review.

190. Zhang, X., Hu, Y., Cheng, Z. & **Archibald, J. M.** 2025. HSDSnake: A SnakeMake pipeline for comprehensive analysis of highly similar gene duplicates in eukaryotic genomes. **Bioinformatics**. [10.1093/bioinformatics/btaf325](https://doi.org/10.1093/bioinformatics/btaf325).

189. Zhang, X., Hu, Y., Cheng, Z. & **Archibald, J. M.** 2025. AMRLearn: A machine learning pipeline for characterization of antimicrobial resistance determinants in microbial genomic data. **STAR Protocols**. 16 103733.

187. Blais, C., Colp, M. J., Sarre, L. A., de Mendoza, A. & **Archibald, J. M.** 2024. Epigenetic silencing and host genome dynamics determine the fate of giant viral endogenizations in *Acanthamoeba*. Submitted. Biorxiv pre-print doi: 10.1101/2024.10.31.621330.

186. Colp, M. J., Blais, C., Curtis, B. A., & **Archibald, J. M.** 2025. The fate of artificial transgenes in *Acanthamoeba castellanii*. **BMC Genomics**. 26:368. 21.

185. **Archibald, J. M.** 2025. Eukaryogenesis: Mosaic evolution of eukaryotic carbon metabolism. **Nature Ecol. Evol.** 02552-4.

184. Richards, T. A., Eme, L., **Archibald, J. M.**, Leonard, G., Coelho, S. M., de Mendoza, A., Dessimoz, C., Dolezal, P., Fritz-Laylin, L. K., Gabaldon, T., Hampl, V., Kops, G. J. P. L., Leger, M. M., Lopez-Garcia, P., McInerney, J. O., Moreira, D., Munoz-Gomez, A., Richter, D. J., Ruiz-Tillo, I., Santoro, A. E., Sebe-Pedros, A., Snel, B., Stairs, C. W., Tromer, E. C., van Hooft, J. J. E., Wickstead, B., Williams, T. A., Roger, A. J., Dacks, J. B., & Wideman, J. G. 2024. Consensus view: reconstructing the last common ancestor of all eukaryotes. **PLOS Biol.** 22 (11): e3002917.

183. LaRoche, J. & Archibald, J. M. 2024. Marine microbiology: how to evolve a nitrogen-fixing organelle. **Curr. Biol.** 34, R826-R829.

182. Schvarcz, C. R., Stancheva, R., Turk-Kubo, K. A., Wilson, S. T., Zehr, J. P., Edwards, K. F., Steward, G. F., **Archibald, J. M.**, Oatley, G., Sinclair, E., Aunin, E., Gettle, N., Santos, C., Paulini, M., McKenna, V., O'Brien, R., Niu, H., Wellcome Sanger Institute Tree of Life Management, Samples and Laboratory Team, Wellcome Sanger Institute Scientific Operations: Sequencing Operations, Wellcome Sanger Institute Tree of Life Core Informatics Team, EBI Aquatic Symbiosis Genomics Data Portal Team, Aquatic

Symbiosis Genomics Project Leadership. 2024. The genome sequences of the marine diatom *Epithemia pelagica* strain UHM3201 (Schvarcz, Stancheva & Steward, 2022) and its nitrogen-fixing, endosymbiotic cyanobacterium. **Wellcome Open Res.** 9:232.

181. Kantor, E. J. H., Robicheau, B., Tolman, J., **Archibald, J. M.**, and LaRoche, J. 2024. Targeted metagenomics reveals pangenomic diversity of the nitroplast (UCYN-A) and its algal host plastid. **ISME Comm.** 4(1): ycae150.

180. Bougon, J., Kadijk, E.C., Gallot-Lavallée, L., Curtis, B.A., Landers, M., **Archibald, J.M.** & Khaperskyy, D. A. 2024. Influenza A virus NS1 effector domain is required for PA-X mediated host shutoff in infected cells. **J. Virol.** 98, e01901-23.

179. Jerlström-Hultqvist, J., Gallot-Lavallée, L., Salas-Leiva, D., Curtis, B. A., Pašuthová, K., Čepička, I., Stairs, C., Pipaliya, S., Dacks, J., **Archibald, J. M.**, & Roger, A. J. 2024. A unique symbiosome in an anaerobic single-celled eukaryote. **Nature Comm.** 15: 9726.

178. Feng X, Zheng J, Irisarri I, Yu H, Zheng B, Ali Z, de Vries S, Keller J, Fürst-Jansen JMR, Dadras A, Zegers JMS, Rieseberg TP, Ashok AD, Darienko T, Bierenbroodspot MJ, Gramzow L, Petroll R, Haas FB, Fernandez-Pozo N, Nousias O, Li T, Fitzek E, Grayburn WS, Rittmeier N, Permann C, Rümpler F, **Archibald J. M.**, Theißen G, Mower JP, Lorenz M, Buschmann H, von Schwartzberg K, Boston L, Hayes RD, Daum C, Barry K, Grigoriev IV, Wang X, Li FW, Rensing SA, Ari JB, Keren N, Mosquna A, Holzinger A, Delaux PM, Zhang C, Huang J, Mutwil M, de Vries J, Yin Y. 2024. Chromosome-level genomes of multicellular algal sisters to land plants illuminate signaling network evolution. **Nature Genet.** 56: 1018-1031.

177. **Archibald, J.M.** 2024. Symbiotic revolutions at the interface of genomics and microbiology. **PLOS Biol.** 22:e3002581.

176. Gallot-Lavallée, L., Jerlström-Hultqvist, J., Stairs, C. W., Cepicka, I., Roger, A. J., & **Archibald, J. M.** 2023. Massive intein content in three *Anaeramoeba* genomes reveals new aspects of intein mobility in eukaryotes. **Proc. Natl. Acad. Sci. USA.** 120, 49: e2306381120.

175. Collier, J. L., Rest, J. S., Lavington, E., Gallot-Lavallée, L., Kuo, A., Jenkins, J., Pangilinan, J. Daum, C., Grigoriev, I. V., Filloramo, G. F., Curtis, B. A., Vanclova, A., & **Archibald, J. M.** 2023. The protist *Aurantiochytrium* has universal subtelomeric rDNAs and is a host for mirusviruses. **Curr. Biol.** 33, 5199-5207.

174. Rius, M., Rest, J. S., Filloramo, G., Vanclova, A., **Archibald, J. M.**, & Collier, J.L. 2023. Horizontal gene transfer and fusion spread carotenogenesis among diverse heterotrophic protists. **Genome. Biol. Evol.** doi.org/10.1093/gbe/evad029.

173. Zhang, X., Hu, Y., Cheng, Z. & **Archibald, J. M.** 2023. HSDecipher: A pipeline for comparative genomic analysis of highly similar duplicate genes in eukaryotic genomes. **STAR Protocols.** 4, 102014.

172. Kim, J. I., Tanifuji, G., Minseok, J., Shin, W., & **Archibald, J. M.** 2022. Gene loss, pseudogenization and genome reduction in non-photosynthetic species of *Cryptomonas* (Cryptophyceae) revealed by comparative nucleomorph genomics. **BMC Biol.** 20:227.

171. Hess, S., Williams, S., Busch, A., Irisarri, I., Delwiche, C.F., de Vries, S., Darienko, T., Roger, A.J., **Archibald, J. M.**, Buschmann, H., von Schwartzberg, K., & de Vries, J. 2022. A phylogenomically informed five-order system for the closest relatives of land plants. *Curr. Biol.* 32, 1-10.
170. Matthey-Doret*, C., Colp*, M. J., Escoll Guerrero, P., Thierry, A., Curtis, B. A., Sarraín, M., Gray, M.W., Lang B.F., **Archibald, J. M.**, Buchrieser, C., & Koszul, R. 2022. Chromosome-scale assemblies of *Acanthamoeba castellanii* genomes provide insights into *Legionella pneumophila* infection-related chromatin re-organization. *Genome Res.* 32, 1698-1710.
169. Kim, J. I., Jo, B. Y., Park, M. G., Yoo, Y. D., Shin, W., & **Archibald, J. M.** 2022. Evolutionary dynamics and lateral gene transfer in raphidophycean plastid genomes. *Frontiers Plant Sci.* 13, doi:10.3389/fpls.2022. 896138.
168. Zhang, X., Hu, Y., Eme, L., Maruyama, S., Eveleigh, R. J. M., Curtis, B. A., Sibbald, S. J., Hopkins, J. F., Filloramo, G. V., van Wijk, K., & **Archibald, J. M.** 2022. Protocol for TreeTuner: A pipeline for minimizing redundancy and complexity in large phylogenetic datasets. *STAR Protocols.* 3, 101175.
167. Lawniczak, M. K. N., Durbin, R., Flicek, P., Lindblad-Toh, K., Wei, X., **Archibald, J. M.**, Baker, W. J., Belov, K., Blaxter, M. L., Marques Bonet, T., Childers, A. K., Coddington, J. A., Crandall, K. A., Crawford, A. J., Davey, R. P., Di Palma, F., Fang, Q., Haerty, W., Hall, N., Hoff, K. J., Howe, K., Jarvis, E. D., Johnson W. E., Johnson, R. N., Kersey, P. J., Liu, X., Lopez, J. V., Myers, E. W., Pettersson, O. V., Phillippy, A. M., Poelchau, M. F., Pruitt, K. D., Rhie, A., Castilla-Rubio, J. C., Sahu, S. K., Salmon, N. A., Soltis, P. S., Swarbreck, D., Thibaud-Nissen, F., Wang, S., Wegrzyn, J. L., Zhang, G., Zhang, H., Lewin, H. A., Richards, S. 2022. Standards recommendations for the Earth BioGenome Project. *Proc. Natl. Acad. Sci. USA.* 119, 4 e2115636118.
166. Blaxter, M., **Archibald, J. M.**, Childers, A. K., Coddington, J. A., Crandall, K. A., Di Palma, F., Durbin, R., Edwards, S. V., Graves, J. A. M., Hackett, K. J., Hall, N., Jarvis, E. D., Johnson, R. N., Karlsson, E. K., Kress, W. J., Kuraku, S., Lawniczak, M. K. N., Lindblad-Toh, K., Lopez, J. V., Moran, N.A., Robinson, G. E., Ryder, O. A., Shapiro, B., Soltis, P. S., Warnow, T., Zhang, G., & Lewin, H. A. 2022. Why sequence all eukaryotes? *Proc. Natl. Acad. Sci. USA.* 119, 4 e2115636118.
165. Lewin, H. A., Richards, S., Lieberman Aiden, E., Allende, M. L., **Archibald, J. M.**, Bálint, M., Barker, K. B., Baumgartner, B., Belov, K., Bertorelle, G., Blaxter, M.L., Cai, J., Caperello, N. D., Carlson, K., Castilla-Rubio, J. C., Chaw, S. M., Chen, L., Childers, A. K., Coddington, J. A., Conde, D. A., Corominas, M., Crandall, K. A., Crawford, A. J., DiPalma, F., Durbin, R., Ebenezer, T. E., Edwards, S. V., Fedrigo, O., Flicek, P., Formenti, G., Gibbs, R. A., Gilbert, M. T. P., Goldstein, M. M., Graves, J. M., Greely, H. T., Grigoriev, I. V., Hackett, K. J., Hall, N., Haussler, D., Helgen, K. M., Hogg, C. J., Isobe, S., Jakobsen, K. S., Janke, A., Jarvis, E. D., Johnson, W. E., Jones, S. J. M., Karlsson, E. K., Kersey, P. J., Kim, J. H., Kress, W. J., Kuraku, S., Lawniczak, M. K. N., Leebens-Mack, J. H., Li, X., Lindblad-Toh, K., Liu, X., Lopez, J. V., Marques-Bonet, T., Mazard, S., Mazet, J. A. K., Mazzoni, C. J., Myers, E. W., O'Neill, R. J., Paez, S., Park, H., Robinson, G. E., Roquet, C., Ryder, O. A., Sabir, J. S. M., Shaffer, H. B., Shank, T. M., Sherkow, J. S., Soltis, P. S., Tang, B., Tedersoo, L., Uliano-Silva, M., Wang, K., Wei, X., Wetzler, R., Wilson, J. L., Xu, X., Yang, H., Yoder, A. D., Zhang, G. 2022. The Earth BioGenome Project 2020: starting the clock. *Proc. Natl. Acad. Sci. USA.* 119, 4 e2115636118.

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162. Salas-Leiva, D. E., Tromer, E. C., Curtis, B. A., Jerlstrom-Hultqvist, J., Kolisko, M., Yi, Z., Salas-Leiva, J. S., Gallot-Lavallée, L., Kops, J. J. P. L., **Archibald, J. M.**, Simpson, A. G. B., & Roger, A. J. 2021. Genomic analysis finds no evidence of canonical eukaryotic DNA processing systems in a free-living protist. *Nat. Comm.* 12:6003.
161. Rowarth, N. M., Curtis, B. A., Einfeldt, A. L., **Archibald, J. M.**, Lacroix, C. R., & Gunawardena, A. H. L. A. N. 2021. RNA-Seq analysis reveals potential regulators involved in program cell death and remodeling of lace plant leaves (*Aponogeton madagascariensis*). *BMC Plant Biol.* 21:375.
160. Filloramo, G. V., Blanche, E., Curtis, B. A., & **Archibald, J. M.** 2021. Re-examination of two diatom reference genomes using long-read sequencing. *BMC Genomics.* 22:379.
159. Blais, C. & **Archibald, J. M.** 2021. The past, present and future of the Tree of Life. *Curr Biol.* 31, R311-329.
158. Sibbald, S. J., Lawton, M. & **Archibald, J. M.** 2021. Mitochondrial genome evolution in pelagophyte algae. *Genome Biol. Evol.* 13(3) Doi: 10.1093/gbe/evab018
157. Gallot-Lavallée, L. & **Archibald, J. M.** 2020. Evolution: viral rhodopsins illuminate algal evolution. *Curr. Biol.* 30, R1469-1471.
156. **Archibald, J. M.** 2020. Quick Guide: Cryptomonads. *Curr. Biol.* 30, R1116-R1115.
155. Kim, J. I., Minseok, J., **Archibald, J. M.** & Shin, W. 2020. Comparative plastid genomics of non-photosynthetic chrysophytes: genome reduction and compaction. *Frontiers Plant Sci.* 11:572703. Doi: 10.3389/fpls.2020.572703.
154. de Vries, S., de Vries, J., **Archibald, J. M.**, & Slamovits, C. S. 2020. Comparative analyses of saprotrophy in *Salisapilia sapeloensis* and diverse plant pathogenic oomycetes reveal lifestyle-specific gene expression. *FEMS Microbiol. Ecol.* 96, fiae184.
153. Sibbald, S. J., Eme, L., **Archibald, J. M.** & Roger, A. J. 2020. Lateral gene transfer mechanisms and pan-genomes in eukaryotes. *Trends Parasitol.* 36, 927-941. (Invited review article).

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150. Colp, M. & **Archibald, J. M.** 2020. The language of symbiosis: insights from protist biology. In: *Cellular dialogs in the holobiont*. Bosch, T. and Hadfield, M. (eds.). CRC Press. (Invited book chapter)

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139. Kim, J. I., Yoon, H. S., Gangman, Y., Shin, W., & **Archibald, J. M.** 2018. Comparative mitochondrial genomics of cryptophyte algae: gene shuffling and dynamic mobile genetic elements. *BMC Genomics*. 19, 275.

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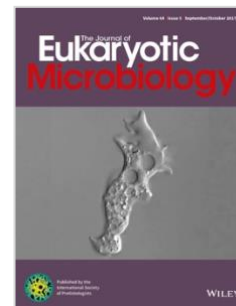
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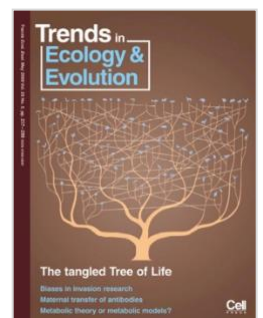
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