

7. References

- Abongâ, B., Gimnig, J., Torr, S., Longman, B., Omoke, D., & Muchoki, M. et al. (2020). Impact of indoor residual spraying with pirimiphos-methyl (Actellic 300CS) on entomological indicators of transmission and malaria case burden in Migori County, western Kenya. *Scientific Reports*, 10(1). <https://doi.org/10.1038/s41598-020-61350-2>
- Abood, S., Eichelbaum, S., Mustafi, S., Veisaga, M., LÃ³pez, L., & Barbieri, M. (2017). Biomedical Properties and Origins of Sesquiterpene Lactones, with a Focus on Dehydroleucodine. *Natural Product Communications*, 12(6), 1934578X1701200. <https://doi.org/10.1177/1934578x1701200638>
- Acquah, F. K., Donu, D., Bredu, D., Eya-Ampah, S., Amponsah, J. A., Quartey, J., Obboh, E. K., Mawuli, B. A., & Amoah, L. E. (2020). Asymptomatic carriage of Plasmodium falciparum by individuals with variant blood groups and haemoglobin genotypes in southern Ghana. *Malaria journal*, 19(217), pp.1-8. <https://doi.org/10.1186/s12936-020-03299-1>
- Adewale, B. (2020). Will long-read sequencing technologies replace short-read sequencing technologies in the next 10 years? *African Journal of Laboratory Medicine*, 9(1). <https://doi.org/10.4102/ajlm.v9i1.1340>
- Amambua-Ngwa, A., Jeffries, D., Amato, R., Worwui, A., Karim, M., & Ceesay, S. et al. (2018). Consistent signatures of selection from genomic analysis of pairs of temporal and spatial Plasmodium falciparum populations from The Gambia. *Scientific Reports*, 8(1). <https://doi.org/10.1038/s41598-018-28017-5>
- Amato, R., Pearson, R. D., Almagro-Garcia, J., Amaralunga, C., Lim, P., Suon, S., ... Kwiatkowski, D. P. (2018). Origins of the current outbreak of multidrug-resistant malaria in southeast Asia: a retrospective genetic study. *The Lancet Infectious Diseases*, 18(3), 337–345. [https://doi.org/10.1016/s1473-3099\(18\)30068-9](https://doi.org/10.1016/s1473-3099(18)30068-9)
- Amir, A., Cheong, F. W., de Silva, J. R., Liew, J., & Lau, Y. L. (2018). *Plasmodium knowlesi* malaria: current research perspectives. *Infection and drug resistance*, 11, 1145–1155. <https://doi.org/10.2147/IDR.S148664>
- Amoah, L.E., Acquah, F.K., Nyarko, P.B. et al. (2020). Comparative analysis of asexual and sexual stage *Plasmodium falciparum* development in different red blood cell types. *Malar Journal*, 19(200), pp.1-10 <https://doi.org/10.1186/s12936-0>

- Anderson, T., Nair, S., McDew-White, M., Cheeseman, I., Nkhoma, S., & Bilgic, F. et al. (2016). Population Parameters Underlying an Ongoing Soft Sweep in Southeast Asian Malaria Parasites. *Molecular Biology and Evolution*, 34(1), 131-144. <https://doi.org/10.1093/molbev/msw228>
- Antinori, S., Galimberti, L., Milazzo, L. and Corbellino, M. (2012) Plasmodium knowlesi: The emerging zoonotic malaria parasite. *Acta Tropica* 125(2013), pp.191–201
- Antonova-Koch, Y., Meister, S., Abraham, M., Luth, M., Otilie, S., & Lukens, A. et al. (2018). Open-source discovery of chemical leads for next-generation chemoprotective antimalarials. *Science*, 362(6419), eaat9446. <https://doi.org/10.1126/science.aat9446>
- Ariey, F., Witkowski, B., Amaratunga, C., Beghain, J., Langlois, A., & Khim, N. et al. (2013). A molecular marker of artemisinin-resistant Plasmodium falciparum malaria. *Nature*, 505(7481), 50-55. <https://doi.org/10.1038/nature12876>
- Ashley, E. A., Phyoe, A. P. & Woodrow, C. J. (2018) Malaria. *The Lancet*, 391(10130), pp.608-1621, ISSN 0140-6736, [https://doi.org/10.1016/S0140-6736\(18\)30324-6](https://doi.org/10.1016/S0140-6736(18)30324-6).
- Ashley, E., & White, N. (2014). The duration of Plasmodium falciparum infections. *Malaria Journal*, 13(1). <https://doi.org/10.1186/1475-2875-13-500>
- Augustina, F., Asamoah, K, K., Fokuo, O. M. and Ndifon Wilfred (2018) Novel Strategies for Malaria Vaccine Design. *Frontiers in Immunology*, 9(1664-3224), 2769, DOI=10.3389/fimmu.2018.02769
- Badugu, S., Nabi, S., Vaidyam, P., Laskar, S., Bhattacharyya, S., & Bhattacharyya, M. (2015). Identification of Plasmodium falciparum DNA Repair Protein Mre11 with an Evolutionarily Conserved Nuclease Function. *PLOS ONE*, 10(5), e0125358. <https://doi.org/10.1371/journal.pone.0125358>
- Baird, J. (2019). 8-Aminoquinoline Therapy for Latent Malaria. *Clinical Microbiology Reviews*, 32(4). <https://doi.org/10.1128/cmr.00011-19>
- Baird, L., & Yamamoto, M. (2020). The Molecular Mechanisms Regulating the KEAP1-NRF2 Pathway. *Molecular and Cellular Biology*, 40(13). <https://doi.org/10.1128/mcb.00099-20>
- Bartoloni, A., & Zammarchi, L. (2012). Clinical aspects of uncomplicated and severe malaria. *Mediterranean Journal of Hematology and Infectious Diseases*, 4(1), e2012026. <https://doi.org/10.4084/MJHID.2012.026>
- Battle, K. E., Lucas, T. C. D., Nguyen, M., Howes, R. E., Nandi, A. K., Twohig, K. A. et al. (2019) Mapping the global endemicity and clinical burden of Plasmodium vivax, 2000–

17: a spatial and temporal modelling study. *Lancet*, 394(10195), pp.332-343
[http://dx.doi.org/10.1016/S0140-6736\(19\)31096-7](http://dx.doi.org/10.1016/S0140-6736(19)31096-7)

Bawa, S., Kumar, S., Drabu, S., & Kumar, R. (2010). Structural modifications of quinoline-based antimalarial agents: Recent developments. *Journal of Pharmacy And Bioallied Sciences*, 2(2), 64. <https://doi.org/10.4103/0975-7406.67002>

Birnbaum, J., Scharf, S., Schmidt, S., Jonscher, E., Hoeijmakers, W., & Flemming, S. et al. (2020). A Kelch13-defined endocytosis pathway mediates artemisinin resistance in malaria parasites. *Science*, 367(6473), 51-59.
<https://doi.org/10.1126/science.aax4735>

Blake TCA, Haase S, Baum J (2020) Actomyosin forces and the energetics of red blood cell invasion by the malaria parasite *Plasmodium falciparum*. *PLOS Pathogens* 16(10), pp.: e1009007. <https://doi.org/10.1371/journal.ppat.1009007>

Blank, A., Färle, K., Jässchke, A., Mikus, G., Lehmann, M., & Häring, J. et al. (2020). Immunization with full-length *Plasmodium falciparum* merozoite surface protein 1 is safe and elicits functional cytophilic antibodies in a randomized first-in-human trial. *Npj Vaccines*, 5(1). <https://doi.org/10.1038/s41541-020-0160-2>

Blasco, B., Leroy, D., & Fidock, D. (2017). Antimalarial drug resistance: linking *Plasmodium falciparum* parasite biology to the clinic. *Nature Medicine*, 23(8), 917-928.
<https://doi.org/10.1038/nm.4381>

Brazier, A. J., Avril, M., Bernabeu, M., Benjamin, M., Smith, J. D. (2017) Pathogenicity Determinants of the Human Malaria Parasite *Plasmodium falciparum* Have Ancient Origins. *American Society for Microbiology*, 2(1), pp.1-13 <https://doi.org/10.1128/mSphere.00348-16>. Basu, S., Aryan, A., Overcash, J., Samuel, G., Anderson, M., &

Bryant, J., Regnault, C., Scheidig-Benatar, C., Baumgarten, S., Guizetti, J., & Scherf, A. (2017). CRISPR/Cas9 Genome Editing Reveals That the Intron Is Not Essential for var2csa Gene Activation or Silencing in *Plasmodium falciparum*. *Mbio*, 8(4).
<https://doi.org/10.1128/mbio.00729-17>

Buffet, P. A., Safeukui, I., Deplaine, G., Brousse, V., Prendki, V., Thellier, M., Turner, G. D. & Mercereau-Puijalon, O. (2011) The pathogenesis of *Plasmodium falciparum* malaria in humans: insights from splenic physiology. *Blood*, 117(2), pp.381–392.
<https://doi.org/10.1182/blood-2010-04-202911>

Burns, A. L., Dans, M. G., Balbin, J. M., de Koning-Ward, T. F., Gilson, P. R., Beeson, J. G., Boyle, M. J., Wilson, D. W. (2019) Targeting malaria parasite invasion of red blood cells as an antimalarial strategy, *FEMS Microbiology Reviews*, 43(3), pp.223–238

- Bushell, E., Gomes, A. R., Sanderson, T., Anar, B., Girling, G., Herd, C., Metcalf, T., Modrzynska, K., Schwach, F., Martin, R. E., Mather, M. W., McFadden, G. I., Parts, L., Rutledge, G. G., Vaidya, A. B., Wengelnik, K., Rayner, J. C., & Billker, O. (2017). Functional Profiling of a Plasmodium Genome Reveals an Abundance of Essential Genes. *Cell*, 170(2), 260–272.e8. <https://doi.org/10.1016/j.cell.2017.06.030>
- Bwire, G. M., Ngasala, B., Mikomangwa, W. P., Kilonzi, M., & Kamuhabwa, A. A. (2020). Detection of mutations associated with artemisinin resistance at k13-propeller gene and a near complete return of chloroquine susceptible falciparum malaria in Southeast of Tanzania. *Scientific Reports*, 10(1). <https://doi.org/10.1038/s41598-020-60549-7>
- Cai, F. Y., DeSimone, T. M., Hansen, E., Jennings, C. V., Bei, A. K., Ahoudi, A. D., Mboup, S., Duraisingh, M. T., & Buckee, C. O. (2020). Accounting for red blood cell accessibility reveals distinct invasion strategies in Plasmodium falciparum strains. *PLoS Computational Biology*, 16(4), pp.1-16 e1007702. <https://doi.org/10.1371/journal.pcbi.1007702>
- Carrasquilla, M. (2019) New approaches for measuring fitness of *Plasmodium falciparum* mutations implicated in drug resistance. Unpublished doctoral dissertation. University of Cambridge, UK
- Carrasquilla, M., Sanderson, T., Montandon, R., Rayner, J., Pance, A., & Lee, M. C. S. (2020). Quantitation of vector uptake reveals non-Poissonian transfection dynamics in Plasmodium falciparum. *Nature Scientific Reports*, 10(10894), 1-11. <https://doi.org/10.1101/681981>
- Carroll, D. (2011). Genome Engineering with Zinc-Finger Nucleases. *Genetics*, 188(4), 773-782. <https://doi.org/10.1534/genetics.111.131433>
- Catteruccia, F., Crisanti, A., & Wimmer, E. (2009). Transgenic technologies to induce sterility. *Malaria Journal*, 8(S2). <https://doi.org/10.1186/1475-2875-8-s2-s7>
- Centres for Disease Control and Prevention (2020). *Where Malaria Occurs*. <https://www.cdc.gov/malaria/about/distribution.html>
- Centres for Disease Control and Prevention, 2020. *Malaria's Impact Worldwide* https://www.cdc.gov/malaria/malaria_worldwide/impact.html
- Cerqueira, G., Cheeseman, I., Schaffner, S., Nair, S., McDew-White, M., & Phy, A. et al. (2017). Longitudinal genomic surveillance of Plasmodium falciparum malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. *Genome Biology*, 18(1). <https://doi.org/10.1186/s13059-017-1204-4>

- Chaorattanakawee, S., Saunders, D. L., Sea, D., Chanarat, N., Yingyuen, K., Sundrakes, S., ... Lanteri, C. A. (2015). Ex VivoDrug Susceptibility Testing and Molecular Profiling of Clinical Plasmodium falciparum Isolates from Cambodia from 2008 to 2013 Suggest Emerging Piperaquine Resistance. *Antimicrobial Agents and Chemotherapy*, 59(8), 4631–4643. <https://doi.org/10.1128/aac.00366-15>
- Choi, L., Pryce, J., & Garner, P. (2019). Indoor residual spraying for preventing malaria in communities using insecticide-treated nets. *Cochrane Database of Systematic Reviews*. <https://doi.org/10.1002/14651858.cd012688.pub2>
- Chugh, M., Scheurer, C., Sax, S., Bilsland, E., van Schalkwyk, D., & Wicht, K. et al. (2014). Identification and Deconvolution of Cross-Resistance Signals from Antimalarial Compounds Using Multidrug-Resistant Plasmodium falciparum Strains. *Antimicrobial Agents and Chemotherapy*, 59(2), 1110-1118. <https://doi.org/10.1128/aac.03265-14>
- Clarkson, C., Temple, H., & Miles, A. (2018). The genomics of insecticide resistance: insights from recent studies in African malaria vectors. *Current Opinion in Insect Science*, 27, 111-115. <https://doi.org/10.1016/j.cois.2018.05.017>
- Clinical Microbiology Reviews, 20 (4) 579-592; DOI: 10.1128/CMR.00027-07
- Collins, W. E. and Jeffery, G. M. (2007) *Plasmodium malariae*: Parasite and Disease.
- Colvin, H. N., & Joice Cordy, R. (2020). Insights into malaria pathogenesis gained from host metabolomics. *PLoS pathogens*, 16(11), e1008930. <https://doi.org/10.1371/journal.ppat.1008930>
- Cooling, L. (2015) Blood Groups in Infection and Host Susceptibility. *Clinical Microbiology Reviews*, 28(3), pp.801-870; DOI: 10.1128/CMR.00109-14
- Coppée, R., Jeffares, D., Miteva, M., Sabbagh, A., & Clain, J. (2019). Comparative structural and evolutionary analyses predict functional sites in the artemisinin resistance malaria protein K13. *Scientific Reports*, 9(1). <https://doi.org/10.1038/s41598-019-47034-6>
- Corey, V. C., Lukens, A. K., Istvan, E. S., Lee, M. C., Franco, V., Magistrado, P., ... Winzeler, E. A. (2016). A broad analysis of resistance development in the malaria parasite. *Nature Communications*, 7(1). <https://doi.org/10.1038/ncomms11901>
- Cowell, A., & Winzeler, E. (2018). Exploration of the Plasmodium falciparum Resistome and Druggable Genome Reveals New Mechanisms of Drug Resistance and Antimalarial Targets. *Microbiology Insights*, 11, 117863611880852. <https://doi.org/10.1177/1178636118808529>

- Cowell, A., & Winzeler, E. (2019). Advances in omics-based methods to identify novel targets for malaria and other parasitic protozoan infections. *Genome Medicine*, 11(1). <https://doi.org/10.1186/s13073-019-0673-3>
- Cowell, A., Istvan, E., Lukens, A., Gomez-Lorenzo, M., Vanaerschot, M., & Sakata-Kato, T. et al. (2018). Mapping the malaria parasite druggable genome by using in vitro evolution and chemogenomics. *Science*, 359(6372), 191-199. <https://doi.org/10.1126/science.aan4472>
- Cowman, A. F. Berry, D., and Jake Baum, J. (2012) The cellular and molecular basis for malaria parasite invasion of the human red blood cell. *Journal of Cell Biology*, 198 (6), pp.961–971
- Cuadrado, A., Rojo, A., Wells, G., Hayes, J., Cousin, S., & Rumsey, W. et al. (2019). Therapeutic targeting of the NRF2 and KEAP1 partnership in chronic diseases. *Nature Reviews Drug Discovery*, 18(4), 295-317. <https://doi.org/10.1038/s41573-018-0008-x>
- Cui, L., Mharakurwa, S., Ndiaye, D., Rathod, P., & Rosenthal, P. (2015). Antimalarial Drug Resistance: Literature Review and Activities and Findings of the ICEMR Network. *The American Journal of Tropical Medicine And Hygiene*, 93(3_Suppl), 57-68. <https://doi.org/10.4269/ajtmh.15-0007>
- Current Protocols in Molecular Biology*, 122(1). <https://doi.org/10.1002/cpmb.59>
- Czechowski, T., Weathers, P., Brodelius, P., Brown, G., & Graham, I. (2020). Editorial: Artemisininâ From Traditional Chinese Medicine to Artemisinin Combination Therapies; Four Decades of Research on the Biochemistry, Physiology, and Breeding of *Artemisia annua*. *Frontiers in Plant Science*, 11. <https://doi.org/10.3389/fpls.2020.594565>
- Dahl, E., & Rosenthal, P. (2008). Apicoplast translation, transcription and genome replication: targets for antimalarial antibiotics. *Trends in Parasitology*, 24(6), 279-284. <https://doi.org/10.1016/j.pt.2008.03.007>
- Dahlem, T. et al. (2015). Silencing of end-joining repair for efficient site-specific gene insertion after TALEN/CRISPR mutagenesis in *Aedes aegypti*. *Proceedings of The National Academy of Sciences*, 112(13), 4038-4043. <https://doi.org/10.1073/pnas.1502370112>
- Davidson, G., Chua, T.H., Cook, A. et al. (2019). Defining the ecological and evolutionary drivers of *Plasmodium knowlesi* transmission within a multi-scale framework. *Malaria Journal*. 18(66), pp.1-13. <https://doi.org/10.1186/s12936-019-2693-2>

- Davies, T., Wixted, W., Coyle, J., Griffiths-Jones, C., Hearn, K., & McMenamin, R. et al. (2016). Monoacidic Inhibitors of the Kelch-like ECH-Associated Protein 1: Nuclear Factor Erythroid 2-Related Factor 2 (KEAP1:NRF2) Protein-Protein Interaction with High Cell Potency Identified by Fragment-Based Discovery. *Journal Of Medicinal Chemistry*, 59(8), 3991-4006. <https://doi.org/10.1021/acs.jmedchem.6b00228>
- de Jong, R. M., Tebeje, S. K., Meerstein-Kessel, L., Tadesse, F. G., Jore, M. M., Stone, W., & Bousema, T. (2020). Immunity against sexual stage Plasmodium falciparum and Plasmodium vivax parasites. *Immunological reviews*, 293(1), pp.190–215. <https://doi.org/10.1111/imr.12828>
- de Koning-Ward, T., Dixon, M., Tilley, L. et al. *Plasmodium* species: master renovators of their host cells. *Nature Reviews Microbiology* 14, 494–507 (2016). <https://doi.org/10.1038/nrmicro.2016.79>
- de Mendonc, V. R. R., Goncalves, M. S. and Barral-Netto, M. (2012) The Host Genetic Diversity in Malaria Infection. *Journal of Tropical Medicine*, 1-17 doi:10.1155/2012/940616
- Debebe, Y., Hill, S. R., Birgersson, G., Tekie, H., & Ignell, R. (2020). Plasmodium falciparum gametocyte-induced volatiles enhance attraction of Anopheles mosquitoes in the field. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03378-3>
- Del Vecchio, F., Mastroiaco, V., Di Marco, A., Compagnoni, C., Capece, D., & Zazzeroni, F. et al. (2017). Next-generation sequencing: recent applications to the analysis of colorectal cancer. *Journal Of Translational Medicine*, 15(1). <https://doi.org/10.1186/s12967-017-1353-y>
- Deshmukh, P., Unni, S., Krishnappa, G., & Padmanabhan, B. (2016). The Keap1-Nrf2 pathway: promising therapeutic target to counteract ROS-mediated damage in cancers and neurodegenerative diseases. *Biophysical Reviews*, 9(1), 41-56. <https://doi.org/10.1007/s12551-016-0244-4>
- Deshpande, S., & Kuppast, B. (2016). 4-aminoquinolines: An Overview of Antimalarial Chemotherapy. *Medicinal Chemistry*, 06(01). <https://doi.org/10.4172/2161-0444.1000315>
- Dhingra, S. K., Small-Saunders, J. L., Ménard, D., & Fidock, D. A. (2019). Plasmodium falciparum resistance to piperaquine driven by PfCRT. *The Lancet Infectious Diseases*, 19(11), 1168–1169. [https://doi.org/10.1016/s1473-3099\(19\)30543-2](https://doi.org/10.1016/s1473-3099(19)30543-2)

- Ding, X. C., Ubben, D., & Wells, T. N. C. (2012). A framework for assessing the risk of resistance for anti-malarials in development. *Malaria Journal*, 11(1). <https://doi.org/10.1186/1475-2875-11-292>
- Dluzewski, A., Ling, I., Hopkins, J., Grainger, M., Margos, G., & Mitchell, G. et al. (2008). Formation of the Food Vacuole in Plasmodium falciparum: A Potential Role for the 19 kDa Duffy, P., & Patrick Gorres, J. (2020). Malaria vaccines since 2000: progress, priorities, products. *Npj Vaccines*, 5(1). <https://doi.org/10.1038/s41541-020-0196-3>
- Draper, S., Sack, B., King, C., Nielsen, C., Rayner, J., & Higgins, M. et al. (2018). Malaria Vaccines: Recent Advances and New Horizons. *Cell Host & Microbe*, 24(1), 43-56. <https://doi.org/10.1016/j.chom.2018.06.008>
- Duraisingh, M. T., Triglia, T., & Cowman, A. F. (2002). Negative selection of Plasmodium falciparum reveals targeted gene deletion by double crossover recombination. *International Journal for Parasitology*, 32(1), 81–89. [https://doi.org/10.1016/s0020-7519\(01\)00345-9](https://doi.org/10.1016/s0020-7519(01)00345-9)
- Duru, V., Khim, N., Leang, R., Kim, S., Domergue, A., Kloeung, N., ... Menard, D. (2015). Plasmodium falciparum dihydroartemisinin-piperaquine failures in Cambodia are associated with mutant K13 parasites presenting high survival rates in novel piperaquine in vitro assays: retrospective and prospective investigations. *BMC Medicine*, 13(1). <https://doi.org/10.1186/s12916-015-0539-5>
- Efficacy and Safety of the RTS,S/AS01 Malaria Vaccine during 18 Months after Vaccination: A Phase 3 Randomized, Controlled Trial in Children and Young Infants at 11 African Sites. (2014), 11(7), e1001685. <https://doi.org/10.1371/journal.pmed.1001685>
- Evidence for Their Role in Chloroquine Resistance. *Molecular Cell*, 6(4), 861-871. [https://doi.org/10.1016/s1097-2765\(05\)00077-8](https://doi.org/10.1016/s1097-2765(05)00077-8)
- Fidock, D., Nomura, T., Talley, A., Cooper, R., Dzekunov, S., & Ferdig, M. et al. (2000). Mutations in the *P. falciparum* Digestive Vacuole Transmembrane Protein PfCRT and Elgoraish, A. G., Elzakia, S. E. G., Ahmeda, R. T., Ahmeda, A. I., Fadlalmulaa, H. A., Mohameda, S. A., Abdallaha, N. I., Abdelgadira, O., Ageepa, T.B. and El-Sayeda, B. B. (2019) Epidemiology and distribution of Plasmodium vivax malaria in Sudan. *The Royal Society of Tropical Medicine and Hygiene*, 113: pp.517–524
- Flannery, E., Fidock, D., & Winzeler, E. (2013). Using Genetic Methods To Define the Targets of Compounds with Antimalarial Activity. *Journal of Medicinal Chemistry*, 56(20), 7761-7771. <https://doi.org/10.1021/jm400325j>

- Fleck, O. (2004). DNA repair. *Journal of Cell Science*, 117(4), 515-517. <https://doi.org/10.1242/jcs.00952>
- Fletcher I.K., Stewart-Ibarra, A.M., Sippy, R., Carrasco-Escobar, G., Silva, M., Beltran-Ayala, E., Ordoñez, T., Adrian, J., Sáenz, F.E., Drakeley, C., Jones, K.E. and Lowe, R. (2020) The Relative Role of Climate Variation and Control Interventions on Malaria Elimination Efforts in El Oro, Ecuador: A Modeling Study. *Frontiers in Environmental Science* 8(135), pp.1-16. doi: 10.3389/fenvs.2020.00135
- Fohl, L., & Roos, D. (2003). Fitness effects of DHFR-TS mutations associated with pyrimethamine resistance in apicomplexan parasites. *Molecular Microbiology*, 50(4), 1319-1327. <https://doi.org/10.1046/j.1365-2958.2003.03756.x>
- Fragment of Merozoite Surface Protein 1 (MSP119). *Plos ONE*, 3(8), e3085. <https://doi.org/10.1371/journal.pone.0003085>
- Frimpong, A., Kusi, K., Ofori, M., & Ndifon, W. (2018). Novel Strategies for Malaria Vaccine Design. *Frontiers In Immunology*, 9. <https://doi.org/10.3389/fimmu.2018.02769>
- Fuseini, G., Phiri, W., von Fricken, M., Smith, J., & Garcia, G. (2019). Evaluation of the residual effectiveness of Fludora® fusion WP-SB, a combination of clothianidin and deltamethrin, for the control of pyrethroid-resistant malaria vectors on Bioko Island, Equatorial Guinea. *Acta Tropica*, 196, 42-47. <https://doi.org/10.1016/j.actatropica.2019.05.006>
- Gabryszewski, S. J., Dhingra, S. K., Combrinck, J. M., Lewis, I. A., Callaghan, P. S., Hassett, M. R., Siriwardana, A., Henrich, P. P., Lee, A. H., Gnädig, N. F., Musset, L., Llinás, M., Egan, T. J., Roepe, P. D., & Fidock, D. A. (2016). Evolution of Fitness Cost-Neutral Mutant PfCRT Conferring *P. falciparum* 4-Aminoquinoline Drug Resistance Is Accompanied by Altered Parasite Metabolism and Digestive Vacuole Physiology. *PLoS pathogens*, 12(11), e1005976. <https://doi.org/10.1371/journal.ppat.1005976>
- Gaj, T., Sirk, S., Shui, S., & Liu, J. (2016). Genome-Editing Technologies: Principles and Applications. *Cold Spring Harbor Perspectives in Biology*, 8(12), a023754. <https://doi.org/10.1101/cshperspect.a023754>
- Gentile, J., Rund, S., & Madey, G. (2015). Modelling sterile insect technique to control the population of *Anopheles gambiae*. *Malaria Journal*, 14(1). <https://doi.org/10.1186/s12936-015-0587-5>
- Ghorbal, M., Gorman, M., Macpherson, C., Martins, R., Scherf, A., & Lopez-Rubio, J. (2014). Genome editing in the human malaria parasite *Plasmodium falciparum* using the

CRISPR-Cas9 system. *Nature Biotechnology*, 32(8), 819-821.
<https://doi.org/10.1038/nbt.2925>

Gnädig, N. F., Stokes, B. H., Edwards, R. L., Kalantarov, G. F., Heimsch, K. C., Kuderjavy, M., ... Fidock, D. A. (2020). Insights into the intracellular localization, protein associations and artemisinin resistance properties of *Plasmodium falciparum* K13. *PLOS Pathogens*, 16(4).
<https://doi.org/10.1371/journal.ppat.1008482>

Godfray, H. (2012). Mosquito ecology and control of malaria. *Journal of Animal Ecology*, 82(1), 15-25. <https://doi.org/10.1111/j.1365-2656.12003>

Goel, N., Dhiman, K., Kalidas, N., Mukhopadhyay, A., Ashish, & Bhattacharjee, S. (2021). *Plasmodium falciparum* Kelch13 and its artemisinin-resistant mutants assemble as hexamers in solution: a SAXS data driven shape restoration study.
<https://doi.org/10.1101/2021.02.07.430181>

Golassa, L., Amenga-Etego, L., Lo, E. et al. (2020). The biology of unconventional invasion of Duffy-negative reticulocytes by *Plasmodium vivax* and its implication in malaria epidemiology and public health. *Malaria Journal*, 19(299).
<https://doi.org/10.1186/s12936-020-03372-9>

Golden, E., Cho, H., Hofman, F., Louie, S., Schönthal, A., & Chen, T. (2015). Quinoline-based antimalarial drugs: a novel class of autophagy inhibitors. *Neurosurgical Focus*, 38(3), E12. <https://doi.org/10.3171/2014.12.focus14748>

Gonçalves, B.P., Sagara, I., Coulibaly, M. et al. Hemoglobin variants shape the distribution of malaria parasites in human populations and their transmission potential. *Scientific Reports* 7(14267). <https://doi.org/10.1038/s41598-017-14627-y>

Goodwin, S., McPherson, J., & McCombie, W. (2016). Coming of age: ten years of next-generation sequencing technologies. *Nature Reviews Genetics*, 17(6), 333-351.
<https://doi.org/10.1038/nrg.2016.49>

Gopalakrishnan, A., & Kumar, N. (2013). DNA Damage and Repair in *Plasmodium*. *Encyclopedia of Malaria*, Springer, New York, 1-8. https://doi.org/10.1007/978-1-4614-8757-9_50-2

Gorka, A. P., Jacobs, L. M., & Roepe, P. D. (2013). Cytostatic versus cytocidal profiling of quinoline drug combinations via modified fixed-ratio isobologram analysis. *Malaria Journal*, 12(1), 332. <https://doi.org/10.1186/1475-2875-12-332>

Govindarajalu, G., Rizvi, Z., Kumar, D. et al. (2019). Lyse-Reseal Erythrocytes for Transfection of *Plasmodium falciparum*. *Scientific Reports*, 9, 19952
<https://doi.org/10.1038/s41598-019-56513-9>

Guerra, C., Tresor Donfack, O., Motobe Vaz, L., Mba Nlang, J., Nze Nchama, L., & Mba Eyono, J. et al. (2021). *Malaria vector control in sub-Saharan Africa in the time of COVID-19: no room for complacency*. *BMJ Global Health*, 5, 1-4, e003880.
doi:10.1136/bmjgh-2020-003880

Gupta, D., Patra, A., Zhu, L., Gupta, A., & Bozdech, Z. (2016). DNA damage regulation and its role in drug-related phenotypes in the malaria parasites. *Scientific Reports*, 6(1).
<https://doi.org/10.1038/srep23603>

Haldar, K., Bhattacharjee, S., & Safeukui, I. (2018). Drug resistance in Plasmodium. *Nature Reviews Microbiology*, 16(3), 156-170. <https://doi.org/10.1038/nrmicro.2017.161>

Hamainza, B., Sikaala, C., Moonga, H., Chanda, J., Chinula, D., & Mwenda, M. et al. (2016). Incremental impact upon malaria transmission of supplementing pyrethroid-impregnated long-lasting insecticidal nets with indoor residual spraying using pyrethroids or the organophosphate, pirimiphos methyl. *Malaria Journal*, 15(1).
<https://doi.org/10.1186/s12936-016-1143-7>

Hamilton, W. L., Amato, R., van der Pluijm, R. W., Jacob, C. G., Quang, H. H., Thuy-Nhien, N. T., ... Miotto, O. (2019). Evolution and expansion of multidrug-resistant malaria in southeast Asia: a genomic epidemiology study. *The Lancet Infectious Diseases*, 19(9), 943–951. [https://doi.org/10.1016/s1473-3099\(19\)30392-5](https://doi.org/10.1016/s1473-3099(19)30392-5)

Hammond, A., Galizi, R., Kyrou, K., Simoni, A., Siniscalchi, C., & Katsanos, D. et al. (2016). A CRISPR-Cas9 gene drive system targeting female reproduction in the malaria mosquito vector *Anopheles gambiae*. *Nature Biotechnology*, 34(1), 78-83.
<https://doi.org/10.1038/nbt.3439>

Hayward, R., Saliba, K., & Kirk, K. (2005). pfmdr1 mutations associated with chloroquine resistance incur a fitness cost in *Plasmodium falciparum*. *Molecular Microbiology*, 55(4), 1285-1295. <https://doi.org/10.1111/j.1365-2958.2004.04470.x>

Heinberg, A., Siu, E., Stern, C., Lawrence, E., Ferdig, M., Deitsch, K., & Kirkman, L. (2013). Direct evidence for the adaptive role of copy number variation on antifolate susceptibility in *Plasmodium falciparum*. *Molecular Microbiology*, 88(4), 702-712.
<https://doi.org/10.1111/mmi.12162>

Henriques, G., Hallett, R. L., Beshir, K. B., Gadalla, N. B., Johnson, R. E., Burrow, R., ... Sutherland, C. J. (2014). Directional Selection at the pfmdr1, pf crt, pfubp1, and

pfap2mu Loci of Plasmodium falciparum in Kenyan Children Treated With ACT. *The Journal of Infectious Diseases*, 210(12), 2001–2008.
<https://doi.org/10.1093/infdis/jiu358>

Herraiz, T., Guillén, H., González-Pérez, D., & Arjón, V. (2019). Antimalarial Quinoline Drugs Inhibit β -Hematin and Increase Free Hemin Catalyzing Peroxidative Reactions and Inhibition of Cysteine Proteases. *Scientific Reports*, 9(1).
<https://doi.org/10.1038/s41598-019-51604-z>

Hill, A. (2011). Vaccines against malaria. *Philosophical Transactions Of The Royal Society B: Biological Sciences*, 366(1579), 2806-2814. <https://doi.org/10.1098/rstb.2011.0091>

Hogan, A. B., Winskill, P., & Ghani, A. C. (2020). Estimated impact of RTS,S/AS01 malaria vaccine allocation strategies in sub-Saharan Africa: A modelling study. *PLOS Medicine*, 17(11). <https://doi.org/10.1371/journal.pmed.1003377>

Hoppe, H., van Schalkwyk, D., Wiehart, U., Meredith, S., Egan, J., & Weber, B. (2004). Antimalarial Quinolines and Artemisinin Inhibit Endocytosis in Plasmodium falciparum. *Antimicrobial Agents and Chemotherapy*, 48(7), 2370-2378.
<https://doi.org/10.1128/aac.48.7.2370-2378.2004>

Hossain, M.S., Commons, R.J., Douglas N.M., Thriemer, K., Alemayehu, B.H., Amaratunga, C. et al. (2020) The risk of Plasmodium vivax parasitaemia after *P. falciparum* malaria: An individual patient data meta-analysis from the WorldWide Antimalarial Resistance Network. *PLoS Medicine* 17(11), pp.1-26 e1003393. <https://doi.org/10.1371/journal.pmed.1003393>

Hott, A., Tucker, M., Casandra, D., Sparks, K., & Kyle, D. (2015). Fitness of artemisinin-resistant Plasmodium falciparum in vitro. *Journal of Antimicrobial Chemotherapy*, 70(10), 2787-2796. <https://doi.org/10.1093/jac/dkv199>

Howes, R. E., Battle K. E., Mendis K. N., Smith D. L., Cibulskis R. E., Baird J. K., Hay S. I. (2016). Global Epidemiology of Plasmodium vivax. *American Journal of Tropical Medicine and Hygiene*. 28;95(6 Suppl):15-34. doi: 10.4269/ajtmh.16-0141
<https://doi.org/10.1016/j.jmii.2019.05.012>.

https://endmalaria.org/sites/default/files/uploads/2017/07/RBM-Strategic-Plan-Template-Test_FINAL.pdf

Hu, L., Magesh, S., Chen, L., Wang, L., Lewis, T., & Chen, Y. et al. (2013). Discovery of a small-molecule inhibitor and cellular probe of Keap1-Nrf2 protein-protein interaction.

Bioorganic & Medicinal Chemistry Letters, 23(10), 3039-3043.
<https://doi.org/10.1016/j.bmcl.2013.03.013>

Huang, R., Pei, L., Liu, Q., Chen, S., Dou, H., & Shu, G. *et al.* (2019). Isobogram Analysis: A Comprehensive Review of Methodology and Current Research. *Frontiers in Pharmacology*, 10. <https://doi.org/10.3389/fphar.2019.01222>

Huang, Z., Li, R., Tang, T., Ling, D., Wang, M., & Xu, D. *et al.* (2020). A novel multistage antiplasmodial inhibitor targeting Plasmodium falciparum histone deacetylase 1. *Cell Discovery*, 6(1). <https://doi.org/10.1038/s41421-020-00215-4>

Hussien, M., Abdel Hamid, M., Elamin, E., Hassan, A., Elaagip, A., & Salama, A. *et al.* (2020). Antimalarial drug resistance molecular makers of Plasmodium falciparum isolates from Sudan during 2015–2017. *PLOS ONE*, 15(8), e0235401. <https://doi.org/10.1371/journal.pone.0235401>

Imai N., White M.T., Ghani A.C. & Drakeley C.J. (2014) Transmission and Control of *Plasmodium knowlesi*: A Mathematical Modelling Study. *PLOS Neglected Tropical Diseases* 8(7): e2978. <https://doi.org/10.1371/journal.pntd.0002978>

Imwong, M., Suwannasin, K., Kunasol, C., Sutawong, K., Mayxay, M., & Rekol, H. *et al.* (2017). The spread of artemisinin-resistant Plasmodium falciparum in the Greater Mekong subregion: a molecular epidemiology observational study. *The Lancet Infectious Diseases*, 17(5), 491-497. [https://doi.org/10.1016/s1473-3099\(17\)30048-8](https://doi.org/10.1016/s1473-3099(17)30048-8)

Jeyaprakasam, N.K., Liew, J. W. K., Low, V. L., Wan-Sulaiman, W.Y., Vythilingam, I. (2020) *Plasmodium knowlesi* infecting humans in Southeast Asia: What's next? *PLOS Neglected Tropical Diseases* 14(12): e0008900. <https://doi.org/10.1371/journal.pntd.0008900>

Jiang, T., Cheng, W., Yao, Y., Tan, H., Wu, K., & Li, J. (2020). Molecular surveillance of anti-malarial resistance Pfdhfr and Pfdhps polymorphisms in African and Southeast Asia Plasmodium falciparum imported parasites to Wuhan, China. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03509-w>

Josling, G. & Llinás, M. Sexual development in *Plasmodium* parasites: knowing when it's time to commit (2015). *Nature Reviews Microbiology*, 13, pp.573–587. <https://doi.org/10.1038/nrmicro3519>

Josling, G. A., Williamson, K. C., & Llinás, M. (2018). Regulation of Sexual Commitment and Gametocytogenesis in Malaria Parasites. *Annual Review of Microbiology*, 72, pp.501–519. <https://doi.org/10.1146/annurev-micro-090817-062712>

- Juma, D., Omondi, A., Ingasia, L., Opot, B., Cheruiyot, A., & Yeda, R. *et al.* (2014). Trends in drug resistance codons in *Plasmodium falciparum* dihydrofolate reductase and dihydropteroate synthase genes in Kenyan parasites from 2008 to 2012. *Malaria Journal*, 13(1), 250. <https://doi.org/10.1186/1475-2875-13-250>
- Kandul, N., Liu, J., Sanchez C., H., Wu, S., Marshall, J., & Akbari, O. (2019). Transforming insect population control with precision guided sterile males with demonstration in *A. gambiae* flies. *Nature Communications*, 10(1). <https://doi.org/10.1038/s41467-018-07964-7>
- Kané, F., Keïta, M., Traoré, B., Diawara, S., Bane, S., & Diarra, S. *et al.* (2020). Performance of IRS on malaria prevalence and incidence using pirimiphos-methyl in the context of pyrethroid resistance in Koulikoro region, Mali. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03357-8>
- Kansanen, E., Kuosmanen, S. M., Leinonen, H., & Levonen, A. L. (2013). The Keap1-Nrf2 pathway: Mechanisms of activation and dysregulation in cancer. *Redox biology*, 1(1), 45–49. <https://doi.org/10.1016/j.redox.2012.10.001>
- Kapesa, A., Kweka, E. J., Atieli, H., Afrane, Y. A., Kamugisha, E., Lee, M.-C., ... Yan, G. (2018). The current malaria morbidity and mortality in different transmission settings in Western Kenya. *PLOS ONE*, 13(8). <https://doi.org/10.1371/journal.pone.0202031>
- Kapishnikov, S., Staals, T., Yang, Y., Lee, J., Párez-Berná, A., & Pereiro, E. *et al.* (2019). Mode of action of quinoline antimalarial drugs in red blood cells infected by *Plasmodium falciparum* revealed in vivo. *Proceedings of The National Academy Of Sciences*, 116(46), 22946-22952. <https://doi.org/10.1073/pnas.1910123116>
- Karema, C., Imwong, M., Fanello, C., Stepniewska, K., Uwimana, A., & Nakeesathit, S. *et al.* (2009). Molecular Correlates of High-Level Antifolate Resistance in Rwandan Children with *Plasmodium falciparum* Malaria. *Antimicrobial Agents and Chemotherapy*, 54(1), 477-483. <https://doi.org/10.1128/aac.00498-09>
- Kayode, A., Ajogbasile, F., Akano, K., Uwanibe, J., Olunyi, P., & Eromon, P. *et al.* (2021). Polymorphisms in *Plasmodium falciparum* dihydropteroate synthetase and dihydrofolate reductase genes in Nigerian children with uncomplicated malaria using high-resolution melting technique. *Scientific Reports*, 11(1). <https://doi.org/10.1038/s41598-020-80017-6>
- Keïta, M., Sogoba, N., Traoré, B., Kané, F., Coulibaly, B., Traoré, S., & Doumbia, S. (2021). Performance of pirimiphos-methyl based Indoor Residual Spraying on entomological parameters of malaria transmission in the pyrethroid resistance region of Koulikoro, Mali. *Acta Tropica*, 216, 105820. <https://doi.org/10.1016/j.actatropica.2020.105820>

- Khamis, D., El Mouden, C., Kura, K., & Bonsall, M. (2018). Optimal control of malaria: combining vector interventions and drug therapies. *Malaria Journal*, 17(1). <https://doi.org/10.1186/s12936-018-2321-6>
- Killeen, G. F., Marshall, J. M., Kiware, S. S., South, A. B., Tusting, L. S., Chaki, P. P., & Govella, N. J. (2017). Measuring, manipulating and exploiting behaviours of adult mosquitoes to optimise malaria vector control impact. *BMJ Global Health*, 2(2). <https://doi.org/10.1136/bmjgh-2016-000212>
- Kleinschmidt, I., Schwabe, C., Shiva, M., Segura, J. L., Sima, V., Mabunda, S. J., & Coleman, M. (2009). Combining indoor residual spraying and insecticide-treated net interventions. *The American journal of tropical medicine and hygiene*, 81(3), 519–524.
- Kotepui, M., Kotepui, K. U., Milanez, G. D., & Masangkay, F. R. (2020). Severity and mortality of severe *Plasmodium ovale* infection: A systematic review and meta-analysis. *PLoS one*, 15(6), e0235014. <https://doi.org/10.1371/journal.pone.0235014>
- Kreppel, K., Viana, M., Main, B., Johnson, P., Govella, N., & Lee, Y. et al. (2020). Emergence of behavioural avoidance strategies of malaria vectors in areas of high LLIN coverage in Tanzania. *Scientific Reports*, 10(1). <https://doi.org/10.1038/s41598-020-71187-4>
- Kublin, J. G., Cortese, J. F., Njunju, E. M., G. Mukadam, R. A., Wirima, J. J., Kazembe, P. N., Plowe, C. V. et al. (2003). Reemergence of Chloroquine-Sensitive *Plasmodium falciparum* Malaria after Cessation of Chloroquine Use in Malawi. *The Journal of Infectious Diseases*, 187(12), 1870–1875. <https://doi.org/10.1086/375419> en
- Kumar, S., Singh, R., Patial, B., Goyal, S., & Bhardwaj, T. (2015). Recent advances in novel heterocyclic scaffolds for the treatment of drug-resistant malaria. *Journal of Enzyme Inhibition And Medicinal Chemistry*, 31(2), 173-186. <https://doi.org/10.3109/14756366.2015.1016513>
- Kümpornsing, K., Kochakarn, T., & Chookajorn, T. (2019). The resistome and genomic reconnaissance in the age of malaria elimination. *Disease Models & Mechanisms*, 12(12), dmm040717. <https://doi.org/10.1242/dmm.040717>
- Kyrou, K., Hammond, A., Galizi, R., Kranjc, N., Burt, A., & Beaghton, A. et al. (2018). A CRISPR/Cas9 gene drive targeting doublesex causes complete population suppression in caged *Anopheles gambiae* mosquitoes. *Nature Biotechnology*, 36(11), 1062-1066. <https://doi.org/10.1038/nbt.4245>
- Lagarce, L., Lerolle, N., Asfar, P., Le Govic, Y., Lainé-Cessac, P., & de Gentile, L. (2016). A non-pharmaceutical form of *Artemisia annua* is not effective in preventing *Plasmodium*

falciparummalaria. *Journal Of Travel Medicine*, 23(5), taw049.
<https://doi.org/10.1093/jtm/taw049>

Laishram, D. D., Sutton, P. L., Nanda, N. et al. (2012). The complexities of malaria disease manifestations with a focus on asymptomatic malaria. *Malar Journal*, 11(29), pp.1-15
<https://doi.org/10.1186/1475-2875-11-29>

Lawrenson, A., Cooper, D., O'Neill, P., & Berry, N. (2018). Study of the antimalarial activity of 4-aminoquinoline compounds against chloroquine-sensitive and chloroquine-resistant parasite strains. *Journal of Molecular Modeling*, 24(9). <https://doi.org/10.1007/s00894-018-3755-z>

Lee W. C., Russell, B. and Rénia, L. (2019) Sticking for a Cause: The Falciparum Malaria Parasites Cytoadherence Paradigm. *Frontiers in Immunology*.
<https://doi.org/10.3389/fimmu.2019.01444>

Lee, A., Symington, L., & Fidock, D. (2014). DNA Repair Mechanisms and Their Biological Roles in the Malaria Parasite Plasmodium falciparum. *Microbiology and Molecular Biology Reviews*, 78(3), 469-486. <https://doi.org/10.1128/mmbr.00059-13>

Lee, M.C.S., Lindner, S., Lopez-Rubio, J., & LlinÁjs, M. (2019). Cutting back malaria: CRISPR/Cas9 genome editing of Plasmodium. *Briefings in Functional Genomics*, 18(5), 281-289. <https://doi.org/10.1093/bfgp/elz012>

Levitz, L., Janko, M., Mwandagaliwa, K., Thwai, K., Likwela, J., & Tshefu, A. et al. (2018). Effect of individual and community-level bed net usage on malaria prevalence among under-fives in the Democratic Republic of Congo. *Malaria Journal*, 17(1).
<https://doi.org/10.1186/s12936-018-2183-y>

Li, L., Wu, L., & Chandrasegaran, S. (1992). Functional domains in Fok I restriction endonuclease. *Proceedings of The National Academy Of Sciences*, 89(10), 4275-4279. <https://doi.org/10.1073/pnas.89.10.4275>

Lo, E., Nguyen, K., Nguyen, J., Hemming-Schroeder, E., Xu, J., Etemesi, H., Githeko, A., & Yan, G. (2017). Plasmodium malariae Prevalence and csp Gene Diversity, Kenya, 2014 and 2015. *Emerging infectious diseases*, 23(4), pp.601–610.
<https://doi.org/10.3201/eid2304.161245>

Lobo, N., Achee, N., Greico, J., & Collins, F. (2017). Modern Vector Control. *Cold Spring Harbor Perspectives in Medicine*, 8(1), a025643.
<https://doi.org/10.1101/cshperspect.a025643>

- Loha, E., Deressa, W., Gari, T., Balkew, M., Kenea, O., & Solomon, T. *et al.* (2019). Long-lasting insecticidal nets and indoor residual spraying may not be sufficient to eliminate malaria in a low malaria incidence area: results from a cluster randomized controlled trial in Ethiopia. *Malaria Journal*, 18(1). <https://doi.org/10.1186/s12936-019-2775-1>
- Loiseau, C., Cooper, M. M., & Doolan, D. L. (2020). Deciphering host immunity to malaria using systems immunology. *Immunol Rev*, 293(1), 115-143. doi:10.1111/imr.12814
- Lubis, I. N. D., Wijaya, H., Lubis, M., Lubis, C. P., Beshir, K. B., Staedke, S. G., & Sutherland, C. J. (2020). Recurrence of *Plasmodium malariae* and *P. falciparum* Following Treatment of Uncomplicated Malaria in North Sumatera With Dihydroartemisinin-Piperaquine or Artemether-Lumefantrine. *Open Forum Infect Dis*, 7(5), ofaa116. doi:10.1093/ofid/ofaa116
- Lukens, A., Ross, L., Heidebrecht, R., Javier Gamo, F., Lafuente-Monasterio, M., & Booker, M. *et al.* (2013). Harnessing evolutionary fitness in *Plasmodium falciparum* for drug discovery and suppressing resistance. *Proceedings Of The National Academy Of Sciences*, 111(2), 799-804. <https://doi.org/10.1073/pnas.1320886110>
- Ma, D., & Liu, F. (2015). Genome Editing and Its Applications in Model Organisms. *Genomics, Proteomics & Bioinformatics*, 13(6), 336-344. <https://doi.org/10.1016/j.gpb.2015.12.001>
- Ménard, D., Khim, N., Beghain, J., Adegnika, A., Shafiu-Alam, M., & Amodu, O. *et al.* (2016). A Worldwide Map of *Plasmodium falciparum* K13-Propeller Polymorphisms. *New England Journal of Medicine*, 374(25), 2453-2464. <https://doi.org/10.1056/nejmoa1513137>
- Mahmoudi, S. and Keshavarz, H. (2018) Malaria Vaccine Development: The Need for Novel Approaches: A Review Article. *Iran Journal of Parasitology*, 13(1), 1-10 <http://ijpa.tums.ac.ir>
- Maïga, H., Damiens, D., Niang, A., Sawadogo, S., Fatherhaman, O., & Lees, R. *et al.* (2014). Mating competitiveness of sterile male *Anopheles coluzzii* in large cages. *Malaria Journal*, 13(1). <https://doi.org/10.1186/1475-2875-13-460>
- Maji, A. K. (2018). Drug susceptibility testing methods of antimalarial agents. *Tropical Parasitology*, 8(2), 70. <https://doi.org/10.4103/2229-5070.248695>
- Marapana, D., & Cowman, A. (2020). Uncovering the ART of antimalarial resistance. *Science*, 367(6473), 22-23. <https://doi.org/10.1126/science.aba0445>

- Marin-Mogollon, C., Salman, A. M., Koolen, K. M., Bolscher, J. M., van Pul, F. J., Miyazaki, S., ... Khan, S. M. (2019). A *P. falciparum* NF54 Reporter Line Expressing mCherry-Luciferase in Gametocytes, Sporozoites, and Liver-Stages. *Frontiers in Cellular and Infection Microbiology*, 9. <https://doi.org/10.3389/fcimb.2019.00096>
- Markus, M. B. (2015). Do hypnozoites cause relapse in malaria? *Trends in Parasitology*, 31(6), 239–245. <https://doi.org/10.1016/j.pt.2015.02.003>
- Martin, N., Nam, V., Lover, A., Phong, T., Tu, T., & Mendenhall, I. (2020). The impact of transfluthrin on the spatial repellency of the primary malaria mosquito vectors in Vietnam: *Anopheles dirus* and *Anopheles minimus*. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-019-3092-4>
- Mathieu, L., Cox, H., Early, A., Mok, S., Lazrek, Y., & Paquet, J. et al. (2020). Local emergence in Amazonia of *Plasmodium falciparum* k13 C580Y mutants associated with in vitro artemisinin resistance. *Elife*, 9. <https://doi.org/10.7554/elife.51015>
- Matthews, H., Duffy, C., & Merrick, C. (2018). Checks and balances? DNA replication and the cell cycle in *Plasmodium*. *Parasites & Vectors*, 11(1). <https://doi.org/10.1186/s13071-018-2800-1>
- Mbengue, A., Bhattacharjee, S., Pandharkar, T., Liu, H., Estiu, G., & Stahelin, R. et al. (2015). A molecular mechanism of artemisinin resistance in *Plasmodium falciparum* malaria. *Nature*, 520(7549), 683-687. <https://doi.org/10.1038/nature14412>
- Ménard, D., & Fidock, D. A. (2019). Accelerated evolution and spread of multidrug-resistant *Plasmodium falciparum* takes down the latest first-line antimalarial drug in southeast Asia. *The Lancet Infectious Diseases*, 19(9), 916–917. [https://doi.org/10.1016/s1473-3099\(19\)30394-9](https://doi.org/10.1016/s1473-3099(19)30394-9)
- Mendes C., Dias F., Figueiredo J., Mora V.G., Cano J., et al. (2011) Duffy Negative Antigen Is No Longer a Barrier to *Plasmodium vivax* – Molecular Evidences from the African West Coast (Angola and Equatorial Guinea). *PLOS Neglected Tropical Diseases* 5(6): e1192. <https://doi.org/10.1371/journal.pntd.0001192>
- Miller, J., Holmes, M., Wang, J., Guschin, D., Lee, Y., & Rupniewski, I. et al. (2007). An improved zinc-finger nuclease architecture for highly specific genome editing. *Nature Biotechnology*, 25(7), 778-785. <https://doi.org/10.1038/nbt1319>
- Miller, R. H., Obuya, C. O., Wanja, E. W., Ogutu, B., Waitumbi, J., Luckhart, S., & Stewart, V. A. (2015). Characterization of *Plasmodium ovale curtisi* and *P. ovale wallikeri* in Western Kenya utilizing a novel species-specific real-time PCR assay. *PLoS*

Neglected Tropical Diseases, 9(1), e0003469.
<https://doi.org/10.1371/journal.pntd.0003469>

Miotto, O., Amato, R., Ashley, E., MacInnis, B., Almagro-Garcia, J., & Amaratunga, C. et al. (2015). Genetic architecture of artemisinin-resistant *Plasmodium falciparum*. *Nature Genetics*, 47(3), 226-234. <https://doi.org/10.1038/ng.3189>

Miotto, O., Sekihara, M., Tachibana, S.-I., Yamauchi, M., Pearson, R. D., Amato, R., ... Mita, T. (2020). Emergence of artemisinin-resistant *Plasmodium falciparum* with kelch13 C580Y mutations on the island of New Guinea. *PLOS Pathogens*, 16(12). <https://doi.org/10.1371/journal.ppat.1009133>

Mkulama, M., Chishimba, S., Sikalima, J., Rouse, P., Thuma, P., & Mharakurwa, S. (2008). Escalating *Plasmodium falciparum* antifolate drug resistance mutations in Macha, rural Zambia. *Malaria Journal*, 7(1), 87. <https://doi.org/10.1186/1475-2875-7-87>

MMV-supported projects | Medicines for Malaria Venture. Mmv.org. (2021). Retrieved 24 February 2021, from <https://www.mmv.org/research-development/mmv-supported-projects>.

Mok, S., Ashley, E., Ferreira, P., Zhu, L., Lin, Z., & Yeo, T. et al. (2014). Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance. *Science*, 347(6220), 431-435. <https://doi.org/10.1126/science.1260403>

Molina-Franky, J., Cuy-Chaparro, L., Camargo, A., Reyes, C., Gómez, M., & Salamanca, D. et al. (2020). *Plasmodium falciparum* pre-erythrocytic stage vaccine development. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-3141-z>

Molnar, C., Jermyn, I. H., Kato, Z., Rahkama, V., Östling, P., Mikkonen, P., Pietäinen, V., & Horvath, P. (2016). Accurate Morphology Preserving Segmentation of Overlapping Cells based on Active Contours. *Scientific reports*, 6, 32412. <https://doi.org/10.1038/srep32412>

Mousa, A., Al-Taiar, A., Anstey, N. M., Badaut, C., Barber, B. E., et al. (2020) The impact of delayed treatment of uncomplicated *P. falciparum* malaria on progression to severe malaria: A systematic review and a pooled multicentre individual-patient meta-analysis. *PLOS Medicine*, 17(10), pp.1-28. e1003359. <https://doi.org/10.1371/journal.pmed.1003359>

Muh, F., Lee, S. K., Hoque, M. R. et al. In vitro invasion inhibition assay using antibodies against *Plasmodium knowlesi* Duffy binding protein alpha and apical membrane antigen protein 1 in human erythrocyte-adapted *P. knowlesi* A1-H.1 strain. *Malaria Journal*, 17(272). <https://doi.org/10.1186/s12936-018-2420-4>

- Mwai, L., Ochong, E., Abdirahman, A., Kiara, S., Ward, S., & Kokwaro, G. et al. (2009). Chloroquine resistance before and after its withdrawal in Kenya. *Malaria Journal*, 8(1), 106. <https://doi.org/10.1186/1475-2875-8-106>
- N'Guessan, R., Boko, P., Odjo, A., Chabi, J., Akogbeto, M., & Rowland, M. (2010). Control of pyrethroid and DDT-resistant *Anopheles gambiae* by application of indoor residual spraying or mosquito nets treated with a long-lasting organophosphate insecticide, chlorpyrifos-methyl. *Malaria Journal*, 9(1). <https://doi.org/10.1186/1475-2875-9-44>
- Nag, S., Dalgaard, M. D., Kofoed, P.-E., Ursing, J., Crespo, M., Andersen, L. O. B., ... Alifrangis, M. (2017). High throughput resistance profiling of *Plasmodium falciparum* infections based on custom dual indexing and Illumina next generation sequencing-technology. *Scientific Reports*, 7(1). <https://doi.org/10.1038/s41598-017-02724-x>
- Nair, S., Li, X., Arya, G. A., McDew-White, M., Ferrari, M., Nosten, F., & Anderson, T. J. (2018). Fitness Costs and the Rapid Spread of kelch13-C580Y Substitutions Conferring Artemisinin Resistance. *Antimicrobial Agents and Chemotherapy*, 62(9). <https://doi.org/10.1128/aac.00605-18>
- Nasamu, A., Falla, A., Pasaje, C., Wall, B., Wagner, J., & Ganesan, S. et al. (2021). An integrated platform for genome engineering and gene expression perturbation in *Plasmodium falciparum*. *Scientific Reports*, 11(1). <https://doi.org/10.1038/s41598-020-77644-4>
- Natasha M. Archer, Nicole Petersen, Martha A. Clark, Caroline O. Buckee, Lauren M. Childs, Manoj T. Duraisingh (2018) Resistance to *Plasmodium falciparum* in sickle cell trait erythrocytes is driven by oxygen-dependent growth inhibition. *Proceedings of the National Academy of Sciences*, 115(28), pp.7350-7355; DOI: 10.1073/pnas.1804388115
- Neafsey, D., Juraska, M., Bedford, T., Benkeser, D., Valim, C., & Griggs, A. et al. (2015). Genetic Diversity and Protective Efficacy of the RTS,S/AS01 Malaria Vaccine. *New England Journal of Medicine*, 373(21), 2025-2037. <https://doi.org/10.1056/nejmoa1505819>
- Ng, C., & Fidock, D. (2019). *Plasmodium falciparum* In Vitro Drug Resistance Selections and Gene Editing. *Methods in Molecular Biology*, 123-140. https://doi.org/10.1007/978-1-4939-9550-9_9
- Ngotho, P., Soares, A. B., Hentzschel, F., Achcar, F., Bertuccini, L., & Marti, M. (2019) Revisiting gametocyte biology in malaria parasites, *FEMS Microbiology Reviews*, 43(4), pp.401–414, <https://doi.org/10.1093/femsre/fuz010>

- Ngufor, C., Fagbohoun, J., Critchley, J., Nguessan, R., Todjinou, D., & Malone, D. et al. (2017). Which intervention is better for malaria vector control: insecticide mixture long-lasting insecticidal nets or standard pyrethroid nets combined with indoor residual spraying? *Malaria Journal*, 16(1). <https://doi.org/10.1186/s12936-017-1987-5>
- Niaré, K., Paloque, L., Tor, P., Doumbo, O. K., Ménard, S., Benoit-Vical, F., ... Dara, A. (2018). Multiple Phenotypic and Genotypic Artemisinin Sensitivity Evaluation of Malian Plasmodium falciparum Isolates. *The American Journal of Tropical Medicine and Hygiene*, 98(4), 1123–1131. <https://doi.org/10.4269/ajtmh.17-0798>
- Nsanzabana, C., Hastings, I., Marfurt, J., Mäller, I., Baea, K., & Rare, L. et al. (2010). Quantifying the Evolution and Impact *The Journal of Infectious Diseases*, 201(3), 435-443. <https://doi.org/10.1086/649784>
- Nsereko, G., Kadobera, D., Okethwangu, D., Nguni, J., Rutazaana, D., & Kyabayinze, D. et al. (2020). Malaria Outbreak Facilitated by Appearance of Vector-Breeding Sites after Heavy Rainfall and Inadequate Preventive Measures: Nwoya District, Northern Uganda, February-May 2018. *Journal of Environmental and Public Health*, 2020, 1-10. <https://doi.org/10.1155/2020/5802401>
- Nureye, D.S. and Assefa, S. (2020) Old and Recent Advances in Life Cycle, Pathogenesis, Diagnosis, Prevention, and Treatment of Malaria Including Perspectives in Ethiopia. *The Scientific World Journal* 2020(1295381) pp.1-17 <https://doi.org/10.1155/2020/1295381>
- Nwakanma, D., Duffy, C., Amambua-Ngwa, A., Oriero, E., Bojang, K., & Pinder, M. et al. (2013). Changes in Malaria Parasite Drug Resistance in an Endemic Population Over a 25-Year Period with Resulting Genomic Evidence of Selection. *The Journal of Infectious Diseases*, 209(7), 1126-1135. <https://doi.org/10.1093/infdis/jit618>
- Ogunah, J., Lalah, J., & Schramm, K. (2020). Malaria vector control strategies. What is appropriate towards sustainable global eradication? *Sustainable Chemistry and Pharmacy*, 18, 100339. <https://doi.org/10.1016/j.scp.2020.100339>
- Okafor C.N., Finnigan N.A. (2020) *Plasmodium Ovale* Malaria. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2020 Jan-. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK519021/>
- Okell, L., Griffin, J., & Roper, C. (2017). Mapping sulphadoxine-pyrimethamine-resistant Plasmodium falciparum malaria in infected humans and in parasite populations in Africa. *Scientific Reports*, 7(1). <https://doi.org/10.1038/s41598-017-06708-9>

Onyedibe, K. I., Iroezindu, M. O., Obishakin, E. T., Ojogba, M. O., Shobowale, E. O., Ita, I. O., Udo, U. O., Isa, S. E. and Egah, D. Z. (2016) Plasmodium knowlesi Infection: Should Africa be Prepared for a New Human Malaria Threat.

Osii, R., S., Otto, T. D., Garside, P., Ndungu, F. M. and Brewer, J. M. (2020) The Impact of Malaria Parasites on Dendritic Cell-T Cell Interaction. *Frontiers in Immunology*, 11(1597), pp1-16. doi: 10.3389/fimmu.2020.01597

Oyedeleji, S., Bassi, P., Oyedeleji, S., Ojurongbe, O., & Awobode, H. (2020). Genetic diversity and complexity of Plasmodium falciparum infections in the microenvironment among siblings of the same household in North-Central Nigeria. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03415-1>

Pacheco, M., Schneider, K., Cheng, Q., Munde, E., Ndege, C., & Onyango, C. et al. (2020). Changes in the frequencies of Plasmodium falciparum dhps and dhfr drug-resistant mutations in children from Western Kenya from 2005 to 2018: the rise of Pfdhps S436H. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03454-8>

Pance, A. (2020). Diversify and Conquer: The Vaccine Escapism of Plasmodium falciparum. *Microorganisms*, 8(11), doi:10.3390/microorganisms8111748

Paone, S., D'Alessandro, S., Parapini, S. et al. Characterization of the erythrocyte GTPase Rac1 in relation to *Plasmodium falciparum* invasion. *Sci Rep* 10, 22054 (2020). <https://doi.org/10.1038/s41598-020-79052-0>

Patel, H., Duncan, C., & Cunningham, A. J. (2020). Predictors of outcome in childhood *Plasmodium falciparum* malaria. *Virulence*, 11(1), pp.199–221. <https://doi.org/10.1080/21505594.2020.1726570>

Patriani, D., Arguni, E., Kenangalem, E., Dini, S., Sugiarto, P., Hasanuddin, A., ... Poespoprodjo, J. R. (2019). Early and late mortality after malaria in young children in Papua, Indonesia. *BMC Infectious Diseases*, 19(1). <https://doi.org/10.1186/s12879-019-4497-y>

Pava, Z., Mok, S., Collins, K., Rebelo, M., Watts, R., & Robinson, G. et al. (2020). Plasmodium falciparum artemisinin-resistant K13 mutations confer a sexual-stage transmission advantage that can be overcome with atovaquone-proguanil. <https://doi.org/10.1101/2020.10.26.20214619>

Penny, M., Camponovo, F., Chitnis, N., Smith, T., & Tanner, M. (2020). Future use-cases of vaccines in malaria control and elimination. *Parasite Epidemiology and Control*, 10, e00145. <https://doi.org/10.1016/j.parepi.2020.e00145>

Pishchany, G., & Skaar, E. (2012). Taste for Blood: Hemoglobin as a Nutrient Source for Pathogens. *Plos Pathogens*, 8(3), e1002535. <https://doi.org/10.1371/journal.ppat.1002535>

Plewes, K., Turner, G. & Dondorp, A. (2018) Pathophysiology, clinical presentation, and treatment of coma and acute kidney injury complicating falciparum malaria, *Current Opinion in Infectious Diseases*: 31(1), 69-77. doi: 10.1097/QCO.0000000000000419

Popovici, J., Roesch, C. and Rougeron V (2020) The enigmatic mechanisms by which *Plasmodium vivax* infects Duffy-negative individuals. *PLOS Pathogens* 16(2): e1008258. <https://doi.org/10.1371/journal.ppat.1008258>

Prajapati, S.K., Ayanful-Torgby, R., Pava, Z. et al. (2020) The transcriptome of circulating sexually committed *Plasmodium falciparum* ring stage parasites forecasts malaria transmission potential. *Nature Communications*, 11(6159), 1-11. <https://doi.org/10.1038/s41467-020-19988->

Protopopoff, N., Mosha, J., Lukole, E., Charlwood, J., Wright, A., & Mwalimu, C. et al. (2018). Effectiveness of a long-lasting piperonyl butoxide-treated insecticidal net and indoor residual spray interventions, separately and together, against malaria transmitted by pyrethroid-resistant mosquitoes: a cluster, randomised controlled, two-by-two factorial design trial. *The Lancet*, 391(10130), 1577-1588. [https://doi.org/10.1016/s0140-6736\(18\)30427-6](https://doi.org/10.1016/s0140-6736(18)30427-6)

Putrianti, E. D., Schmidt-Christensen, A., Heussler, V., Matuschewski, K., Ingmundson, A. (2020) A Plasmodium cysteine protease required for efficient transition from the liver infection stage. *PLoS Pathogen*, 16(9), pp.1-20 e1008891. <https://doi.org/10.1371/journal.ppat.1008891>

Quan, H., Igbasi, U., Oyibo, W., Omilabu, S., Chen, S., & Shen, H. et al. (2020). High multiple mutations of Plasmodium falciparum-resistant genotypes to sulphadoxine-pyrimethamine in Lagos, Nigeria. *Infectious Diseases of Poverty*, 9(1). <https://doi.org/10.1186/s40249-020-00712-4>

Rajapakse, C., Lisai, M., Deregnaucourt, C., Sinou, V., Latour, C., & Roy, D. et al. (2015). Synthesis of New 4-Aminoquinolines and Evaluation of Their In Vitro Activity against Chloroquine-Sensitive and Chloroquine-Resistant Plasmodium falciparum. *PLOS ONE*, 10(10), e0140878. <https://doi.org/10.1371/journal.pone.0140878>

Rampling, T., Ewer, K., Bowyer, G., Edwards, N., Wright, D., & Sridhar, S. et al. (2018). Safety and efficacy of novel malaria vaccine regimens of RTS,S/AS01B alone, or with

concomitant ChAd63-MVA-vectored vaccines expressing ME-TRAP. *Npj Vaccines*, 3(1). <https://doi.org/10.1038/s41541-018-0084-2>

Rathmehs, G., Rumisha, S. F., Lucas, T. C., Twohig, K. A., Python, A., Nguyen, M., ... Weiss, D. J. (2020). Global estimation of anti-malarial drug effectiveness for the treatment of uncomplicated *Plasmodium falciparum* malaria 1991–2019. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03446-8>

Ravenhall, M., Benavente, E., Sutherland, C., Baker, D., Campino, S., & Clark, T. (2019). An analysis of large structural variation in global *Plasmodium falciparum* isolates identifies a novel duplication of the chloroquine resistance associated gene. *Scientific Reports*, 9(1). <https://doi.org/10.1038/s41598-019-44599-0>

Raynes, K. (1999). Invited review Bisquinaline antimalarials: their role in malaria chemotherapy. *International Journal for Parasitology*, 29(3), 367-379. [https://doi.org/10.1016/s0020-7519\(98\)00217-3](https://doi.org/10.1016/s0020-7519(98)00217-3)

Rénia, L., Howland, S. W., Claser, C., Charlotte Gruner, A., Suwanarusk, R., Hui Teo, T., Russell, B., & Ng, L. F. (2012). Cerebral malaria: mysteries at the blood-brain barrier. *Virulence*, 3(2), 193–201. <https://doi.org/10.4161/viru.19013>

Reteng, P., Vrisca, V., Sukarno, I., Djarkoni, I. H., Kalangi, J. A., Jacobs, G. E., ... Tuda, J. (2017). Genetic polymorphisms in *Plasmodium falciparum* chloroquine resistance genes, pfcr1 and pfmdr1, in North Sulawesi, Indonesia. *BMC Research Notes*, 10(1). <https://doi.org/10.1186/s13104-017-2468-1>

Rocamora, F., & Winzeler, E. A. (2020). Genomic Approaches to Drug Resistance in Malaria. *Annual Review of Microbiology*, 74(1), 761–786. <https://doi.org/10.1146/annurev-micro-012220-064343>

Rogerson, S., Beeson, J., Laman, M., Poespoprodjo, J., William, T., Simpson, J., & Price, R. (2020). Identifying and combating the impacts of COVID-19 on malaria. *BMC Medicine*, 18(1). <https://doi.org/10.1186/s12916-020-01710-x>

Roll Back Malaria (2018) RBM Partnership Strategic Plan 2018–2020

Roncalés, M., Vidal, J., Torres, P.A. and Herreros, E. (2015) *In Vitro Culture of Plasmodium falciparum: Obtention of Synchronous Asexual Erythrocytic Stages*. *Open Journal of Epidemiology*, 5, pp.71-80.

Rosenthal, P. (2003). Antimalarial drug discovery: old and new approaches. *Journal Of Experimental Biology*, 206(21), 3735-3744. <https://doi.org/10.1242/jeb.00589>

- Ross, L., Lafuente-Monasterio, M., Sakata-Kato, T., Mandt, R., Gamo, F., Wirth, D., & Lukens, A. (2018). Identification of Collateral Sensitivity to Dihydroorotate Dehydrogenase Inhibitors in *Plasmodium falciparum*. *ACS Infectious Diseases*, 4(4), 508-515. <https://doi.org/10.1021/acsinfecdis.7b00217>
- SÁj, J., Kaslow, S., Krause, M., Melendez-Muniz, V., Salzman, R., & Kite, W. et al. (2018). Artemisinin resistance phenotypes and K13 inheritance in a *Plasmodium falciparum* cross and Aotus model. *Proceedings of The National Academy Of Sciences*, 115(49), 12513-12518. <https://doi.org/10.1073/pnas.1813386115>
- Saifi, A. (2013). Antimalarial drugs: Mode of action and status of resistance. *African Journal Of Pharmacy And Pharmacology*, 7(5), 148-156. <https://doi.org/10.5897/ajppx12.015>
- Salamanca, D. R., Gómez, M., Camargo, A., Cuy-Chaparro, L., Molina-Franky, J., Reyes, C., ... Patarroyo, M. E. (2019). Plasmodium falciparum Blood Stage Antimalarial Vaccines: An Analysis of Ongoing Clinical Trials and New Perspectives Related to Synthetic Vaccines. *Frontiers in Microbiology*, 10. <https://doi.org/10.3389/fmicb.2019.02712>
- Sallum, M.A.M., Obando, R.G., Carrejo, N. et al. (2020) Identification keys to the *Anopheles* mosquitoes of South America (Diptera: Culicidae). I. Introduction. *Parasites Vectors* 13(583). <https://doi.org/10.1186/s13071-020-04298-6>
- Sánchez, L., Vidal, M., Jairoce, C., Aguilar, R., Ubillos, I., & Cuamba, I. et al. (2020). Antibody responses to the RTS,S/AS01E vaccine and *Plasmodium falciparum* antigens after a booster dose within the phase 3 trial in Mozambique. *Npj Vaccines*, 5(1). <https://doi.org/10.1038/s41541-020-0192-7>
- Schlott, A. C., Mayclin, S., Reers, A. R., Coburn-Flynn, O., Bell, A. S., Green, J., ... Holder, A. A. (2019). Structure-Guided Identification of Resistance Breaking Antimalarial N-Myristoyltransferase Inhibitors. *Cell Chemical Biology*, 26(7). <https://doi.org/10.1016/j.chembiol.2019.03.015>
- Schwach, F., Bushell, E., Gomes, A. R., Anar, B., Girling, G., Herd, C., Rayner, J. C., & Billker, O. (2015). PlasmoGEM, a database supporting a community resource for large-scale experimental genetics in malaria parasites. *Nucleic acids research*, 43(Database issue), D1176–D1182. <https://doi.org/10.1093/nar/gku1143>
- Schwartz, L., Brown, G.V., Genton, B. et al. (2012). A review of malaria vaccine clinical projects based on the WHO rainbow table. *Malaria Journal* 11(11) <https://doi.org/10.1186/1475-2875-11-11>

Scott, J. (2020) Proposed Integrated Control of Zoonotic Plasmodium knowlesi in Southeast Asia Using Themes of One Health. *Tropical Medicine Infectious Disease*. 5(175), pp.1-17. doi:10.3390/tropicalmed5040175

Shandilya, A., Chacko, S., Jayaram, B., & Ghosh, I. (2013). A plausible mechanism for the antimalarial activity of artemisinin: A computational approach. *Scientific Reports*, 3(1). <https://doi.org/10.1038/srep02513>

Sharma, A., Shin, S., Bopp, S., Volkman, S., Hartl, D., & Wirth, D. (2020). Genetic background and PfKelch13 affect artemisinin susceptibility of PfCoronin mutants in Plasmodium falciparum. *PLOS Genetics*, 16(12), e1009266. <https://doi.org/10.1371/journal.pgen.1009266>

Shibeshi, M., Kifle, Z., & Atnafie, S. (2020). <p>Antimalarial Drug Resistance and Novel Targets for Antimalarial Drug Discovery</p>. *Infection and Drug Resistance, Volume 13*, 4047-4060. <https://doi.org/10.2147/idr.s279433>

Shinzawa, N., Nishi, T., Hiyoshi, F., Motooka, D., Yuda, M., & Iwanaga, S. (2020). Improvement of CRISPR/Cas9 system by transfecting Cas9-expressing Plasmodium berghei with linear donor template. *Communications Biology*, 3(1). <https://doi.org/10.1038/s42003-020-01138-2>

Siciliano, G. and Alano, P. (2015) Enlightening the malaria parasite life cycle: bioluminescent Plasmodium in fundamental and applied research. *Frontiers in Microbiology*. 6(391), 1-8. doi: 10.3389/fmicb.2015.00391

Siddiqui, F., Boonhok, R., Cabrera, M., Mbenda, H., Wang, M., & Min, H. et al. (2020). Role of Plasmodium falciparum Kelch 13 Protein Mutations in *P. falciparum* Populations from Northeastern Myanmar in Mediating Artemisinin Resistance. *Mbio*, 11(1). <https://doi.org/10.1128/mbio.01134-19>

Simoni, A., Hammond, A., Beaghton, A., Galizi, R., Taxiarchi, C., & Kyrou, K. et al. (2020). A male-biased sex-distorter gene drive for the human malaria vector Anopheles gambiae. *Nature Biotechnology*, 38(9), 1054-1060. <https://doi.org/10.1038/s41587-020-0508-1>

Singh, B., & Daneshvar, C. (2013). Human infections and detection of Plasmodium knowlesi. *Clinical microbiology reviews*, 26(2), 165–184. <https://doi.org/10.1128/CMR.00079-12>

Singh, G., Goel, P., & Sharma, A. (2016). Structural mapping of Kelch13 mutations associated with artemisinin resistance in malaria. *Journal of Structural And Functional Genomics*, 17(2-3), 51-56. <https://doi.org/10.1007/s10969-016-9205-1>

- Sinha, S., Radotra, B., Medhi, B., Batovska, D., Markova, N., & Sehgal, R. (2020). Ultrastructural alterations in *Plasmodium falciparum* induced by chalcone derivatives. *BMC Research Notes*, 13(1). <https://doi.org/10.1186/s13104-020-05132-z>
- Sinha, S., Sarma, P., Sehgal, R., & Medhi, B. (2017). Development in Assay Methods for in Vitro Antimalarial Drug Efficacy Testing: A Systematic Review. *Frontiers in Pharmacology*, 8. <https://doi.org/10.3389/fphar.2017.00754>
- Sinka, M.E., Bangs, M.J., Manguin, S. et al. (2010). The dominant *Anopheles* vectors of human malaria in Africa, Europe and the Middle East: occurrence data, distribution maps and bionomic précis. *Parasites Vectors*, 3(117), <https://doi.org/10.1186/1756-3305-3-117>
- Sitali, L., Miller, J.M., Mwenda, M.C. et al. (2019). Distribution of *Plasmodium* species and assessment of performance of diagnostic tools used during a malaria survey in Southern and Western Provinces of Zambia. *Malaria Journal*, 18(130). <https://doi.org/10.1186/s12936-019-2766-2>
- Skwarczynski, M., Chandrudu, S., Rigau-Planella, B., Islam, M., Cheong, Y., & Liu, G. et al. (2020). Progress in the Development of Subunit Vaccines against Malaria. *Vaccines*, 8(3), 373. <https://doi.org/10.3390/vaccines8030373>
- Slatko, B. E., Gardner, A. F., & Ausubel, F. M. (2018). Overview of Next-Generation Sequencing Technologies. *Current Protocols in Molecular Biology*, 122(1). <https://doi.org/10.1002/cpmb.59>
- Smith Gueye, C., Newby, G., Gosling, R. D., Whittaker, M. A., Chandramohan, D., Slutsker, L., & Tanner, M. (2016). Strategies and approaches to vector control in nine malaria-eliminating countries: a cross-case study analysis. *Malaria Journal*, 15(1). <https://doi.org/10.1186/s12936-015-1054-z>
- Smith, L. M., Motta, F. C., Chopra, G., Moch, J. K., Nerem, R. R., Cummins, B., Roche, K. E., Kelliher, C. M., Leman, A. R., Harer, J., Gedeon, T., Waters, N. C., & Haase, S. B. (2020). An intrinsic oscillator drives the blood stage cycle of the malaria parasite *Plasmodium falciparum*. *Science*, 368(6492), pp.754–759. <https://doi.org/10.1126/science.aba4357>
- Stocks, P., Raynes, K., Bray, P., Park, B., O'Neill, P., & Ward, S. (2002). Novel Short Chain Chloroquine Analogues Retain Activity Against Chloroquine Resistant K1 Plasmodium falciparum. *Journal of Medicinal Chemistry*, 45(23), 4975-4983. <https://doi.org/10.1021/jm0108707>

- Stokes, B., Rubiano, K., Dhingra, S., Mok, S., Straimer, J., & Gnädig, N. et al. (2021). Plasmodium falciparum K13 mutations in Africa and Asia present varying degrees of artemisinin resistance and an elevated fitness cost in African parasites. <https://doi.org/10.1101/2021.01.05.425445>
- Straimer, J., Gnädig, N. F., Stokes, B. H., Ehrenberger, M., Crane, A. A., & Fidock, D. A. (2017). Plasmodium falciparum K13 Mutations Differentially Impact Ozonide Susceptibility and Parasite Fitness In Vitro. *MBio*, 8(2). <https://doi.org/10.1128/mbio.00172-17>
- Straimer, J., Gnädig, N. F., Witkowski, B., Amaratunga, C., Duru, V., Ramadani, A. P., Dacheux, M., Khim, N., Zhang, L., Lam, S., Gregory, P. D., Urnov, F. D., Mercereau-Puijalon, O., Benoit-Vical, F., Fairhurst, R. M., Ménard, D., & Fidock, D. A. (2015). Drug resistance. K13-propeller mutations confer artemisinin resistance in Plasmodium falciparum clinical isolates. *Science (New York, N.Y.)*, 347(6220), 428–431. <https://doi.org/10.1126/science.1260867>
- Straimer, J., Lee, M., Lee, A., Zeitler, B., Williams, A., & Pearl, J. et al. (2012). Site-specific genome editing in Plasmodium falciparum using engineered zinc-finger nucleases. *Nature Methods*, 9(10), 993-998. <https://doi.org/10.1038/nmeth.2143>
- Su, X-z., Zhang, C. and Joy, D. A. (2020) Host-Malaria Parasite Interactions and Impacts on Mutual Evolution. *Frontiers Cellular and Infectious Microbiology*, 10:587933. doi: 10.3389/fcimb.2020.587933
- Sugaram, R., Suwannasin, K., Kunasol, C., Mathema, V. B., Day, N. P., Sudathip, P., ... Imwong, M. (2020). Molecular characterization of Plasmodium falciparum antifolate resistance markers in Thailand between 2008 and 2016. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03176-x>
- Sullivan, D. (2002). Theories on malarial pigment formation and quinoline action. *International Journal for Parasitology*, 32(13), 1645-1653. [https://doi.org/10.1016/s0020-7519\(02\)00193-5](https://doi.org/10.1016/s0020-7519(02)00193-5)
- Sullivan, JR D. J., Gluzman, I. Y., Russell, D. and Goldberg, D. (1996). On the molecular mechanism of chloroquine's antimalarial action (Plasmodium/hemozoin/heme/histidine-rich protein). *Proceedings of the National Academy of Sciences*, 93, 11865-11870,
- Sy, O., Niang, E., Diallo, A., Ndiaye, A., Konaté, L., & Ba, E. et al. (2019). Evaluation of the effectiveness of a targeted community-based IRS approach for malaria elimination in

an area of low malaria transmission of the central-western Senegal. *Parasite Epidemiology and Control*, 6, e00109. <https://doi.org/10.1016/j.parepi.2019.e00109>

Taguchi, K., & Yamamoto, M. (2017). The KEAP1-NRF2 System in Cancer. *Frontiers in Oncology*, 7. <https://doi.org/10.3389/fonc.2017.00085>

Tangena, J., Hendriks, C., Devine, M., Tammaro, M., Trett, A., & Williams, I. et al. (2020). Indoor residual spraying for malaria control in sub-Saharan Africa 1997 to 2017: an adjusted retrospective analysis. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03216-6>

Tindall, S. M., Vallières, C., Lakhani, D. H., Islahudin, F., Ting, K.-N., & Avery, S. V. (2018). Heterologous Expression of a Novel Drug Transporter from the Malaria Parasite Alters Resistance to Quinoline Antimalarials. *Scientific Reports*, 8(1). <https://doi.org/10.1038/s41598-018-20816-0>

Tirrell, A. R., Vendrely, K. M., Checkley, L. A., Davis, S. Z., McDew-White, M., Cheeseman, I. H., ... Ferdig, M. T. (2019). Pairwise growth competitions identify relative fitness relationships among artemisinin resistant Plasmodium falciparum field isolates. *Malaria Journal*, 18(1). <https://doi.org/10.1186/s12936-019-2934-4>

Tizifa, T., Kabaghe, A., McCann, R., van den Berg, H., Van Vugt, M., & Phiri, K. (2018). Prevention Efforts for Malaria. *Current Tropical Medicine Reports*, 5(1), 41-50. <https://doi.org/10.1007/s40475-018-0133-y>

Tola, M., Ajibola, O., Idowu, E., Omidiji, O., Awolola, S., & Amambua-Ngwa, A. (2020). Molecular detection of drug resistant polymorphisms in Plasmodium falciparum isolates from Southwest, Nigeria. *BMC Research Notes*, 13(1). <https://doi.org/10.1186/s13104-020-05334-5>

Toro-Moreno, M., Sylvester, K., Srivastava, T., Posfai, D., Derbyshire, E.R. (2020). RNA-Seq analysis illuminates the early stages of *Plasmodium* liver infection. *mBio* 11(1), pp.1-14. :e03234-19. <https://doi.org/10.1128/mBio.03234-19>.

Trager, W. and Jensen, J B (1976). Human malaria parasites in Continuous culture. *Science* 193, pp.673-675

Trager, W., & Jensen, J. (1976). Human malaria parasites in continuous culture. *Science*, 193(4254), 673-675. <https://doi.org/10.1126/science.781840>

Tse, E., Korsik, M., & Todd, M. (2019). The past, present and future of anti-malarial medicines. *Malaria Journal*, 18(1). <https://doi.org/10.1186/s12936-019-2724-z>

- Turkiewicz, A., Manko, E., Sutherland, C., Diez Benavente, E., Campino, S., & Clark, T. (2020). Genetic diversity of the *Plasmodium falciparum* GTP-cyclohydrolase 1, dihydrofolate reductase and dihydropteroate synthetase genes reveals new insights into sulfadoxine-pyrimethamine antimalarial drug resistance. *PLOS Genetics*, 16(12), e1009268. <https://doi.org/10.1371/journal.pgen.1009268>
- Tusting, L. S., Thwing, J., Sinclair, D., Fillinger, U., Gimnig, J., Bonner, K. E., ... Lindsay, S. W. (2013). Mosquito larval source management for controlling malaria. *Cochrane Database of Systematic Reviews*. <https://doi.org/10.1002/14651858.cd008923.pub2>
- Twohig K.A., Pfeffer D.A., Baird J.K., Price R.N., Zimmerman P.A., Hay, S. I., Gething, P. W., Battle, K. E., Howes, R.E. (2019) Growing evidence of *Plasmodium vivax* across malaria-endemic Africa. *PLOS Neglected Tropical Diseases* 13(1): e0007140. <https://doi.org/10.1371/journal.pntd.0007140>
- Ursing, J., Kofoed, P., Rodrigues, A., & Rombo, L. (2009). No Seasonal Accumulation of Resistant *P. falciparum* when High-Dose Chloroquine Is Used. *Plos ONE*, 4(8), e6866. <https://doi.org/10.1371/journal.pone.0006866>
- Usui, M., Prajapati, S. K., Ayanful-Torgby, R., Acquah, F. K., Cudjoe, E., Kakaney, C., Amponsah, J. A., Obboh, E. K., Reddy, D. K., Barbeau, M. C., Simons, L. M., Czesny, B., Raiciulescu, S., Olsen, C., Abuaku, B. K., Amoah, L. E., & Williamson, K. C. (2019). Plasmodium falciparum sexual differentiation in malaria patients is associated with host factors and GDV1-dependent genes. *Nature Communications*, 10(1), 2140, pp.1-15. <https://doi.org/10.1038/s41467-019-10172-6>
- Uwimana, A., Legrand, E., Stokes, B., Ndikumana, J., Warsame, M., & Umulisa, N. et al. (2020). Emergence and clonal expansion of in vitro artemisinin-resistant *Plasmodium falciparum* kelch13 R561H mutant parasites in Rwanda. *Nature Medicine*, 26(10), 1602-1608. <https://doi.org/10.1038/s41591-020-1005-2>
- van der Pluijm, R., Imwong, M., Chau, N., Hoa, N., Thuy-Nhien, N., & Thanh, N. et al. (2019). Determinants of dihydroartemisinin-piperaquine treatment failure in *Plasmodium falciparum* malaria in Cambodia, Thailand, and Vietnam: a prospective clinical, pharmacological, and genetic study. *The Lancet Infectious Diseases*, 19(9), 952-961. [https://doi.org/10.1016/s1473-3099\(19\)30391-3](https://doi.org/10.1016/s1473-3099(19)30391-3)
- Vaughan, A. M., & Kappe, S. (2017). Malaria Parasite Liver Infection and Exoerythrocytic Biology. *Cold Spring Harbor perspectives in medicine*, 7(6), pp.1-21 a025486. <https://doi.org/10.1101/cshperspect.a025486>

- Vaughan, A. M., Aly, A. S. I. and Kappe, S. H. I. (2008) Malaria Parasite Pre-Erythrocytic Stage Infection: Gliding and Hiding. *Cell Host & Microbe*, 4, pp.209-218
- Vaughan, A. M., Mikolajczak, S. A., Wilson, E. M., Grompe, M., Kaushansky, A., Camargo, N., Kappe, S. H. et al. (2012). Complete *Plasmodium falciparum* liver-stage development in liver-chimeric mice. *Journal of Clinical Investigations*, 122(10), 3618-3628. doi:10.1172/JCI62684
- Venugopal, K., Hentzschel, F., Valkiūnas, G., & Marti, M. (2020). Plasmodium asexual growth and sexual development in the haematopoietic niche of the host. *Nature reviews. Microbiology*, 18(3), pp.177–189. <https://doi.org/10.1038/s41579-019-0306-2>
- Wagman, J., Cissé, I., Kone, D., Fomba, S., Eckert, E., & Mihigo, J. et al. (2020). Combining next-generation indoor residual spraying and drug-based malaria control strategies: observational evidence of a combined effect in Mali. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03361-y>
- Wagner, J., Platt, R., Goldfless, S., Zhang, F., & Niles, J. (2014). Efficient CRISPR-Cas9-mediated genome editing in *Plasmodium falciparum*. *Nature Methods*, 11(9), 915-918. <https://doi.org/10.1038/nmeth.3063>
- Walliker, D., Quakyi, I., Wellemes, T., McCutchan, T., Szarfman, A., & London, W. et al. (1987). Genetic analysis of the human malaria parasite *Plasmodium falciparum*. *Science*, 236(4809), 1661-1666. <https://doi.org/10.1126/science.3299700>
- Wangdi, K., Furuya-Kanamori, L., Clark, J., Barendregt, J., Gatton, M., & Banwell, C. et al. (2018). Comparative effectiveness of malaria prevention measures: a systematic review and network meta-analysis. *Parasites & Vectors*, 11(1). <https://doi.org/10.1186/s13071-018-2783-y>
- Wanjala, C. L., Mbugi, J. P., Ototo, E., Gesuge, M., Afrane, Y. A., Atieli, H. E., et al. (2015). Pyrethroid and DDT Resistance and Organophosphate Susceptibility among Anopheles spp. Mosquitoes, Western Kenya. *Emerging infectious diseases*, 21(12), 2178–2181. <https://doi.org/10.3201/eid2112.150814>
- Weiss, D. J., Lucas, T. C., Nguyen, M., Nandi, A. K., Bisanzio, D., Battle, K. E., ... Gething, P. W. (2019). Mapping the global prevalence, incidence, and mortality of *Plasmodium falciparum*, 2000–17: a spatial and temporal modelling study. *The Lancet*, 394(10195), 322–331. [https://doi.org/10.1016/s0140-6736\(19\)31097-9](https://doi.org/10.1016/s0140-6736(19)31097-9)
- Wesolowski, R., Wozniak, A., Mila-Kierzenkowska, C., & Szewczyk-Golec, K. (2015). *Plasmodium knowlesi* as a Threat to Global Public Health. *The Korean journal of parasitology*, 53(5), 575–581. <https://doi.org/10.3347/kjp.2015.53.5.575>

- White N. J. (2017). Malaria parasite clearance. *Malaria journal*, 16(88), pp.1-14. <https://doi.org/10.1186/s12936-017-1731-1>
- White, N. J., Pukrittayakamee, S. X., Hien,T. T., et al. (2014) Malaria. *The Lancet*, 383(9918), 723-735
- Wilson, A., Courtenay, O., Kelly-Hope, L., Scott, T., Takken, W., Torr, S., & Lindsay, S. (2020). The importance of vector control for the control and elimination of vector-borne diseases. *PLOS Neglected Tropical Diseases*, 14(1), e0007831. <https://doi.org/10.1371/journal.pntd.0007831>
- Winer, B., Edgel, K.A., Zou, X. et al. Identification of Plasmodium falciparum proteoforms from liver stage models. *Malaria Journal*, 19, 10 (2020). <https://doi.org/10.1186/s12936-019-3093-3>
- Winkel, A. F., Engel, C. K., Margerie, D., Kannt, A., Szillat, H., Glombik, H., ... Schmoll, D. (2015). Characterization of RA839, a Noncovalent Small Molecule Binder to Keap1 and Selective Activator of Nrf2 Signaling. *Journal of Biological Chemistry*, 290(47), 28446–28455. <https://doi.org/10.1074/jbc.m115.678136>
- Witkowski, B., Amaratunga, C., Khim, N., Sreng, S., Chim, P., & Kim, S. et al. (2013). Novel phenotypic assays for the detection of artemisinin-resistant Plasmodium falciparum malaria in Cambodia: in-vitro and ex-vivo drug-response studies. *The Lancet Infectious Diseases*, 13(12), 1043-1049. [https://doi.org/10.1016/s1473-3099\(13\)70252-4](https://doi.org/10.1016/s1473-3099(13)70252-4)
- Witmer, K., Dahalan, F. A., Delves, M. J., Yahiya, S., Watson, O. J., Straschil, U., ... Baum, J. (2020). Transmission of Artemisinin-Resistant Malaria Parasites to Mosquitoes under Antimalarial Drug Pressure. *Antimicrobial Agents and Chemotherapy*, 65(1). <https://doi.org/10.1128/aac.00898-20>
- Wootton, J., Feng, X., Ferdig, M., Cooper, R., Mu, J., & Baruch, D. et al. (2002). Genetic diversity and chloroquine selective sweeps in Plasmodium falciparum. *Nature*, 418(6895), 320-323. <https://doi.org/10.1038/nature00813>
- World Health Organisation, 2016. Eliminating Malaria https://apps.who.int/iris/bitstream/handle/10665/205565/WHO_HTM_GMP_2016.3_en.pdf;jsessionid=C781C183B9A9DD3A1A67675B32A95AE4?ua=1?sequence=1
- Wu, Y., Encheva, V., Green, J. L., Lasonder, E., Prommaban, A., Kunzelmann, S., ... Holder, A. A. (2019). Protein ubiquitylation is essential for the schizont to merozoite transition in Plasmodium falciparum blood-stage development. <https://doi.org/10.1101/755439>

- Xia, J., Wu, D., Sun, L., Zhu, H., Li, K., Zhang, J., ... Liu, S. (2020). Characteristics of imported *Plasmodium ovale* spp. and *Plasmodium malariae* in Hubei Province, China, 2014–2018. *Malaria Journal*, 19(1). <https://doi.org/10.1186/s12936-020-03337-y>
- Xiao, B., Yin, S., Hu, Y., Sun, M., Wei, J., & Huang, Z. et al. (2018). Epigenetic editing by CRISPR/dCas9 in *Plasmodium falciparum*. *Proceedings of The National Academy Of Sciences*, 116(1), 255-260. <https://doi.org/10.1073/pnas.1813542116>
- Xie, S., Ralph, S., & Tilley, L. (2020). K13, the Cytostome, and Artemisinin Resistance. *Trends in Parasitology*, 36(6), 533-544. <https://doi.org/10.1016/j.pt.2020.03.006>
- Xu, R., Liu, Y., Fan, R., Liang, R., Yue, L., & Liu, S. et al. (2019). Generation and functional characterisation of *Plasmodium yoelii* csp deletion mutants using a microhomology-based CRISPR/Cas9 method. *International Journal for Parasitology*, 49(9), 705-714. <https://doi.org/10.1016/j.ijpara.2019.04.003>
- Yamamoto, D. S., Sumitani, M., Kasashima, K., Sezutsu H., Matsuoka, H. (2016) Inhibition of Malaria Infection in Transgenic Anopheline Mosquitoes Lacking Salivary Gland Cells. *PLoS Pathogens* 12(9): e1005872. <https://doi.org/10.1371/journal.ppat.1005872>
- Yamamoto, D., Sumitani, M., Kasashima, K., Sezutsu, H., Matsuoka, H., & Kato, H. (2019). A synthetic male-specific sterilization system using the mammalian pro-apoptotic factor in a malaria vector mosquito. *Scientific Reports*, 9(1). <https://doi.org/10.1038/s41598-019-44480-0>
- Yewhalaw, D., Balkew, M., Shililu, J., Suleman, S., Getachew, A., & Ashenbo, G. et al. (2017). Determination of the residual efficacy of carbamate and organophosphate insecticides used for indoor residual spraying for malaria control in Ethiopia. *Malaria Journal*, 16(1). <https://doi.org/10.1186/s12936-017-2122-3>
- Yman V., Wandell G., Mutemi D.D., Miglar A., Asghar M., Hammar U. Karlsson, M., Lind, I., Nordfjell, C., Rooth, I., Ngasala, B., Homann, M. V., Färnert, A. (2019) Persistent transmission of *Plasmodium malariae* and *Plasmodium ovale* species in an area of declining *Plasmodium falciparum* transmission in eastern Tanzania. *PLoS Neglected Tropical Diseases*, 13(5): e0007414. <https://doi.org/10.1371/journal.pntd.0007414>
- Yobi, D. M., Kayiba, N. K., Mvumbi, D. M., Boreux, R., Bontems, S., Kabututu, P. Z., ... Hayette, M.-P. (2020). The lack of K13-propeller mutations associated with artemisinin resistance in *Plasmodium falciparum* in Democratic Republic of Congo (DRC). *PLOS ONE*, 15(8). <https://doi.org/10.1371/journal.pone.0237791>
- Yongkiettrakul, S., Kolié, F. R., Kongkasuriyachai, D., Sattabongkot, J., Nguiragool, W., Nawattanapaibool, N., ... Buates, S. (2020). Validation of PfSNP-LAMP-Lateral Flow

Dipstick for Detection of Single Nucleotide Polymorphism Associated with Pyrimethamine Resistance in *Plasmodium falciparum*. *Diagnostics*, 10(11), 948. <https://doi.org/10.3390/diagnostics10110948>

Yusuf, Y., Yoshii, T., Iyori, M., Mizukami, H., Fukumoto, S., & Yamamoto, D. et al. (2019). A Viral-Vectored Multi-Stage Malaria Vaccine Regimen with Protective and Transmission-Blocking Efficacies. *Frontiers in Immunology*, 10. <https://doi.org/10.3389/fimmu.2019.02412>

Yuthavong, Y. (2013). Antifolate Drugs. *Encyclopedia of Malaria*, 1-12. https://doi.org/10.1007/978-1-4614-8757-9_2-1

Zaw, M. T. and Lin, Z. (2019) Human *Plasmodium knowlesi* infections in South-East Asian countries. *Journal of Microbiology, Immunology and Infection*, 52(5), pp.679-684, ISSN 1684-1182,

Zaw, M. T., Lin, Z., & Emran, N. A. (2020). Importance of kelch 13 C580Y mutation in the studies of artemisinin resistance in *Plasmodium falciparum* in Greater Mekong Subregion. *Journal of Microbiology, Immunology and Infection*, 53(5), 676–681. <https://doi.org/10.1016/j.jmii.2019.07.006>

Zekar, L. and Sharman, T. (2020) *Plasmodium Falciparum Malaria*. [Updated 2020 Oct 1]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; pp.1-9. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK555962/?report=classic>

Zhao, Y., Liu, Z., Soe, M., Wang, L., Soe, T., & Wei, H. et al. (2019). Genetic Variations Associated with Drug Resistance Markers in Asymptomatic *Plasmodium falciparum* Infections in Myanmar. *Genes*, 10(9), 692. <https://doi.org/10.3390/genes10090692>