

References

- Abnizova, Irina et al. (Apr. 2012). "Analysis of Context-Dependent Errors for Illumina Sequencing". In: *Genome Science and Technology* 10.02, p. 1241005 (cit. on pp. 26, 58).
- Al-Khedery, Basima and David R Allred (Dec. 2005). "Antigenic variation in *Babesia bovis* occurs through segmental gene conversion of the ves multi-gene family, within a bidirectional locus of active transcription". In: *Molecular microbiology* 59.2, pp. 402–414 (cit. on p. 93).
- Altschul, Stephen F et al. (Oct. 1990). "Basic local alignment search tool". In: *J. Mol. Biol* 215.3, pp. 403–410 (cit. on pp. 135, 152).
- Anderson, Tim (Apr. 2009). "Mapping the spread of malaria drug resistance". In: *PLoS medicine* 6.4, e1000054 (cit. on p. 2).
- Andrej Trampuz, Matjaz Jereb Igor Muzlovic Rajesh M Prabhu (2003). "Clinical review: Severe malaria". In: *Critical Care* 7.4, p. 315 (cit. on p. 4).
- Ariey, Frédéric et al. (July 2001). "Association of Severe Malaria with a Specific *Plasmodium falciparum* Genotype in French Guiana". In: *The Journal of infectious diseases* 184.2, pp. 237–241 (cit. on pp. 15, 128).
- Assefa, Samuel et al. (2009). "ABACAS: algorithm-based automatic contiguation of assembled sequences." In: *Bioinformatics (Oxford, England)* 25, pp. 1968–1969 (cit. on pp. 33, 95, 102, 177).
- Avril, Marion et al. (May 2012). "A restricted subset of var genes mediates adherence of *Plasmodium falciparum*-infected erythrocytes to brain endothelial cells". In: *PNAS* 109.26, E1782–E1790 (cit. on pp. 15, 129, 174).
- Barry, AE et al (2007). "Population genomics of the immune evasion (var) genes of *Plasmodium falciparum*," in: *PLoS Pathogens* 3.3, e34 (cit. on pp. 11, 16, 17).

- Barry, Alyssa E et al. (Mar. 2007). "Population Genomics of the Immune Evasion (var) Genes of *Plasmodium falciparum*". In: *PLoS Pathogens* 3.3, e34 (cit. on p. 135).
- Baruch, D I et al. (July 1995). "Cloning the *P. falciparum* gene encoding PfEMP1, a malarial variant antigen and adherence receptor on the surface of parasitized human erythrocytes". In: *Cell* 82.1, pp. 77–87 (cit. on p. 6).
- Batzoglou, Serafim et al. (Jan. 2002). "ARACHNE: A Whole-Genome Shotgun Assembler". In: *Genome Research* 12.1, pp. 177–189 (cit. on p. 23).
- Baumeister, Stefan et al. (Nov. 2009). "The malaria parasite *Plasmodium falciparum*: cell biological peculiarities and nutritional consequences". In: *Proto-plasma* 240.1-4, pp. 3–12 (cit. on p. 3).
- Bentley, David R (Dec. 2006). "Whole-genome re-sequencing". In: *Current Opinion in Genetics & Development* 16.6, pp. 545–552 (cit. on p. 20).
- Bentley, David R et al. (Nov. 2008). "Accurate whole human genome sequencing using reversible terminator chemistry". In: *Nature* 456.7218, pp. 53–59 (cit. on p. 20).
- Biggs, B A (July 1990). "Knob-independent cytoadherence of *Plasmodium falciparum* to the leukocyte differentiation antigen CD36". In: *Journal of Experimental Medicine* 171.6, pp. 1883–1892 (cit. on p. 6).
- Boetzer, M et al. (Feb. 2011). "Scaffolding pre-assembled contigs using SSPACE". In: *Bioinformatics (Oxford, England)* 27.4, pp. 578–579 (cit. on pp. 23, 27, 68).
- Brayton, Kelly A et al. (2002). "Antigenic variation of *Anaplasma marginale* msp2 occurs by combinatorial gene conversion". In: *Molecular microbiology* 43, pp. 1151–1159 (cit. on p. 93).
- Buckee, Caroline O and Mario Recker (Apr. 2012). "Evolution of the Multi-Domain Structures of Virulence Genes in the Human Malaria Parasite, *Plasmodium falciparum*". In: *PLoS Computational Biology* 8.4, e1002451 (cit. on p. 174).
- Bull, P C et al. (Mar. 1998). "Parasite antigens on the infected red cell surface are targets for naturally acquired immunity to malaria". In: *Nature medicine* 4.3, pp. 358–360 (cit. on p. 15).
- Bull, P C et al. (July 2000). "*Plasmodium falciparum*–Infected Erythrocytes: Agglutination by Diverse Kenyan Plasma Is Associated with Severe Disease

- and Young Host Age". In: *Journal of Infectious Diseases* 182.1, pp. 252–259 (cit. on p. 15).
- Bull, Peter C et al. (Nov. 2005). "Plasmodium falciparum variant surface antigen expression patterns during malaria". In: *PLoS Pathogens* 1.3, e26 (cit. on pp. 11, 15, 128, 152).
- Bull, Peter C et al. (July 2007). "An approach to classifying sequence tags sampled from Plasmodium falciparum var genes". In: *The International Journal of Biochemistry & Cell Biology* 154.1, pp. 98–102 (cit. on pp. 14, 60, 79, 81, 132, 142, 147, 148, 152, 174).
- Bull, Peter C et al. (June 2008). "Plasmodium falciparum antigenic variation. Mapping mosaic var gene sequences onto a network of shared, highly polymorphic sequence blocks". In: *Molecular microbiology* 68.6, pp. 1519–1534 (cit. on pp. 16, 17, 89, 126, 135, 152, 159).
- Butler, J et al (May 2008). "ALLPATHS: de novo assembly of whole-genome shotgun microreads". In: *Genome Research* 18.5, pp. 810–820 (cit. on p. 26).
- Calderwood, M S et al. (June 2003). "Plasmodium falciparum var Genes Are Regulated by Two Regions with Separate Promoters, One Upstream of the Coding Region and a Second within the Intron". In: *Journal of Biological Chemistry* 278.36, pp. 34125–34132 (cit. on p. 9).
- Carver, T J et al. (Aug. 2005). "ACT: the Artemis comparison tool". In: *Bioinformatics (Oxford, England)* 21.16, pp. 3422–3423 (cit. on pp. 34, 97).
- Carver, Tim et al. (2010). "BamView: viewing mapped read alignment data in the context of the reference sequence." In: *Bioinformatics* 26, pp. 676–677 (cit. on pp. 36, 97, 102).
- Chaisson MJ, Pevzner PA (2008). "Short read fragment assembly of bacterial genomes." In: *Genome Res.* 18.2, p. 324 (cit. on pp. 24, 26).
- Cham, G K K et al. (Oct. 2010). "Hierarchical, Domain Type-Specific Acquisition of Antibodies to Plasmodium falciparum Erythrocyte Membrane Protein 1 in Tanzanian Children". In: *Infection and immunity* 78.11, pp. 4653–4659 (cit. on pp. 15, 128).
- Cheeseman, Ian H et al. (Apr. 2012). "A Major Genome Region Underlying Artemisinin Resistance in Malaria". In: *Science* 336.6077, pp. 79–82 (cit. on pp. 2, 174).

- Chen, Donald S et al. (Feb. 2011). "A Molecular Epidemiological Study of var Gene Diversity to Characterize the Reservoir of Plasmodium falciparum in Humans in Africa". In: *PLoS ONE* 6.2, e16629 (cit. on pp. 11, 16).
- Chen, Jian-Min et al. (2001). "Gene Conversion in Evolution and Disease". In: *Life Sciences* (cit. on p. 93).
- Chen, Jian-Min et al. (Sept. 2007). "Gene conversion: mechanisms, evolution and human disease". In: *Nature Reviews Genetics* 8.10, pp. 762–775 (cit. on pp. 92, 93).
- Chen, Qijun (2007). "The naturally acquired immunity in severe malaria and its implication for a PfEMP-1 based vaccine." In: *Microbes and infection / Institut Pasteur* 9, pp. 777–783 (cit. on pp. 15, 16).
- Cheng, Qin et al. (Nov. 1998). "stevor and rif are Plasmodium falciparum multicopy gene families which potentially encode variant antigens". In: *Molecular and Biochemical Parasitology* 97.1-2, pp. 161–176 (cit. on p. 3).
- Chookajorn, T et al. (Jan. 2007). "Epigenetic memory at malaria virulence genes". In: *PNAS* 104.3, pp. 899–902 (cit. on p. 9).
- Chookajorn, Thanat et al. (Oct. 2008). "Mutually exclusive var gene expression in the malaria parasite: multiple layers of regulation". In: *Trends in parasitology* 24.10, pp. 455–461 (cit. on p. 8).
- Claessens, Antoine et al. (May 2012). "A subset of group A-like var genes encodes the malaria parasite ligands for binding to human brain endothelial cells". In: *PNAS* 109.26, E1772–E1781 (cit. on pp. 15, 129, 174).
- Compeau, Phillip E C et al. (Nov. 2011). "How to apply de Bruijn graphs to genome assembly". In: *Nature* 29.11, pp. 987–991 (cit. on p. 25).
- Conway, D J et al (1999). "High recombination rate in natural populations of ..." In: *Proc Natl Acad Sci U S A*. 96.8, pp. 4506–4511 (cit. on p. 16).
- Dayarian, Adel et al. (2010). "SOPRA: Scaffolding algorithm for paired reads via statistical optimization". In: *BMC Bioinformatics* 11.1, p. 345 (cit. on p. 23).
- Deitsch, Kirk W et al. (1999). "Intra-cluster recombination and var transcription switches in the antigenic variation of Plasmodium falciparum". In: *Molecular and Biochemical Parasitology* 101, pp. 107–116 (cit. on p. 126).

- Dohm, Juliane C et al. (Oct. 2007). "SHARCGS, a fast and highly accurate short-read assembly algorithm for de novo genomic sequencing". In: *Genome Research* 17.11, pp. 1697–6435207 (cit. on p. 26).
- Dzikowski, Ron et al. (Aug. 2007). "Mechanisms underlying mutually exclusive expression of virulence genes by malaria parasites". In: *Nature* 8.10, pp. 959–965 (cit. on p. 9).
- Earl, Dent et al. (Feb. 2011). "Assemblathon 1: A competitive assessment of de novo short read assembly methods". In: *Genome Research* 21, pp. 2224–2241 (cit. on p. 172).
- Enderes, C et al. (Oct. 2011). "Var Gene Promoter Activation in Clonal *Plasmodium falciparum* Isolates Follows a Hierarchy and Suggests a Conserved Switching Program that Is Independent of Genetic Background". In: *Journal of Infectious Diseases* 204.10, pp. 1620–1631 (cit. on p. 9).
- Erlich, Yaniv et al. (July 2008). "Alta-Cyclic: a self-optimizing base caller for next-generation sequencing". In: *Nature methods* 5.8, pp. 679–682 (cit. on p. 21).
- Fairhurst, Rick M et al. (Aug. 2012). "Abnormal PfEMP1/knob display on *Plasmodium falciparum*-infected erythrocytes containing hemoglobin variants: fresh insights into malaria pathogenesis and protection". In: *Microbes and Infection* 14.10, pp. 851–862 (cit. on p. 6).
- Falk, Nicole et al. (Aug. 2009). "Analysis of *Plasmodium falciparum* varGenes Expressed in Children from Papua New Guinea". In: *Journal of Infectious Diseases* 200.3, pp. 347–356 (cit. on pp. 15, 128).
- Flick, Kirsten and Qijun Chen (Apr. 2004). "var genes, PfEMP1 and the human host". In: *Molecular and Biochemical Parasitology* 134.1, pp. 3–9 (cit. on p. 6).
- Fowler, Elizabeth V et al. (Mar. 2002). "Genetic diversity of the DBL region in *Plasmodium falciparum* var genes among Asia-Pacific isolates". In: *Molecular and Biochemical Parasitology* 120.1, pp. 117–126 (cit. on p. 11).
- Fowler, Elizabeth V et al. (Oct. 2006). "Physical Linkage to Drug Resistance Genes Results in Conservation of varGenes among West Pacific *Plasmodium falciparum* Isolates". In: *Journal of Infectious Diseases* 194.7, pp. 939–948 (cit. on p. 174).

- Frank, Matthias and Kirk Deitsch (Aug. 2006). "Activation, silencing and mutually exclusive expression within the var gene family of *Plasmodium falciparum*". In: *International Journal for Parasitology* 36.9, pp. 975–985 (cit. on p. 8).
- Frank, Matthias et al. (Aug. 2008). "Frequent recombination events generate diversity within the multi-copy variant antigen gene families of *Plasmodium falciparum*". In: *International Journal for Parasitology* 38.10, pp. 1099–1109 (cit. on pp. 18, 60, 89, 92, 125).
- Freitas-Junior, L H et al. (2000). "Frequent ectopic recombination of virulence factor genes in telomeric chromosome clusters of *P. falciparum*." In: *Nature* 407, pp. 1018–1022 (cit. on pp. 9, 18, 92, 93, 125, 126).
- Fried, M and P E Duffy (June 1996). "Adherence of *Plasmodium falciparum* to Chondroitin Sulfate A in the Human Placenta". In: *Science* 272.5267, pp. 1502–1504 (cit. on p. 14).
- Frith, M C et al. (Apr. 2010). "Incorporating sequence quality data into alignment improves DNA read mapping". In: *Nucleic acids research* 38.7, e100–e100 (cit. on p. 26).
- Gaida, Annette et al. (2011). "Cloning of the repertoire of individual *Plasmodium falciparum* var genes using transformation associated recombination (TAR)." In: *PLoS ONE* 6, e17782 (cit. on p. 16).
- Gao, Ling et al. (2005). "Meiotic recombination hotspots in eukaryotes". In: *Yi chuan Hereditas Zhongguo yi chuan xue hui bian ji* 27, pp. 641–650 (cit. on p. 93).
- Gardner, M J et al. (Oct. 2002). "Genome sequence of the human malaria parasite *Plasmodium falciparum*". In: *Nature* 419.6906, pp. 498–511 (cit. on pp. 3, 9, 11–13, 16, 29, 104, 125).
- Gething, Peter W et al. (Dec. 2011). "A new world malaria map: *Plasmodium falciparum* endemicity in 2010". In: *Malaria Journal* 10.1, p. 378 (cit. on p. 2).
- Giladi, Eldar et al. (Oct. 2010). "Error Tolerant Indexing and Alignment of Short Reads with Covering Template Families". In: *Journal of Computational Biology* 17.10, pp. 1397–1411 (cit. on p. 26).
- Greenwood, B M et al (2005). "Malaria". In: *Lancet* 365.9469, pp. 1487–1498 (cit. on p. 1).

- Gupta, Sunetra et al. (Mar. 1999). "Immunity to non-cerebral severe malaria is acquired after one or two infections". In: *Nature medicine* 5.3, pp. 340–343 (cit. on p. 15).
- Haldar, Kasturi and Narla Mohandas (May 2007). "Erythrocyte remodeling by malaria parasites". In: *Current Opinion in Hematology* 14.3, pp. 203–209 (cit. on p. 3).
- Havlak, P et al. (Apr. 2004). "The Atlas Genome Assembly System". In: *Genome Research* 14.4, p. 721 (cit. on p. 23).
- Hayton, Karen et al. (July 2008). "Erythrocyte Binding Protein PfRH5 Polymorphisms Determine Species-Specific Pathways of Plasmodium falciparum Invasion". In: *Cell Host and Microbe* 4.1, pp. 40–51 (cit. on p. 18).
- Hernandez, D et al (May 2008). "De novo bacterial genome sequencing: millions of very short reads assembled on a desktop computer". In: *Genome Research* 18.5, pp. 802–809 (cit. on pp. 23, 26).
- Hernandez-Rivas, Rosaura et al. (2010). "Telomeric Heterochromatin in Plasmodium falciparum". In: *Journal of Biomedicine and Biotechnology* 2010, pp. 1–12 (cit. on p. 9).
- Hicks, Wade M (2010). "Mitotic Gene Conversion". In: *Science* 82 (cit. on p. 93).
- Holliday, Robin (1964). "A mechanism for gene conversion in fungi". In: *Genetics Research* 5, pp. 282–304 (cit. on p. 92).
- Huang, X (Sept. 2003). "PCAP: A Whole-Genome Assembly Program". In: *Genome Research* 13.9, pp. 2164–2170 (cit. on p. 23).
- Huang, X and A Madan (Sept. 1999). "CAP3: A DNA sequence assembly program". In: *Genome Research* 9.9, pp. 868–877 (cit. on p. 23).
- Hughes, Katie R et al. (Feb. 2009). "Continued cytoadherence of Plasmodium falciparum infected red blood cells after antimalarial treatment". In: *Molecular and Biochemical Parasitology* 169.2, pp. 71–78 (cit. on p. 6).
- Huson, Daniel H et al. (Sept. 2002). "The greedy path-merging algorithm for contig scaffolding". In: *Journal of the ACM* 49.5, pp. 603–615 (cit. on p. 27).
- Hviid, Lars (Oct. 2011). "The case for PfEMP1-based vaccines to protect pregnant women against Plasmodium falciparum malaria". In: *Cellular microbiology* 10.10, pp. 1405–1414 (cit. on p. 16).

- Imelfort, Michael and David Edwards (Nov. 2009). "De novo sequencing of plant genomes using second-generation technologies". In: *Briefings in Bioinformatics* 10.6, pp. 609–618 (cit. on p. 26).
- Iqbal, Zamin et al. (Jan. 2012). "De novo assembly and genotyping of variants using colored de Bruijn graphs". In: *Nature Genetics* 44.2, pp. 226–232 (cit. on p. 170).
- Jackson, Andrew P et al. (Feb. 2012). "Antigenic diversity is generated by distinct evolutionary mechanisms in African trypanosome species". In: *PNAS* 109.9, pp. 3416–3421 (cit. on p. 93).
- Jeck, WR et al (2007). "Extending assembly of short DNA sequences to handle error". In: *Bioinformatics* 23, pp. 2942–2944 (cit. on p. 26).
- Jemmely, Noelle Yvonne et al. (May 2010). "Small variant surface antigens and Plasmodium evasion of immunity". In: *Future Microbiology* 5.4, pp. 663–682 (cit. on p. 13).
- Jensen, A T R (Apr. 2004). "Plasmodium falciparum Associated with Severe Childhood Malaria Preferentially Expresses PfEMP1 Encoded by Group A var Genes". In: *Journal of Experimental Medicine* 199.9, pp. 1179–1190 (cit. on pp. 15, 128).
- Jiang, Hongying et al. (2011). "High recombination rates and hotspots in a Plasmodium falciparum genetic cross." In: *Genome Biology* 12, R33 (cit. on pp. 13, 93, 124, 126).
- Kaestli, Mirjam et al. (May 2004). "Longitudinal Assessment of Plasmodium falciparum varGene Transcription in Naturally Infected Asymptomatic Children in Papua New Guinea". In: *The Journal of infectious diseases* 189.10, pp. 1942–1951 (cit. on pp. 15, 128).
- Kaestli, Mirjam et al. (June 2006). "Virulence of Malaria Is Associated with Differential Expression of Plasmodium falciparum varGene Subgroups in a CaseControl Study". In: *The Journal of infectious diseases* 193.11, pp. 1567–1574 (cit. on pp. 15, 128).
- Kalmbach, Yvonne et al. (July 2010). "Differential varGene Expression in Children with Malaria and Antidromic Effects on Host Gene Expression". In: *The Journal of infectious diseases* 202.2, pp. 313–317 (cit. on pp. 15, 128).

- Kantibhattacharyya, M et al. (June 2004). "Molecular players of homologous recombination in protozoan parasites: implications for generating antigenic variation". In: *Infection, Genetics and Evolution* 4.2, pp. 91–98 (cit. on p. 18).
- Kim, Pan-Gyu et al. (2008). "A Scaffold Analysis Tool Using Mate-Pair Information in Genome Sequencing". In: *Journal of Biomedicine and Biotechnology* 2008, pp. 1–8 (cit. on p. 27).
- Kingsford, Carl et al. (2010). "Assembly complexity of prokaryotic genomes using short reads". In: *BMC Bioinformatics* 11.1, p. 21 (cit. on p. 24).
- Kirchgatter, Karin and Hernando A del Portilo (Jan. 2002). "Association of severe noncerebral *Plasmodium falciparum* malaria in Brazil with expressed PfEMP1 DBL1 alpha sequences lacking cysteine residues." In: *Molecular Medicine* 8.1, pp. 16–23 (cit. on pp. 15, 128).
- Kozarewa, Iwanka et al. (Apr. 2009). "Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes". In: *Nat. Methods* 6.4, pp. 291–295 (cit. on pp. 30, 31, 94).
- Kraemer, Susan M and Joseph D Smith (Nov. 2003). "Evidence for the importance of genetic structuring to the structural and functional specialization of the *Plasmodium falciparum* var gene family". In: *Molecular microbiology* 50.5, pp. 1527–1538 (cit. on p. 17).
- (Aug. 2006). "A family affair: var genes, PfEMP1 binding, and malaria disease". In: *Current opinion in microbiology* 9.4, pp. 374–380 (cit. on pp. 8, 11, 14).
- Kraemer, Susan M et al. (2007). "Patterns of gene recombination shape var gene repertoires in *Plasmodium falciparum*: comparisons of geographically diverse isolates." In: *BMC genomics* 8, p. 45 (cit. on pp. 9–11, 13, 16, 17, 34, 60, 89, 126, 128, 158).
- Kyes, S A (Aug. 1999). "Rifins: A second family of clonally variant proteins expressed on the surface of red cells infected with *Plasmodium falciparum*". In: *Proceedings of the National Academy of Sciences* 96.16, pp. 9333–9338 (cit. on p. 3).
- Kyes, S A et al. (Sept. 2007). "Antigenic Variation in *Plasmodium falciparum*: Gene Organization and Regulation of the var Multigene Family". In: *Eukaryotic Cell* 6.9, pp. 1511–1520 (cit. on pp. 9, 10).

- Kyriacou, Helen M et al. (Dec. 2006). "Differential var gene transcription in *Plasmodium falciparum* isolates from patients with cerebral malaria compared to hyperparasitaemia". In: *Molecular and Biochemical Parasitology* 150.2, pp. 211–218 (cit. on pp. 15, 128).
- Langmead, Ben et al. (2009). "Ultrafast and memory-efficient alignment of short DNA sequences to the human genome". In: *Genome Biology* 10.3, R25 (cit. on p. 35).
- Lavstsen, Thomas et al. (2003). "Sub-grouping of *Plasmodium falciparum* 3D7 var genes based on sequence analysis of coding and non-coding regions". In: *Malaria Journal* 2.1, p. 27 (cit. on p. 13).
- Lavstsen, Thomas et al. (2005). "Expression of *Plasmodium falciparum* erythrocyte membrane protein 1 in experimentally infected humans". In: *Malaria Journal* 4.21 (cit. on pp. 15, 128).
- Lavstsen, Thomas et al. (May 2012). "*Plasmodium falciparum* erythrocyte membrane protein 1 domain cassettes 8 and 13 are associated with severe malaria in children". In: *PNAS* 109.26, E1791–E1800 (cit. on pp. 15, 129, 174).
- Le Roch, K G et al. (Feb. 2012). "Genomics and integrated systems biology in *Plasmodium falciparum*: a path to malaria control and eradication". In: *Parasite Immunology* 34.2-3, pp. 50–60 (cit. on p. 20).
- Leech, J H et al. (June 1984). "Identification of a strain-specific malarial antigen exposed on the surface of *Plasmodium falciparum*-infected erythrocytes". In: *Journal of Experimental Medicine* 159.6, pp. 1567–1575 (cit. on p. 6).
- Li, H and R Durbin (July 2009). "Fast and accurate short read alignment with Burrows-Wheeler transform". In: *Bioinformatics (Oxford, England)* 25.14, pp. 1754–1760 (cit. on p. 35).
- Li, Heng et al. (Aug. 2009a). "The Sequence Alignment/Map format and SAM-tools." In: *Bioinformatics* 25.16, pp. 2078–2079 (cit. on pp. 36, 62, 96).
- Li, Ruiqiang et al. (Dec. 2009b). "The sequence and de novo assembly of the giant panda genome". In: *Nature* 463.7279, pp. 311–317 (cit. on pp. 23, 24, 26).
- Li, Ruiqiang et al. (Feb. 2010). "De novo assembly of human genomes with massively parallel short read sequencing". In: *Genome Research* 20.2, pp. 265–272 (cit. on pp. 23, 32).

- Lieber, Michael R (2010). "The Mechanism of Double-Strand DNA Break Repair by the Nonhomologous DNA End Joining Pathway". In: *Annual review of biochemistry* 79, p. 181 (cit. on p. 18).
- MacPherson, G G et al. (June 1985). "Human cerebral malaria. A quantitative ultrastructural analysis of parasitized erythrocyte sequestration." In: *The American Journal of Pathology* 119.3, p. 385 (cit. on p. 4).
- Maier, Alexander G et al. (June 2009). "Malaria parasite proteins that remodel the host erythrocyte". In: *PLoS ONE* 7.5, pp. 341–354 (cit. on p. 3).
- Maizels, Nancy (2005). "Immunoglobulin gene diversification." In: *Annual review of genetics* 39, pp. 23–46 (cit. on p. 93).
- Manske, Magnus et al. (July 2012). "Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing." In: *Nature* (cit. on pp. 17, 168, 172).
- Mardis, Elaine R (Mar. 2008). "The impact of next-generation sequencing technology on genetics". In: *Trends in Genetics* 24.3, pp. 133–141 (cit. on p. 20).
- Miller, Louis et al. (Feb. 2002). "The pathogenic basis of malaria". In: *Nature* 415.6872, pp. 673–679 (cit. on pp. 4, 8).
- Milner Jr, Danny A et al. (Dec. 2008). "Severe malaria in children and pregnancy: an update and perspective". In: *PLoS ONE* 24.12, pp. 590–595 (cit. on p. 4).
- Montgomery, Jacqui et al. (Aug. 2007). "Differential var gene expression in the organs of patients dying of falciparum malaria". In: *Molecular microbiology* 65.4, pp. 959–967 (cit. on pp. 8, 15, 128).
- Mugasa, Joseph et al. (2012). "Genetic diversity of expressed Plasmodium falciparum var genes from Tanzanian children with severe malaria". In: *Malaria Journal* 11.1, p. 230 (cit. on p. 16).
- Mullikin, J C and Z Ning (Dec. 2002). "The Phusion Assembler". In: *Genome Research* 13.1, pp. 81–90 (cit. on p. 23).
- Murray, Christopher JI et al. (2012). "Global malaria mortality between 1980 and 2010: a systematic analysis". In: *The Lancet* 379, pp. 413–431 (cit. on p. 1).
- Myers, E W (Jan. 1995). "Toward simplifying and accurately formulating fragment assembly". In: *Journal of computational biology : a journal of computational molecular cell biology* 2.2, pp. 275–290 (cit. on p. 22).

- Myers, Eugene W et al. (Mar. 2000). "A Whole-Genome Assembly of *Drosophila*". In: *Science* 287.5461, pp. 2196–2204 (cit. on p. 23).
- Narzisi, Giuseppe and Bud Mishra (2011). "Comparing de novo genome assembly: the long and short of it." In: *PLoS ONE* 6, e19175 (cit. on p. 23).
- Neghina, Raul et al. (Dec. 2010). "Malaria, a journey in time: in search of the lost myths and forgotten stories." In: *The American journal of the medical sciences* 340.6, pp. 492–498 (cit. on p. 1).
- Newbold, C I (1999). "Antigenic variation in *Plasmodium falciparum*: mechanisms and consequences." In: *Current opinion in microbiology* 2, pp. 420–425 (cit. on p. 6).
- Newbold, Chris et al. (June 1999). "Cytoadherence, pathogenesis and the infected red cell surface in *Plasmodium falciparum*". In: *International Journal for Parasitology* 29.6, pp. 927–937 (cit. on p. 6).
- Nielsen, K M (May 2003). "Gene Conversion as a Source of Nucleotide Diversity in *Plasmodium falciparum*". In: *Molecular biology and evolution* 20.5, pp. 726–734 (cit. on p. 93).
- Nielsen, Morten A et al. (Dec. 2002). "Plasmodium falciparum Variant Surface Antigen Expression Varies Between Isolates Causing Severe and Nonsevere Malaria and Is Modified by Acquired Immunity". In: *Plasmodium falciparum Variant Surface Antigen Expression Varies Between Isolates Causing Severe and Nonsevere Malaria and Is Modified by Acquired Immunity* 168, pp. 3444–3450 (cit. on pp. 15, 128).
- Ning, Z et al. (Oct. 2001). "SSAHA: a fast search method for large DNA databases." In: *Genome Research* 11.10, pp. 1725–1729 (cit. on p. 96).
- Normark, Johan et al. (Oct. 2007). "PfEMP1-DBL1CE± amino acid motifs in severe disease states of *Plasmodium falciparum* malaria". In: *PNAS* 104.40, pp. 15835–15840 (cit. on pp. 15, 128).
- Otto, Thomas D et al. (July 2010a). "Iterative Correction of Reference Nucleotides (iCORN) using second generation sequencing technology." In: *Bioinformatics* 26.14, pp. 1704–1707 (cit. on pp. 22, 26, 95).
- Otto, Thomas D et al. (2010b). "New insights into the blood-stage transcriptome of *Plasmodium falciparum* using RNA-Seq." In: *Molecular microbiology* 76.1, pp. 12–24 (cit. on p. 10).

- Oyola, Samuel O et al. (Jan. 2013). "Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing". In: *Journal of Clinical Microbiology* 51.3, pp. 745–751 (cit. on p. 130).
- Ozarkar, Aarti et al. (2009). "Analysis of PfEMP1—var Gene Sequences in Different Plasmodium falciparum Malarial Parasites". In: *Scholarly Research Exchange* 2009, pp. 1–10 (cit. on p. 16).
- Pain, A et al. (Oct. 2008). "The genome of the simian and human malaria parasite Plasmodium knowlesi." In: *Nature* 455.7214, pp. 799–803 (cit. on p. 2).
- Pasternak, Noa D and Ron Dzikowski (July 2009). "PfEMP1: An antigen that plays a key role in the pathogenicity and immune evasion of the malaria parasite Plasmodium falciparum". In: *The International Journal of Biochemistry & Cell Biology* 41.7, pp. 1463–1466 (cit. on pp. 3, 6, 7).
- Pop, M (Dec. 2003). "Hierarchical Scaffolding With Bambus". In: *Genome Research* 14.1, pp. 149–159 (cit. on pp. 23, 27).
- Pop, Mihai (July 2009). "Genome assembly reborn: recent computational challenges". In: *Briefings in Bioinformatics* 10.4, pp. 354–366 (cit. on pp. 24, 26, 57).
- Pop, Mihai and Steven L Salzberg (Mar. 2008). "Bioinformatics challenges of new sequencing technology". In: *Trends in Genetics* 24.3, pp. 142–149 (cit. on p. 24).
- Prabakaran, Ponraj et al. (2011). "454 antibody sequencing - error characterization and correction". In: *BMC research notes* 4, p. 404 (cit. on p. 26).
- Ranson, Hilary et al. (2009). "Insecticide resistance in Anopheles gambiae: data from the first year of a multi-country study highlight the extent of the problem". In: *Malaria Journal* 8.1, p. 299 (cit. on p. 2).
- Rask, Thomas S et al. (Sept. 2010). "Plasmodium falciparum Erythrocyte Membrane Protein 1 Diversity in Seven Genomes – Divide and Conquer". In: *PLoS computational biology* 6.9, e1000933 (cit. on pp. 11, 15, 16, 34, 60, 128, 129, 174).
- RBM, WHO (2010). "Roll Back Malaria Partnership: Malaria in Africa". In: (cit. on p. 1).

- Recker, Mario et al. (2011). "Antigenic variation in *Plasmodium falciparum* malaria involves a highly structured switching pattern." In: *PLoS Pathogens* 7, e1001306 (cit. on p. 8).
- Roberts, D J et al. (June 1992). "Rapid switching to multiple antigenic and adhesive phenotypes in malaria". In: *Nature* 357.6380, pp. 689–692 (cit. on p. 8).
- Rogerson, Stephen J et al. (Dec. 2007). "Malaria in Pregnancy: Linking Immunity and Pathogenesis to Prevention". In: *Am J. Trop. Med. Hyg* 77.6, pp. 14–22 (cit. on p. 15).
- Rottmann, Matthias et al. (Dec. 2006). "Differential Expression of var Gene Groups Is Associated with Morbidity Caused by *Plasmodium falciparum* Infection in Tanzanian Children". In: *Infection and immunity* 74.7, pp. 3904–3911 (cit. on pp. 15, 128).
- Rowe, J Alexandra et al. (May 2009). "Adhesion of *Plasmodium falciparum*-infected erythrocytes to human cells: molecular mechanisms and therapeutic implications". In: *Expert Reviews in Molecular Medicine* 11, e16 (cit. on p. 8).
- Ruiqiang Li, Hongmei Zhu Jue Ruan Wubin Qian Xiaodong Fang Zhongbin Shi Yingrui Li Shengting Li Gao Shan Karsten Kristiansen Songgang Li Huanming Yang Jian Wang Jun Wang (Feb. 2010). "De novo assembly of human genomes with massively parallel short read sequencing". In: *Genome Research* 20.2, pp. 265–272 (cit. on pp. 24, 26, 32).
- Salanti, A (Nov. 2004). "Evidence for the Involvement of VAR2CSA in Pregnancy-associated Malaria". In: *Journal of Experimental Medicine* 200.9, pp. 1197–1203 (cit. on p. 14).
- Salzberg, Steven L et al. (Sept. 2008). "Gene-Boosted Assembly of a Novel Bacterial Genome from Very Short Reads". In: *PLoS Computational Biology* 4.9, e1000186 (cit. on p. 169).
- Samarakoon, Upeka et al. (2011). "High-throughput 454 resequencing for allele discovery and recombination mapping in *Plasmodium falciparum*". In: *BMC genomics* 12, p. 116 (cit. on p. 93).
- San Filippo, Joseph et al. (June 2008). "Mechanism of Eukaryotic Homologous Recombination". In: *Annual review of biochemistry* 77.1, pp. 229–257 (cit. on pp. 18, 19).

- Santoyo, Gustavo and David Romero (2005). "Gene conversion and concerted evolution in bacterial genomes." In: *FEMS microbiology reviews* 29, pp. 169–183 (cit. on p. 93).
- Scherf, A et al. (1998). "Antigenic variation in malaria : in situ switching , relaxed and mutually exclusive transcription of var genes during intra-erythrocytic development in *Plasmodium falciparum*". In: *The EMBO Journal* 17, pp. 5418–5426 (cit. on pp. 6, 8).
- Scherf, Artur et al. (2008). "Antigenic Variation in *Plasmodium falciparum*". In: *Annual review of microbiology* 62.1, pp. 445–470 (cit. on pp. 8, 9).
- Schmid-Hempel, Paul (Feb. 2011). *Evolutionary Parasitology. The Integrated Study of Infections, Immunology, Ecology, and Genetics*. Oxford University Press (cit. on p. 175).
- Sharma, Yagya D (Jan. 1991). "Knobs, knob proteins and cytoadherence in *falciparum* malaria". In: *Current Opinion in Microbiology* 23.9, pp. 775–789 (cit. on p. 6).
- Shendure, Jay and Hanlee Ji (Oct. 2008). "Next-generation DNA sequencing". In: *Nature* 26.10, pp. 1135–1145 (cit. on p. 22).
- Simpson, Jared T and Richard Durbin (Apr. 2012). "Efficient de novo assembly of large genomes using compressed data structures." In: *Genome Research* 22.3, pp. 549–556 (cit. on pp. 23, 170).
- Simpson, JT et al (June 2009). "ABYSS: a parallel assembler for short read sequence data". In: *Genome Research* 19.6, pp. 1117–1123 (cit. on pp. 23, 24, 26).
- Smith, J D et al. (July 1995). "Switches in expression of *Plasmodium falciparum* var genes correlate with changes in antigenic and cytoadherent phenotypes of infected erythrocytes". In: *Cell* 82.1, pp. 101–110 (cit. on p. 6).
- Su, X Z et al. (July 1995). "The large diverse gene family var encodes proteins involved in cytoadherence and antigenic variation of *Plasmodium falciparum*-infected erythrocytes". In: *Cell* 82.1, pp. 89–100 (cit. on p. 6).
- Sue Kyes et al. (Dec. 2001). "Antigenic variation at the infected red cell surface in malaria". In: *Annual review of microbiology* 55, pp. 657–707 (cit. on pp. 6, 8).

- Sutton, Granger G et al. (Jan. 1995). "TIGR Assembler: A New Tool for Assembling Large Shotgun Sequencing Projects". In: *Genome Science and Technology* 1.1, pp. 9–19 (cit. on p. 23).
- Swain, Martin T et al. (June 2012). "A post-assembly genome-improvement toolkit (PAGIT) to obtain annotated genomes from contigs". In: *Nature Protocols* 7.7, pp. 1260–1284 (cit. on p. 177).
- Swamy, L et al. (Apr. 2011). "Plasmodium falciparum var Gene Silencing Is Determined by cis DNA Elements That Form Stable and Heritable Interactions". In: *Eukaryotic Cell* 10.4, pp. 530–539 (cit. on p. 9).
- Symington, L S et al. (1991). "Genetic Analysis of a Meiotic Recombination Hotspot on Chromosome III of *Saccharomyces Cerevisiae*". In: *Genetics* 128, pp. 717–727 (cit. on p. 93).
- Szostak, Jack W et al. (May 1983). "The double-strand-break repair model for recombination". In: *Cell* 33.1, pp. 25–35 (cit. on p. 18).
- Taylor, H M et al. (Jan. 2000a). "A study of var gene transcription in vitro using universal var gene primers". In: *Molecular and Biochemical Parasitology* 105.1, pp. 13–23 (cit. on pp. 10, 16, 93, 126).
- Taylor, H M et al. (Oct. 2000b). "Var gene diversity in *Plasmodium falciparum* is generated by frequent recombination events". In: *Molecular and Biochemical Parasitology* 110.2, pp. 391–397 (cit. on pp. 10, 11, 18, 60).
- Taylor, Helen M et al. (Jan. 2000c). "A study of var gene transcription in vitro using universal var gene primers". In: *Molecular and Biochemical Parasitology* 105.1, pp. 13–23 (cit. on p. 125).
- Tilley, Leann et al. (June 2011). "The *Plasmodium falciparum*-infected red blood cell". In: *The International Journal of Biochemistry & Cell Biology* 43.6, pp. 839–842 (cit. on p. 3).
- Treangen, Todd J and Steven L Salzberg (Nov. 2011). "Repetitive DNA and next-generation sequencing: computational challenges and solutions". In: *Nature Reviews Genetics* 13.1, pp. 36–46 (cit. on p. 24).
- Trimnell, Adama R et al. (Aug. 2006). "Global genetic diversity and evolution of var genes associated with placental and severe childhood malaria". In: *The International Journal of Biochemistry & Cell Biology* 148.2, pp. 169–180 (cit. on p. 11).

- Tsai, Isheng J et al. (2010). "Improving draft assemblies by iterative mapping and assembly of short reads to eliminate gaps". In: *Genome Biology* 11.4, R41 (cit. on p. 69).
- Voss, Till S et al. (Feb. 2006). "A var gene promoter controls allelic exclusion of virulence genes in *Plasmodium falciparum* malaria". In: *Nature* 439, pp. 1004–1008 (cit. on p. 9).
- Walliker, D (Nov. 2005). "The hitchhiker's guide to malaria parasite genes". In: *Trends in Parasitology* 21.11, pp. 489–493 (cit. on p. 173).
- Walliker, David et al. (July 1987). "Genetic Analysis of the Human Malaria Parasite *Plasmodium falciparum*". In: *Science* 236.4809, pp. 1661–1666 (cit. on pp. 18, 93, 94).
- Warimwe, GM et al (2009). "Plasmodium falciparum var gene expression is modified by host immunity". In: *Proc Natl Acad Sci U S A*. 106.51, pp. 21801–21806 (cit. on p. 15).
- Warren, Ren L et al. (Dec. 2006). "Assembling millions of short DNA sequences using SSAKE". In: *Bioinformatics (Oxford, England)* 23.4, pp. 500–501 (cit. on p. 26).
- Webb, James L A (Dec. 2008). *Humanity's Burden. A Global History of Malaria*. Cambridge University Press (cit. on p. 1).
- Wei-Chun Kao, Kristian Stevens Yun S Song (Oct. 2009). "BayesCall: A model-based base-calling algorithm for high-throughput short-read sequencing". In: *Genome Research* 19.10, p. 1884 (cit. on p. 21).
- wellems, T E et al. (May 1990). *Chloroquine resistance not linked to mdr-like genes in a Plasmodium falciparum cross*. URL: <http://www.nature.com/nature/journal/v345/n6272/pdf/345253a0.pdf> (cit. on p. 18).
- WHO (2011). "World Malaria Report 2011". In: (cit. on pp. 1, 2).
- Zerbino, Daniel and Ewan Birney (Mar. 2008). "Velvet: algorithms for de novo short read assembly using de Bruijn graphs". In: *Genome Research* 18.5, gr.074492.107–829 (cit. on pp. 23, 24, 26, 31, 67, 102).
- Zhao, Xiaohong et al. (Nov. 2010). "EDAR: An Efficient Error Detection and Removal Algorithm for Next Generation Sequencing Data". In: *Journal of Computational Biology* 17.11, pp. 1549–1560 (cit. on p. 26).