

REFERENCES

- Akika, R., Awada, Z., Mogharbil, N., & Zgheib, N. K. (2017). Region of interest methylation analysis: a comparison of MSP with MS-HRM and direct BSP. *Molecular Biology Reports*, *44*(3), 295–305. <https://doi.org/10.1007/s11033-017-4110-7>
- Al Harrasi, I., Al-Yahyai, R., & Yaish, M. W. (2017). Detection of Differential DNA Methylation Under Stress Conditions Using Bisulfite Sequence Analysis (pp. 121–137). Humana Press, New York, NY. https://doi.org/10.1007/978-1-4939-7136-7_7
- Applied Biosystems. (2009). A Guide to High Resolution Melting (HRM) Analysis, (C).
- Brenner, H., Kloor, M., & Pox, C. P. (2014). Colorectal cancer. *The Lancet*, *383*(9927), 1490–1502. [https://doi.org/10.1016/S0140-6736\(13\)61649-9](https://doi.org/10.1016/S0140-6736(13)61649-9)
- Cancer Treatment Centers of America. (2016). Colorectal cancer types. Retrieved March 28, 2018 from <https://www.cancercenter.com/colorectal-cancer/types/tab/other-colorectal-cancer-types/>
- Chen, Q. W., Zhu, X. Y., Li, Y. Y., & Meng, Z. Q. (2014). Epigenetic regulation and cancer (review). *Oncology Reports*, *31*(2), 523–532. <https://doi.org/10.3892/or.2013.2913>
- Dahl, C., & Guldborg, P. (2003). DNA methylation analysis techniques. *Biogerontology*, *4*(4), 233–250. <https://doi.org/10.1023/A:1025103319328>
- De Rosa, M., Pace, U., Rega, D., Costabile, V., Duraturo, F., Izzo, P., & Delrio, P. (2015). Genetics, diagnosis and management of colorectal cancer (Review). *Oncology Reports*, *34*(3), 1087–1096. <https://doi.org/10.3892/or.2015.4108>
- Fermentas Life Sciences. (n.d.). Troubleshooting Guide for DNA Electrophoresis, 447–452. Retrieved from http://res.hmu.edu.iq/Portals/0/Users/Bazhdar/DNA_Troubleshooting.pdf
- Genetics Home Reference. (2015). MLH1 gene, 1–6. Retrieved from <https://ghr.nlm.nih.gov/gene/MLH1#sourcesforpage>
- Granados-Romero, J. J., Valderrama-Treviño, A. I., Contreras-Flores, E. H., Barrera-Mera, B., Herrera Enríquez, M., Uriarte-Ruíz, K., ... Arauz-Peña, G. (2017). Colorectal cancer: a review. *International Journal of Research in Medical Sciences*, *5*(11), 4667. <https://doi.org/10.18203/2320-6012.ijrms20174914>
- Hattori, N., & Ushijima, T. (2011). Analysis of Gene-specific DNA Methylation. *Handbook of Epigenetics*, 125–134. <https://doi.org/10.1016/B978-0-12-375709-8.00008-3>
- International Agency for Research on Cancer. (2012). Colorectal Cancer: Estimated Incidence, Mortality and Prevalence in 2012. *GLOBOCAN 2012*. Retrieved January 30, 2018 from http://globocan.iarc.fr/Pages/fact_sheets_cancer.aspx?cancer=colorectal
- Kristensen, L. S., Mikeska, T., Krypuy, M., & Dobrovic, A. (2008). Sensitive Melting Analysis after Real Time- Methylation Specific PCR (SMART-MSP): high-throughput and probe-free quantitative DNA methylation detection. *Nucleic Acids Research*, *36*(7), e42. <https://doi.org/10.1093/nar/gkn113>
- Kurdyukov, S., & Bullock, M. (2016). DNA Methylation Analysis: Choosing the Right Method. *Biology*, *5*(1), 3. <https://doi.org/10.3390/biology5010003>

- Levine, A. J., Phipps, A. I., Baron, J. A., Buchanan, D. D., Ahnen, D. J., Cohen, S. A., ... Weisenberger, D. J. (2016). Clinicopathological risk factor distributions for MLH1 promoter region methylation in CIMP positive tumors. *Cancer Epidemiol Biomarkers Prev*, *25*(1), 68–75. <https://doi.org/10.1158/1055-9965.EPI-15-0935>.
- Ma, Y., Chen, Y., & Petersen, I. (2017). Expression and promoter DNA methylation of MLH1 in colorectal cancer and lung cancer, 6–11.
- MethylDetect. (2017). MethylDetect DNA Methylation Assay Kit Protocol, (October), 1–11.
- Pérez-Carbonell, L., Alenda, C., Payá, A., Castillejo, A., Barberá, V. M., Guillén, C., ... Jover, R. (2010). Methylation analysis of MLH1 improves the selection of patients for genetic testing in Lynch syndrome. *Journal of Molecular Diagnostics*, *12*(4), 498–504. <https://doi.org/10.2353/jmoldx.2010.090212>
- Poynter, J. N., Siegmund, K. D., Weisenberger, D. J., Long, T. I., Thibodeau, S. N., Lindor, N., ... Laird, P. W. (2008). Molecular characterization of MSI-H colorectal cancer by MLH1 promoter methylation, immunohistochemistry and mismatch repair germline mutation screening. *Cancer Epidemiol Biomarkers Prev*, *17*(11), 3208–3215. <https://doi.org/10.1158/1055-9965.EPI-08-0512>.Molecular
- Ryan, E., Sheahan, K., Creavin, B., Mohan, H. M., & Winter, D. C. (2017). The current value of determining the mismatch repair status of colorectal cancer: A rationale for routine testing. *Critical Reviews in Oncology/Hematology*, *116*, 38–57. <https://doi.org/10.1016/j.critrevonc.2017.05.006>
- Sclafani, F., Gullo, G., Sheahan, K., & Crown, J. (2013). BRAF mutations in melanoma and colorectal cancer: A single oncogenic mutation with different tumour phenotypes and clinical implications. *Critical Reviews in Oncology/Hematology*, *87*(1), 55–68. <https://doi.org/10.1016/j.critrevonc.2012.11.003>
- Tariq, K., & Ghas, K. (2016). Colorectal cancer carcinogenesis : a review of mechanisms, 7–9. <https://doi.org/10.28092/j.issn.2095-3941.2015.0103>
- Vaiopoulos, A. G., Athanasoula, K. C., & Papavassiliou, A. G. (2014). Epigenetic modifications in colorectal cancer: Molecular insights and therapeutic challenges. *Biochimica et Biophysica Acta - Molecular Basis of Disease*, *1842*(7), 971–980. <https://doi.org/10.1016/j.bbadis.2014.02.006>
- Wajed, S. A., Laird, P. W., & DeMeester, T. R. (2001). DNA methylation: An alternative pathway to cancer. *Annals of Surgery*, *234*(1), 10–20. <https://doi.org/10.1097/00000658-200107000-00003>
- Wojdacz, T. K. (2012). Methylation-sensitive high-resolution melting in the context of legislative requirements for validation of analytical procedures for diagnostic applications. *Expert Review of Molecular Diagnostics*, *12*(1), 39–47. <https://doi.org/10.1586/erm.11.88>
- Wojdacz, T. K., & Dobrovic, A. (2007). Methylation-sensitive high resolution melting (MS-HRM): A new approach for sensitive and high-throughput assessment of methylation. *Nucleic Acids Research*, *35*(6). <https://doi.org/10.1093/nar/gkm013>
- Wojdacz, T. K., Dobrovic, A., & Hansen, L. L. (2008). Methylation-sensitive high-resolution melting. *Nature Protocols*, *3*(12), 1903–1908. <https://doi.org/10.1038/nprot.2008.191>
- Wojdacz, T. K., Møller, T. H., Thestrup, B. B., Kristensen, L. S., & Hansen, L. L. (2010). Limitations and advantages of MS-HRM and bisulfite sequencing for single locus methylation studies. *Expert Review of Molecular Diagnostics*, *10*(5), 575–580. <https://doi.org/10.1586/erm.10.46>

- World Health Organization. (2014). Indonesia. *Cancer Country Profiles*. Retrieved January 31, 2018 from http://www.who.int/cancer/country-profiles/idn_en.pdf
- Zaanan, A., Meunier, K., Sangar, F., Fléjou, J.-F., & Praz, F. (2011). Microsatellite instability in colorectal cancer: from molecular oncogenic mechanisms to clinical implications. *Cellular Oncology (Dordrecht)*, 34(3), 155–176. <https://doi.org/10.1007/s13402-011-0024-x>
- Zakhari, S. (2013). Alcohol metabolism and epigenetics changes. *Alcohol Research : Current Reviews*, 35(1), 6–16. Retrieved from <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=3860421&tool=pmcentrez&rendertype=abstract>
- Zhang, W., Bauer, M., Croner, R. S., Pelz, J. O. W., Lodygin, D., Hermeking, H., ... Matzel, K. E. (2007). DNA stool test for colorectal cancer: Hypermethylation of the secreted frizzled-related protein-1 gene. *Diseases of the Colon and Rectum*, 50(10), 1618–1626. <https://doi.org/10.1007/s10350-007-0286-6>
- Zillner, K. (2011). Epi-combining - a novel method for the analysis of DNA methylation patterns at single DNA molecules. Retrieved July 15, 2018, from <https://www.elitenetzwerk.bayern.de/elitenetzwerk-home/forschungsarbeiten/lebenswissenschaften/2011/zillner-forschungsbericht0/>
- Zymo Research. (2000). Instruction Manual - EZ DNA Methylation™ Kit, (949), 5–6.