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Resumo	Non-Hodgkin's lymphomas (NHLs) comprise a diverse group of diseases, either of mature B-cell or of T-cell derivation, characterized by heterogeneous molecular features and clinical manifestations. While most of the patients are responsive to standard chemotherapy, immunotherapy, radiation and/or stem cell transplantation, relapsed and/or refractory cases still have a dismal outcome. Deep sequencing analysis have pointed out that epigenetic dysregulations, including mutations in epigenetic enzymes, such as chromatin modifiers and DNA methyltransferases (DNMTs), are prevalent in both B- cell and T-cell lymphomas. Accordingly, over the past decade, a large number of epigenetic-modifying agents have been developed and introduced into the clinical management of these entities, and a few specific inhibitors have already been approved for clinical use. Here we summarize the main epigenetic alterations described in B- and T-NHL, that further supported the clinical development of a selected set of epidrugs in determined diseases, including inhibitors of DNMTs, histone deacetylases (HDACs), and extra-terminal domain proteins (bromodomain and extra-terminal motif; BETs). Finally, we highlight the most promising future directions of research in this area, explaining how bioinformatics approaches can help to identify new epigenetic targets in B- and T-cell lymphoid neoplasms.
Fomento	