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A proteomic approach for leukemia epigenetics research

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Propositions

1. Proteomics can be used to study leukemia epigenetics.

this thesis

2. Dysfunctional epigenetic protein expressions confer prognostic information beyond the existence of mutations or chromosomal abnormalities in pediatric and adult acute myeloid leukemia, acute lymphoblastic leukemia and chronic lymphocytic leukemia.

this thesis

3. In adult AML, additional measurement of H3K27me3 at time of diagnosis can lead to a more precise outcome prediction complementing cytogenetic and molecular genetic subgrouping.

this thesis

4. Subgroup analysis is an essential step in the evaluation of efficacy in randomized clinical trials when outcomes are not different between the study groups.

this thesis

5. High-HME conveys more transposase-accessible chromatin, predicts higher relapse risk after standard chemotherapeutic treatment, but improves overall survival after bortezomib-containing chemotherapy compared to low-HME.

this thesis

6. The proteasome inhibitor bortezomib is beneficial for pediatric AML with low-RelA-pSer⁵³⁶.

this thesis

7. CLL patients with low-HMM are more eligible candidates for BTK inhibition than for chemotherapy or antibody-based treatment.

this thesis

8. What we see depends mainly on what we look for.

John Lubbock

9. Not everything that can be counted counts and not everything that counts can be counted.

Albert Einstein

10. Wisdom begins in wonder.

Socrates