Janus Kinase 3–Activating Mutations Identified in Natural Killer/T-cell Lymphoma


Précis: The presence of activating JAK3 mutations in 35.4% of natural killer/T-cell lymphomas suggests that JAK inhibition may be an effective therapeutic strategy.

Chimeric Transcript Generated by cis-Splicing of Adjacent Genes Regulates Prostate Cancer Cell Proliferation

Y. Zhang, M. Gong, H. Yuan, H.G. Park, H.F. Frierson, and H. Li

Précis: RNA transcription across the SLC45A3–ELK4 gene boundary results in a putative oncogenic fusion product in the absence of chromosomal rearrangements.

The HIF-1α Hypoxia Response in Tumor-Infiltrating T Lymphocytes Induces Functional CD137 (4-1BB) for Immunotherapy


Précis: Selective expression of CD137 by tumor-infiltrating lymphocytes in response to hypoxia can be targeted with anti-CD137 immunotherapy.
A Bioluminescent Transposon Reporter-Trap Identifies Tumor-Specific Microenvironment-Induced Promoters in *Salmonella* for Conditional Bacterial-Based Tumor Therapy ........................... 624

Précis: Tumor colonization by Salmonella and activation of Salmonella genes in response to the tumor microenvironment can be exploited for tumor-specific expression of toxic transgenes.

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- T-DM1 “Smart Bomb” Hits Breast Cancer Targets
- Neoadjuvant Drug Combination Eliminates Some Prostate Tumors
- BRAF and MEK Inhibitors Offer Good News in Melanoma
- Anti-PD-1 Drug Shows Strong Promise
- Pushing the Science of Prostate Screening
- Aggressive Pediatric Cancers Respond to ALK Inhibitor

The Transcription Factor ZNF217 Is a Prognostic Biomarker and Therapeutic Target during Breast Cancer Progression ........................... 638

Précis: ZNF217 overexpression in breast cancer is associated with poor survival and response to neoadjuvant chemotherapy but may be a predictor of triciribine efficacy.

Zhang and colleagues observed that transcription occurs across the boundary of 2 adjacent genes, *solute carrier family 45, member 3* (*SLC45A3*) and *ETS-domain protein SRF accessory protein 1* (*ELK4*), in prostate cancers in association with decreased CCCTC-binding factor (CTCF) occupancy at intergenic insulator sequences. Multiple prostate cancer cell lines were dependent on *SLC45A3–ELK4* expression, and chimeric *SLC45A3–ELK4* RNA levels correlated with Gleason score. These findings establish cis-splicing as a mechanism by which oncogenic gene fusions can potentially occur and implicate *SLC45A3–ELK4* as a putative driver of prostate cancer development. For details, please see the article by Zhang and colleagues on page 598.