In Focus

Connecting Genomic Alterations to Cancer Biology with Proteomics: The NCI Clinical Proteomic Tumor Analysis Consortium


ceRNA Cross-Talk in Cancer: When ce-bling Rivalries Go Awry

F.A. Karreth and P.P. Pandolfi

SF3B1 Mutations Are Associated with Alternative Splicing in Uveal Melanoma


Précis: Mutations in splicing factor 3b, subunit 1 (SF3B1) occur in approximately 15% of uveal melanomas and are associated with specific alternative splicing events.

Prostate Cancer Cell Telomere Length Variability and Stromal Cell Telomere Length as Prognostic Markers for Metastasis and Death


Précis: The combination of more variable telomere length among prostate cancer cells and shorter telomeres in cancer-associated stromal cells is associated with increased risk of tumor progression and death.

See commentary, p. 1096

Hypoxia Signaling—License to Metastasize

S. Vanharanta and J. Massagué

See article, p. 1103

Glycolysis Back in the Limelight: Systemic Targeting of HK2 Blocks Tumor Growth

S. Ros and A. Schulze

See commentary, p. 1096

MINI REVIEW

ceRNA Cross-Talk in Cancer: When ce-bling Rivalries Go Awry

F.A. Karreth and P.P. Pandolfi

RESEARCH ARTICLES

Prostate Cancer Cell Telomere Length Variability and Stromal Cell Telomere Length as Prognostic Markers for Metastasis and Death


Précis: The combination of more variable telomere length among prostate cancer cells and shorter telomeres in cancer-associated stromal cells is associated with increased risk of tumor progression and death.

See commentary, p. 1096
Bouwman and colleagues developed high-throughput functional complementation assays to predict the pathogenicity of BRCA1 variants of unknown significance (VUS). BRCA1 VUSs were evaluated for their ability to rescue proliferation defects, cisplatin sensitivity, and olaparib sensitivity in murine embryonic stem cells lacking endogenous Brca1. The ability of BRCA1 VUSs to rescue growth defects and drug sensitivity correlated with their homologous recombination activity, indicating that these assays can predict BRCA1 functionality. Interestingly, all unambiguously predicted pathogenic BRCA1 variants were located in the RING and BRCT domains. This approach has the potential to rapidly characterize BRCA1 sequence variants identified during screening for germline mutations associated with increased risk of breast and ovarian cancer. For details, please see the article by Bouwman and colleagues on page 1142.

DEAR1 Is a Chromosome 1p35 TumorSuppressor and Master Regulator ofTGF-β-DrivenEpithelial-MesenchymalTransition

Précis: Loss of DEAR1 drives tumor formation and enhances TGF-β-induced EMT and anoikis resistance via upregulation of SMAD3 signaling.

Hypoxia-Dependent Modification ofCollagen Networks PromotesSarcoma Metastasis

Précis: Induction of the procollagen lysyl hydroxylase PLOD2 by HIF-1α alters extracellular collagen organization to facilitate migration and metastasis of sarcoma cells.

See commentary, p. 1103
**CANCER DISCOVERY**

3 (10)


<table>
<thead>
<tr>
<th>Updated version</th>
<th>Access the most recent version of this article at:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><a href="http://cancerdiscovery.aacrjournals.org/content/3/10">http://cancerdiscovery.aacrjournals.org/content/3/10</a></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>E-mail alerts</th>
<th>Sign up to receive free email-alerts related to this article or journal.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reprints and Subscriptions</td>
<td>To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubsWith AACR.org.</td>
</tr>
<tr>
<td>Permissions</td>
<td>To request permission to re-use all or part of this article, contact the AACR Publications Department at permissionsWith AACR.org.</td>
</tr>
</tbody>
</table>