## Contents

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<table>
<thead>
<tr>
<th>ARTICLES</th>
<th>Authors</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neurofibromin (Nf1) is required for skeletal muscle development</td>
<td>N. Kossler, S. Stricker, C. Rödelsperger, P.N. Robinson, J. Kim, C. Dietrich, M. Osswald, J. Kühnisch, D.A. Stevenson, T. Braun, S. Mundlos, and M. Kolanczyk</td>
<td>2697</td>
</tr>
<tr>
<td>A point mutation in the ubiquitin-associated domain of SQSMT1 is sufficient to cause a Paget's disease-like disorder in mice</td>
<td>A. Daroszewska, R.J. van 't Hof, J.A. Rojas, R. Layfield, E. Landao-Basonga, L. Rose, K. Rose, and S.H. Ralston</td>
<td>2734</td>
</tr>
<tr>
<td>Transgenic mice expressing caspase-6-derived N-terminal fragments of mutant huntingtin develop neurologic abnormalities with predominant cytoplasmic inclusion pathology composed largely of a smaller proteolytic derivative</td>
<td>A.T.N. Tebbenkamp, C. Green, G. Xu, E.M. Denovan-Wright, A.C. Rising, S.E. Fromholt, H.H. Brown, D. Swing, R.J. Mandel, L. Tessarollo, and D.R. Borchelt</td>
<td>2770</td>
</tr>
<tr>
<td>Perturbation of the Akt/Gsk3-β signalling pathway is common to <em>Drosophila</em> expressing expanded untranslated CAG, CUG and AUUCU repeat RNAs</td>
<td>C.L. van Eyk, L.V. O’Keefe, K.T. Lawlor, S.E. Samaranweera, C.J. McLeod, G.R. Price, D.J. Venter, and R.I. Richards</td>
<td>2783</td>
</tr>
<tr>
<td>Disrupted-in-Schizophrenia-1 (Disc1) is necessary for migration of the pyramidal neurons during mouse hippocampal development</td>
<td>K. Tomita, K. Kubo, K. Ishii, and K. Nakajima</td>
<td>2834</td>
</tr>
</tbody>
</table>
HD CAG-correlated gene expression changes support a simple dominant gain of function


ASSOCIATION STUDIES ARTICLES

A genome-wide association study reveals association between common variants in an intergenic region of 4q25 and high-grade myopia in the Chinese Han population


Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer


Fine-mapping of colorectal cancer susceptibility loci at 8q23.3, 16q22.1 and 19q13.11: refinement of association signals and use of in silico analysis to suggest functional variation and unexpected candidate target genes


A gender-specific association of CNV at 6p21.3 with NPC susceptibility


Chromosome 7p11.2 (EGFR) variation influences glioma risk


Cover: A schematic of the relationships, within a hierarchy of ‘energy’ category processes, depicting the response of mouse embryonic stem cells to lengthening the polyglutamine tract in endogenous huntingtin or to lack of huntingtin, as determined by gene expression analyses. Depicted are processes uniquely correlated with Hdh knock-in CAG repeat size (red), altered by Hdh inactivation (blue) and altered in both scenarios (yellow). Thus, while the two genetic paradigms probing huntingtin function produced non-overlapping single gene responses, the membership of these genes in unique or common pathways, might be expected to produce similar, as well as unique, phenotypic outcomes. For further details, see the article by Jacobsen et al., pp. 2846–2860.