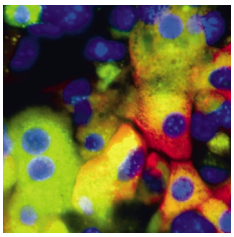
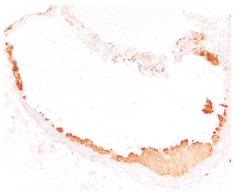
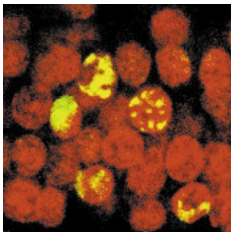


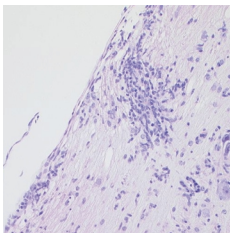
Long-lost liver progenitors found. The adult liver is a quiescent organ, except when subjected to injury, when it responds with neoproliferation of mature hepatocytes and other liver cells to the point of complete organ regeneration. There is also a contribution from resident hepatic stem cells, about which little is known. Miguel Marcos and colleagues now describe a population of 11-dpc c-Kit^{low}(CD45/TER119)$^{-}$ embryonic liver progenitors that selectively express hepatospecific genes and proteins in vivo (pages 1152–1163). The cultured cells were proliferative and were able to simultaneously differentiate into functional hepatocytes and bile duct cells. Cells were evaluated for their growth potential, differentiation, and clonal growth in media supplemented with different growth factors. The purified progenitor cells cocultured with cell-depleted fetal liver fragments engrafted and repopulated hepatic compartments, suggesting that they may be the embryonic stem cells responsible for liver development.



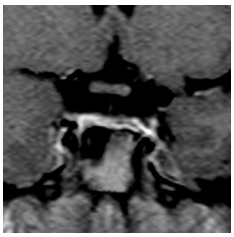
Enigmatic role for NF-κB in atherosclerosis. The role of the transcription factor NF-κB in atherosclerosis remains controversial. NF-κB is known to induce expression of inflammatory genes that play detrimental roles in atherosclerosis; on the other hand, NF-κB is a survival factor and may promote expression of certain anti-inflammatory cytokines. To investigate the role of NF-κB activation in macrophages during atherogenesis, Menno de Winther and colleagues used *Ldlr*$^{-/-}$ mice with a macrophage-restricted deletion of IκB kinase 2 (*IKK2*), which is essential for NF-κB activation (pages 1176–1185). The authors show that NF-κB–defective macrophages enhance rather than inhibit atherosclerosis. Lesions were larger in size, more advanced, and contained more necrosis, and early lesions contained more macrophages. In vitro studies revealed that *IKK2*-deleted macrophages produced less TNF and IL-10. These data indicate that inhibition of NF-κB activation in macrophages aggravates atherosclerosis.



FGF-2 to the rescue in the brain. Specific subsets of progenitor cells residing in the CNS have been known to proliferate after traumatic brain injury (TBI). However, the proliferation of these cells is minimal, and the injury suffered is often difficult to overcome. Michael Moskowitz and colleagues now demonstrate that FGF-2 plays a pivotal role in the proliferation of neural progenitor cells in the adult subgranular zone of dentate gyrus in response to TBI (pages 1202–1210). Fewer progenitor cells proliferated after TBI in *FGF-2*$^{-/-}$ mice than in controls. Overexpression of FGF-2 after TBI increased numbers of dividing cells and prevented the death of existing neurons. FGF-2 supplementation might provide a rational strategy to treat brain injury by simultaneously enhancing neurogenesis and reducing neurodegeneration.



Tug of war between IL-12 and IL-23. Microglia and macrophages that reside within the CNS are a source of the inflammatory cytokines IL-23 and IL-12. In particular, IL-23 has been shown to be critical for the pathogenesis of EAE. Burkhard Becher and colleagues now show that the p40 subunit, shared by both IL-12 and IL-23, plays a critical role in maintaining encephalitogenicity during the course of disease (pages 1186–1191). Adoptive transfer and bone marrow chimeras were used to show that in the absence of expression of p40 within the CNS, EAE was delayed and less severe. Cellular infiltration was not affected, but there was a decrease in Th1 cytokine expression by the infiltrating cells. This study suggests that cells resident in the CNS can control the degree of T cell encephalitogenicity.



***Hesx1* puts a hex on the pituitary gland.** The *paired*-like homeobox gene *Hesx1* encodes a developmental repressor and is expressed in early development in the forebrain and later in the anterior pituitary gland. Mutations within *Hesx1* are associated with septo-optic dysplasia and mild hypopituitarism. Mehul Dattani and colleagues now describe the clinical phenotype and functional consequence of only the second homozygous mutation within *Hesx1* (pages 1192–1201). The authors identify a missense mutation in the critical Engrailed homology repressor domain of *Hesx1* that normally mediates recruitment of Groucho homolog/Transducin-like enhancer of split-1 (TLE1). The authors present a phenotypic description of the mutation, followed by functional analyses demonstrating disruption of Hesx1/TLE1 interaction and transcriptional repression in cultured cells. These results provide a striking example of clinical disorder associated with the loss of repressor/corepressor interactions.