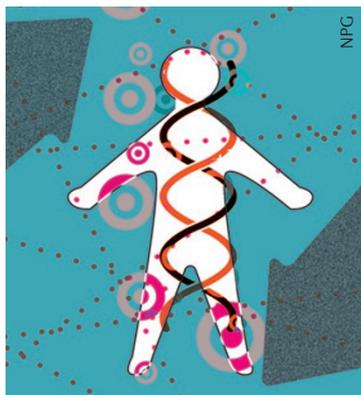
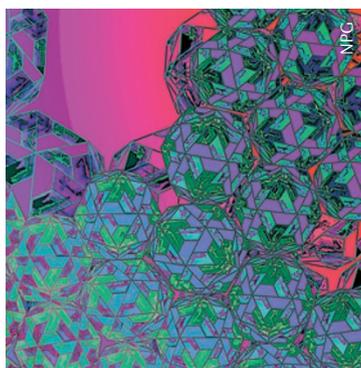


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The high failure rate of compounds in clinical trials is largely responsible for the high costs of drug development. These failures reflect the limited predictive capacity of standard preclinical disease models, and in our first Review Plenge and colleagues propose that greater use of knowledge from human genetics — in particular on naturally occurring mutations that affect the activity of specific proteins — could help to address this problem. They present examples supporting the use of genetics in target validation, propose objective criteria for prioritizing drug targets and consider the limitations of this approach. In the second Review, Manns and von Hahn discuss the recent acceleration in the development of therapies for hepatitis C virus (HCV). They summarize the molecular targets of antiviral therapy and assess the various classes of compounds currently under development while considering the key challenges faced in HCV treatment. Next, Turkson and colleagues review the abnormal activation of STAT (signal transducer and activator of transcription) signalling pathways in various disorders, including cancer, autoimmune diseases, asthma and diabetes. Various strategies and agents that are currently under investigation for the modulation of individual STAT protein activity, as well as future directions for the field, are highlighted. Finally, Sexton and colleagues focus on the growing interest in allosteric ligands of G protein-coupled receptors, which influence receptor activity by binding to a site distinct to that of endogenous ligands. They discuss recent advances in understanding the complex actions of allosteric modulators, such as the induction of biased signaling, and consider how this knowledge may be therapeutically exploited.

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