IN BRIEF

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COMPUTATIONAL CHEMISTRY

Diverse, high quality test set for the validation of protein–ligand docking performance.

Hartshorn, M. J. *et al. J. Med. Chem.* **50**, 726–741 (2007)

Despite the success of docking methods used in virtual screening, there is still a need to improve the performance of these programmes. Hartshorn and colleagues have developed a procedure for analysing and classifying publicly available crystal structures. They used it to identify 85 high-resolution protein–ligand complexes that are relevant to drug discovery targets. This new, freely available validation set will be useful in benchmarking the performance of different computational-docking programmes.

ANTICANCER DRUGS

Improvement of cancer-targeting therapy, using nanocarriers for intractable solid tumours by inhibition of TGF-β signalling.

Kano, M. R. *et al. Proc. Natl Acad. Sci. USA* **104**, 3460–3465 (2007)

Although transforming growth factor-β (TGFβ) plays a role in the progression of cancer, adverse effects could be caused by the inhibition of TGFβ signalling. Kano and colleagues have shown that a low-dose, short-acting TGFβ-type-1-receptor (TGFβR1) inhibitor is effective against experimental intractable solid tumours, including pancreatic adenocarcinoma and diffuse-type gastric cancer. The inhibitor did not alter TGFβ signalling in cancer cells but promoted accumulation of anticancer nanocarriers in tumours. Therefore, the use of TGFβR1 inhibitors combined with nanocarriers could be beneficial in treating intractable solid-tumour cancers.

HIV

Structural definition of a conserved neutralization epitope of HIV-1 and gp120.

Zhou, T. *et al. Nature* **445**, 732–737 (2007)

Binding of HIV-1 to the CD4 receptor causes rearrangement of the gp120 glycoprotein, which allows HIV-1 to evade antibody-mediated neutralization. By creating variants of gp120 that are stabilized in the CD4-bound state, Zhou and colleagues identified a functionally conserved antibody-binding surface on the HIV-1 envelope that is involved in the initial attachment of CD4, before the gp120 rearrangement required for stable engagement. The identification of a site related to a functional requirement for efficient association with CD4 could therefore be targeted by antibodies against HIV-1.

GENE THERAPY

Targeted gene addition into specified location in the human genome using designed zinc finger nucleases.

Moehle, E. A. *et al. Proc. Natl Acad. Sci. USA* **104**, 3055–3060 (2007)

Efficient incorporation of novel DNA sequences into a specific site in the genome remains a challenge. Moehle and colleagues found that a precisely placed double-strand break induced by engineered zinc-finger nucleases can stimulate integration of long DNA stretches into a predetermined genomic location, resulting in high-efficiency site-specific gene addition. Zinc-finger nucleases could drive the addition of 8-kb sequences at a frequency of 6% in the absence of any selection. These experiments open up the possibility of zinc-finger-nuclease-driven gene therapy.