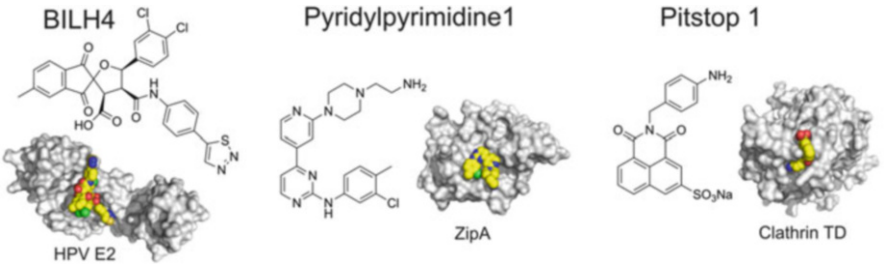

Fig. 3 Small-molecule inhibitors of HPV E2 (human papillomavirus E2 protein) binding to HPV E1, interaction of bacterial ZipA (Z interacting protein A) with FtsZ (filamenting temperature-sensitive mutant Z), and CTD's (clathrin terminal domain) binding to amphiphysin. The PDB codes of the crystal structures are 1R6N, 1Y2F, and 2XZG, respectively

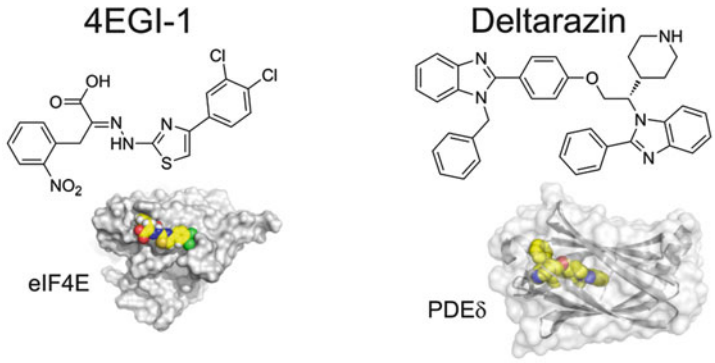

Fig. 4 Small-molecule inhibitors of eIF4E's (eukaryotic translation initiation factor 4E) binding to eIF4G and of PDEδ's (phosphodiesterase delta subunit) interaction with KRAS (Kirsten rat sarcoma). The PDB codes of the crystal structures are 4TQC and 4JVF, respectively

development, apoptosis, synaptic plasticity, and axon guidance, the authors suggest that they could also represent a new strategy for small-molecule cancer therapy. Their most active compound – **4EGI-1** – was just recently crystallized in complex with eIF4E revealing an allosteric mechanism of PPI inhibition (Papadopoulos et al. 2014). The group of Wilding found inhibitors of the androgen receptor (AR)/JunD interaction by screening a 27,000-compound library with a luciferase complementation assay (Mehraein-Ghomi et al. 2014). Inhibiting the AR/JunD complex is expected to reduce production of carcinogenic reactive oxygen species (ROS) in prostate epithelial cells. Their best hit – **GWARJD10** – significantly reduced androgen-induced transcriptional activity. The group of Waldmann reported the identification and medicinal chemistry optimization of inhibitors of the PDEδ/KRAS interaction by screening a compound library with an AlphaScreen assay (Fig. 4) (Zimmermann et al. 2013).