



Figure 1.3 Representative crystal structures of the three types of AMEs and respective sites of aminoglycoside modification. (a) Structure of the aminoglycoside 2''-phosphotransferase APH(2'')-Ia from *Staphylococcus aureus*, in complex with gentamycin and GDP (Caldwell et al. 2016). The neamine-like moiety is circumscribed by a dashed blue line. (b) Dimeric structure of aminoglycoside 6''-N-acetyltransferase AAC(6'')-Ig from *Acinetobacter haemolyticus* in complex with tobramycin. Chains A and B are depicted in blue and red ribbons, respectively, while the yellow star marks the putative binding site of acetyl-CoA in each monomer (Stogios et al. 2017). (c) Structure of aminoglycoside nucleotidyltransferase ANT(2'')-Ia from *Klebsiella pneumoniae* in complex with kanamycin (Cox et al. 2015). All protein structures are shown in surface representation. AGAs and GDP are represented as stick model; magnesium atoms and water molecules are represented as green and red spheres, respectively. Hydrogen bonds are represented by thin blue lines. Hydrogen atoms are omitted for simplicity. *Source:* All images were produced with program Chimera (Pettersen et al. 2004). (See insert for color representation of the figure.)