



**Figure 3 | Pseudoknots and internal ribosome entry.** **a** | A secondary structure representation of the hepatitis C virus (HCV) internal ribosome entry site (IRES) with the pseudoknot shown in blue. **b** | A surface representation of the human 80S ribosome (grey) in complex with the HCV IRES (red) derived from the cryo-electron microscopy (cryo-EM) structure<sup>36</sup>. Density corresponding to the pseudoknot is indicated in blue. **c** | A secondary structure representation of the *Plautia stali* intestine virus (PSIV) IRES is shown above a ribbon representation of the RNA (domains 1 and 2) derived from the crystal structure<sup>27</sup>. Domain 3 remains to be solved. The secondary structure of the cricket paralysis virus (CrPV) IRES (not shown) is similar. **d** | A surface representation of the yeast 80S ribosome (grey) is shown in complex with the CrPV IRES (red) derived from the cryo-EM structure<sup>26</sup>. Below is a fit of the density to the modelled CrPV IRES showing the interactions that occur between the various domains and ribosomal components. Ribosomal proteins are cyan, 25S ribosomal RNA (rRNA) is purple and 18S rRNA is brown.