Exploring sequence-structure relationships

• Demo
  – Multalign Viewer - sequence alignment viewer with many features, including crosstalk to and from associated structures
  – MatchMaker - constructs pairwise sequence alignments with standard methods, matches structures accordingly
  – Match -> Align - constructs pairwise or multiple sequence alignments based on pre-existing structural superpositions

• Hands-on experience
  – Sequences and Structures tutorial (the online version can be accessed from the Chimera Help menu)