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)