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| **Software** | **Version** | **Parameters** | **Context** |
| hhblits | 3.0.0 | -d uniprot20\_2016\_02 -n 2 | All network building exercises |
| hhsearch | 3.0.0 | -d <species> | All network building exercises |
| psipred | 3.5 | hhsuite defaults | Adding secondary structure predictions |
| mcl | 14-137 | -I 2.5 | Clustering |
| PyMol | 1.8.0.5 | NA | Structural alignments |
| Chimera | 1.10.2 | NA | Conservation maps |
| TM-align | Pymol | default | Structural alignments |
| Jalview | 2.9.0b.2 | NA | Sequence alignments |
| GLProbs | jalview | default | Sequence alignments |
| Muscle | jalview | default | Sequence alignments |
| MAAFT | Jalview | default | Sequence alignments |
| PSI-/BLAST | online server | default | Sequence collection for MSAs |
| MergeAlign | online server | default | Sequence alignments |
| Cytoscape | 3.4 | NA | Network Visualisation |
| Bingo | 3.0.3 | GO bio. process | Network Validation |
| HHRepID | Online server | -n 3 | Nse5/6 analysis |