Table 1: Peer-reviewed alignment tools for gas-chromatography data. Note: Unlisted are programs using mass-spectra of GC-MS runs.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Program | Year | Open access | Platform | Visualisation | Limitations | Source |
|  |  |  |  |  |  |  |
| GCALIGNER 1.0 | 2013 | Yes | Java | None | *Last RT1 of every sample remains unaligned* | {Dellicour 2013 #8} |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

1 RT = Retention time