|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| species\* | **T** | **Q** | **S** | **N** | **D** | **E** | **P** | **V** | **G** |
| Cpar | 1427 | 234 | 318 | 119 | 25 | 248 | 69 | 0 | 0 |
| Chom TU502\_new | 1220 | 248 | 280 | 115 | 40 | 316 | 0 | 21 | 0 |
| Chom Udea | 1138 | 279 | 238 | 95 | 59 | 243 | 0 | 21 | 0 |
| Cmel | 793 | 307 | 164 | 100 | 0 | 304 | 93 | 0 | 0 |
| Cubi | 554 | 198 | 290 | 226 | 31 | 156 | 58 | 0 | 25 |
| Cand | 22 | 51 | 29 | 144 | 26 | 22 | 0 | 0 | 0 |
| Cmur | 178 | 60 | 30 | 292 | 117 | 32 | 21 | 0 | 0 |
| Cbai | 1128 | 29 | 400 | 1692 | 96 | 38 | 0 | 0 | 0 |

Table S2. Cumulative SAAR length for 7 species and eight genomes calculated by amino acid using XSTREAM.

\*Cpar, *C. parvum* ;Chom, *C. hominis*; Cmel, *C. meleagridis*; Cubi, *C. ubiquitum*; Cand, *C. andersoni*; Cmur, *C. muris* ; Cbai, *C. baileyi*.