|    | Ec SufE | Pf SufE | Pf MnmA | Bm MnmA | Ta MnmA | Tg MnmA | Et MnmA |
|----|---------|---------|---------|---------|---------|---------|---------|
|    |         |         | HHIDYIHEYIYNFLMSY |         |         | RSTQROVQLRQLESREEE |         |         | PS^PRS--KEIAKL--  |
|    |         |         | 138     | 249     | 380     | 708     | 444     |

**Figure 3- figure supplement 8- source data 3.** Multiple sequence alignment used for Figure 3- figure supplement 8(H).