



**Supplementary Figure S3. Seqlogo was done using <https://weblogo.berkeley.edu/> server with default paraameters and is based on alignment of 36 amino acid C-terminal conserved regions of the following proteins:**  
**WP\_007542093\_1, WP\_008322016\_1, WP\_049890737\_1, WP\_083857055\_1, WP\_089672923\_1, WP\_006653064\_1, WP\_097381164\_1, AGB14781\_1, WP\_004216539\_1, WP\_007109788\_1, WP\_007701607\_1, WP\_008455678\_1, WP\_049888012\_1, WP\_049901575\_1, WP\_049923820\_1.**