

Multiple sequence alignment of the R50 region (residues 44-118) for various *Vibrio* species. The alignment shows conserved regions highlighted in yellow. The species listed include *V. anguillarum*, *V. parahaemolyticus*, *V. vulnificus*, *V. cholerae*, *V. shilonii*, *V. parahaemolyticus*, *V. vulnificus*, *V. fluvialis*, *P. marinus*, *P. arcticus*, *S. woodyi*, *S. alifanensis*, *A. succinogenes*, *P. multicauda*, *H. influenzae*, *P. putida*, *P. fluorescens*, *P. syringae*, *X. axonopodis*, *X. campestris*, *X. fastidiosa*, *E. coli*, *S. enterica*, *E. xiangfangensis*, *Enterobacter* sp. 638, *Y. pestis*, *P. polaris*, *P. atrosepticum*, *S. dentrificans*, *S. amazonensis*, *Shewanella* sp. MR-4, *S. ballina*, *S. putrefaciens*, *P. tunicata*, *P. aeruginosa*, and *P. mendocina*.

Multiple sequence alignment of the R190 region (residues 119-193) for various *Vibrio* species. The alignment shows conserved regions highlighted in yellow. The species listed include *V. anguillarum*, *V. parahaemolyticus*, *V. vulnificus*, *V. cholerae*, *V. shilonii*, *V. parahaemolyticus*, *V. vulnificus*, *V. fluvialis*, *P. marinus*, *P. arcticus*, *S. woodyi*, *S. alifanensis*, *A. succinogenes*, *P. multicauda*, *H. influenzae*, *P. putida*, *P. fluorescens*, *P. syringae*, *X. axonopodis*, *X. campestris*, *X. fastidiosa*, *E. coli*, *S. enterica*, *E. xiangfangensis*, *Enterobacter* sp. 638, *Y. pestis*, *P. polaris*, *P. atrosepticum*, *S. dentrificans*, *S. amazonensis*, *Shewanella* sp. MR-4, *S. ballina*, *S. putrefaciens*, *P. tunicata*, *P. aeruginosa*, and *P. mendocina*.