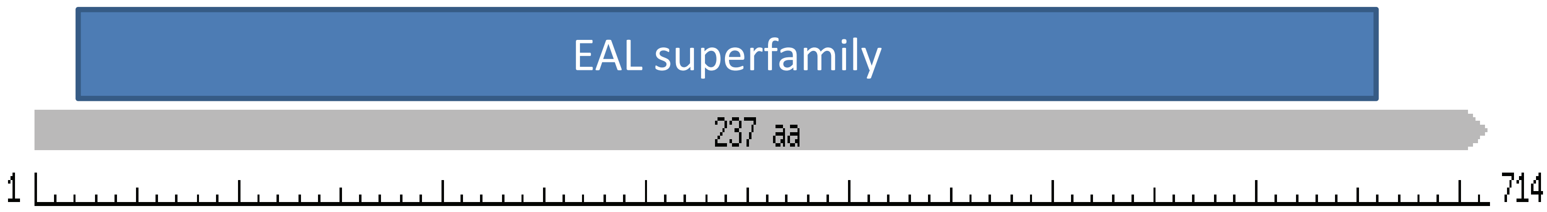

```
MKIFLENLYHSDCYFLPIRDNQQDLVGVELITHFSSEDGTVRIPTSRVIAQLTVEQHWQLFSEQLELLKS
    ^   ^ *   ^ *       *   ^    *         *               *
CQHFFIQHKLFAWLNLTPQVATLLLDRDNFAGELLKYPFIELLINENYPHFNEGKDNRDLLSLSQMYPLV
    *                   ^             ^ ^^   *  *    **    ^        ^
LGNLGAGNSTMKAVFDGLFTRVMLDKSFIQQQITHRSFEPFIRAIQAQISPCCNCIIAGGIDTPEILAQI
* ^ * *        *^*^ ^^ ^^^ ^         ^ ^^       ^   ^      ^ ^
IPFDFHALQGCLWPAVPINQITTLVQR
        *
```

* 100% conserved in 21 YdiV homolog alignment
^ 90-95% conserved in 21 YdiV homolog alignment
Red = site directed mutation to alanine
Bold = EAL domain