

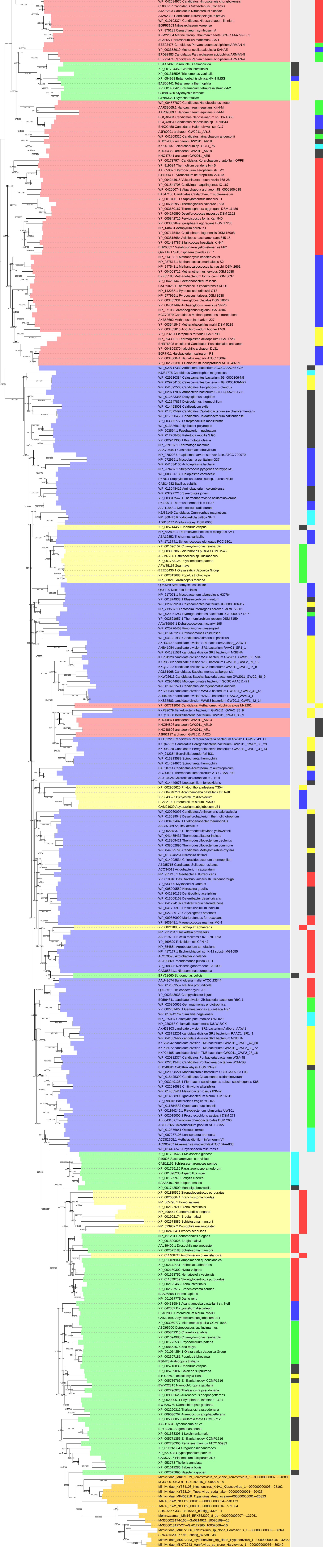
Supplementary Data

Phylogenetic trees of aaRSs of NCLDV and their close relatives in cellular organisms. Background was color-coded based on domain-level taxonomy: green for eukaryotes, blue for bacteria, red for archaea, and orange for NCLDV. Numbers on branches represent bootstrap values: left and right ones are SH-aLRT and Ultrafast Bootstrap values, respectively. The root was decided based on Furukawa et al (Furukawa et al. 2017). The substitution models were selected by ModelFinder from IQ-TREE. The trees are ordered alphabetically by the one-letter code of each amino acid. The substitution models for each aaRS tree were listed below.

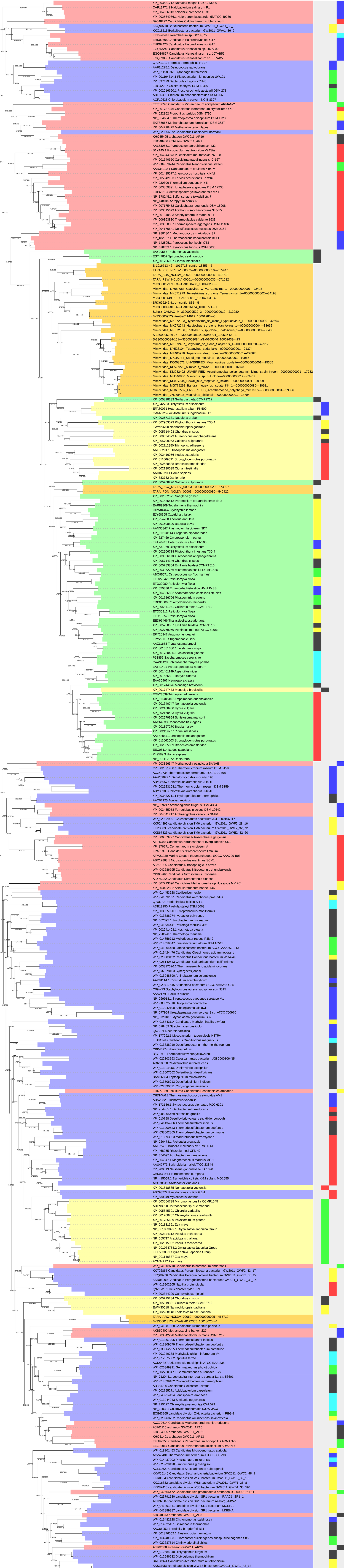
AlaRS: LG+R10
CysRS: LG+R10
AspRS: LG+R10
GluRS: Q.pfam+F+R10
PheRS: LG+R9
GlyRS: LG+R9
HisRS: LG+R10
IleRS: Q.pfam+F+R10
LysRS: LG+R10
LeuRS: LG+R10
MetRS: LG+R10
AsnRS: LG+F+R10
ProRS: LG+R10
GlnRS: LG+R8
ArgRS: Q.pfam+F+R10
SerRS: LG+R9
ThrRS: LG+R9
ValRS: LG+R10
TrpRS: LG+R9
TyrRS: LG+R9

AlaRS

substitution per site: 1

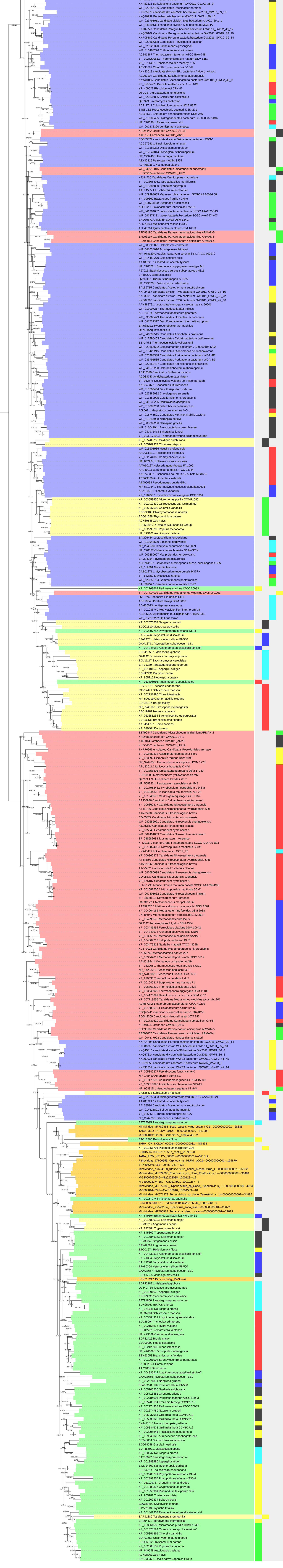


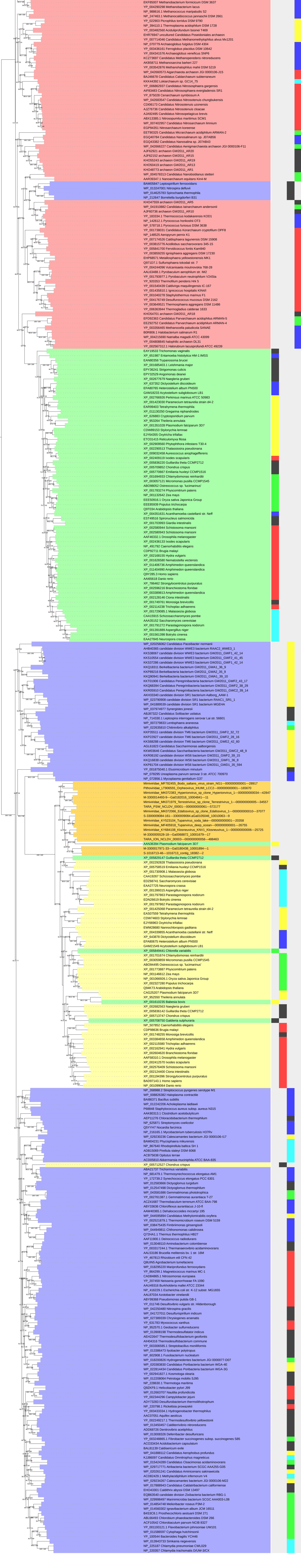
substitution per site: 1



AspRS

substitution per site: 1

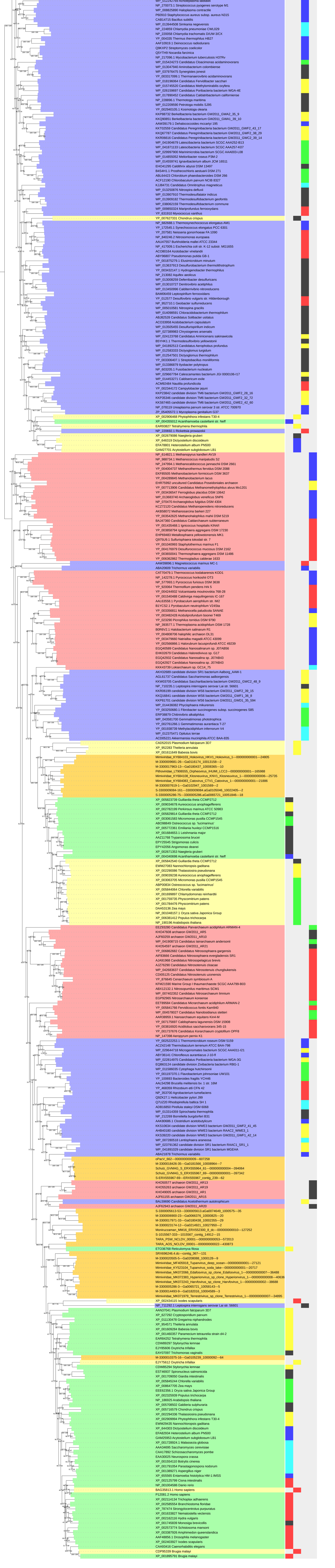




GlyRS

substitution per site: 1



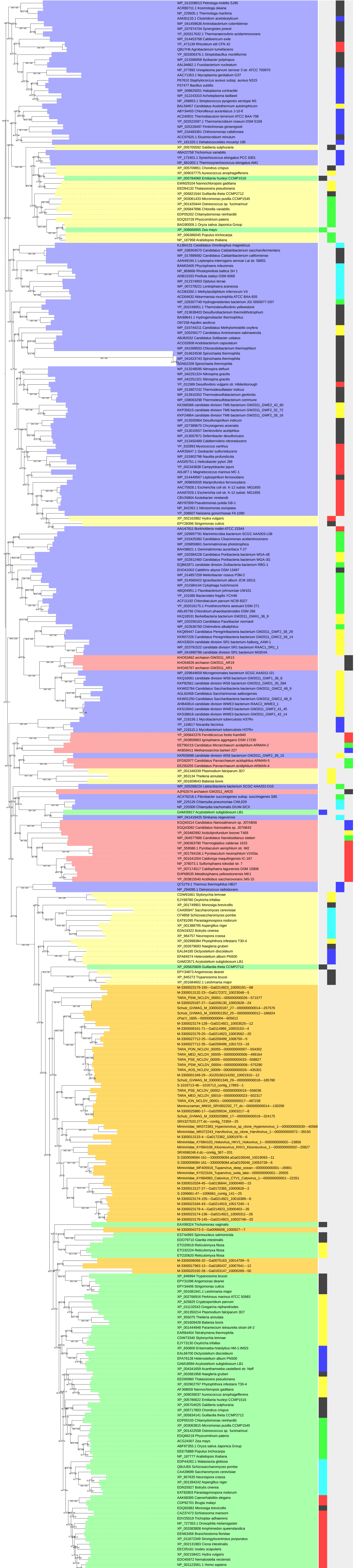


substitution per site: 1



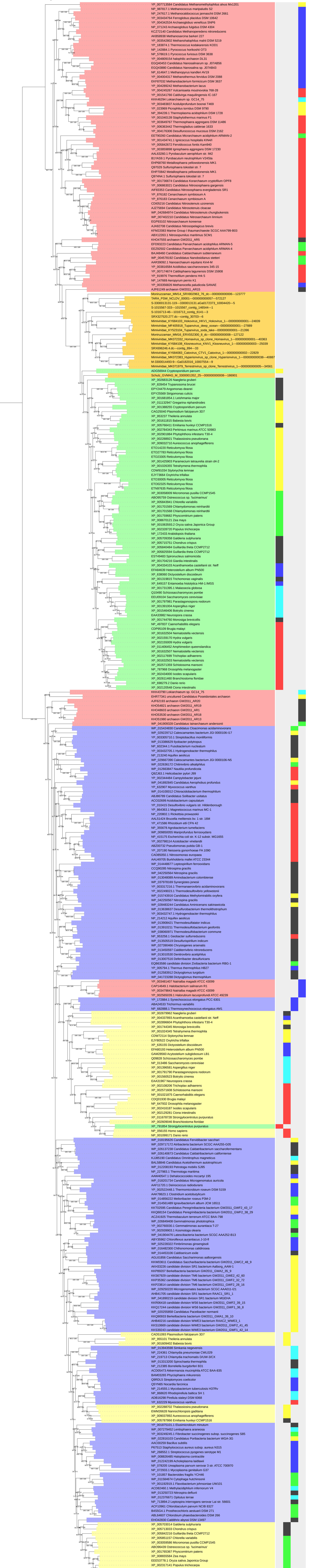
LysRS

substitution per site: 1



LeuRS

substitution per site: 1



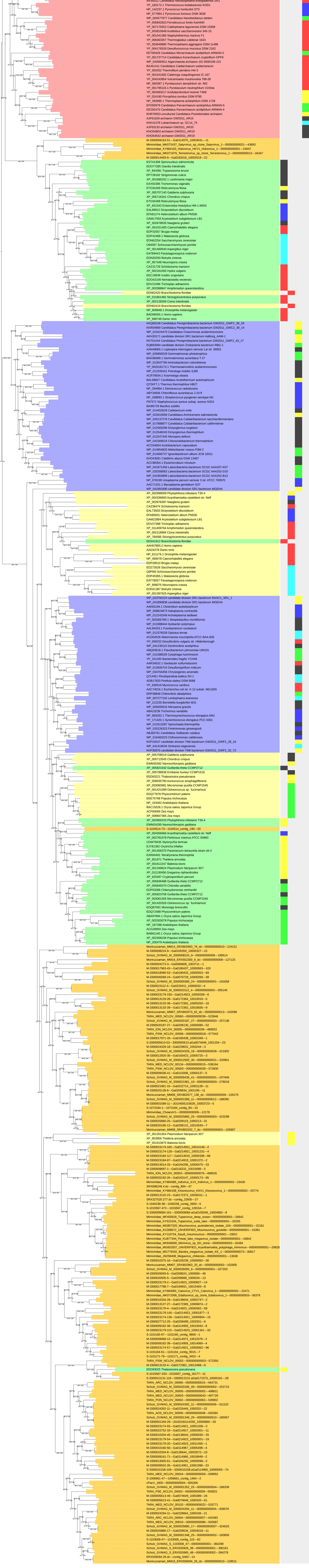
MetRS

substitution per site: 1



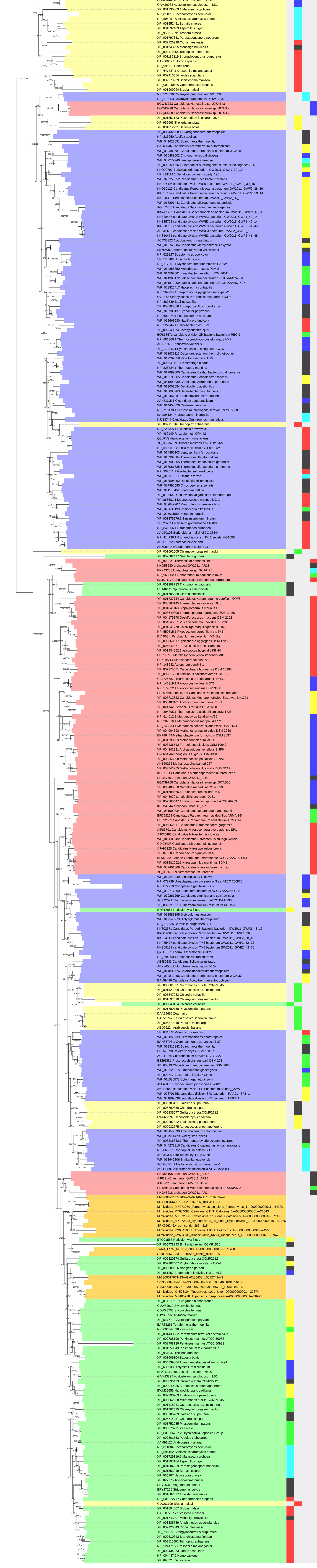
AsnRS

substitution per site: 1



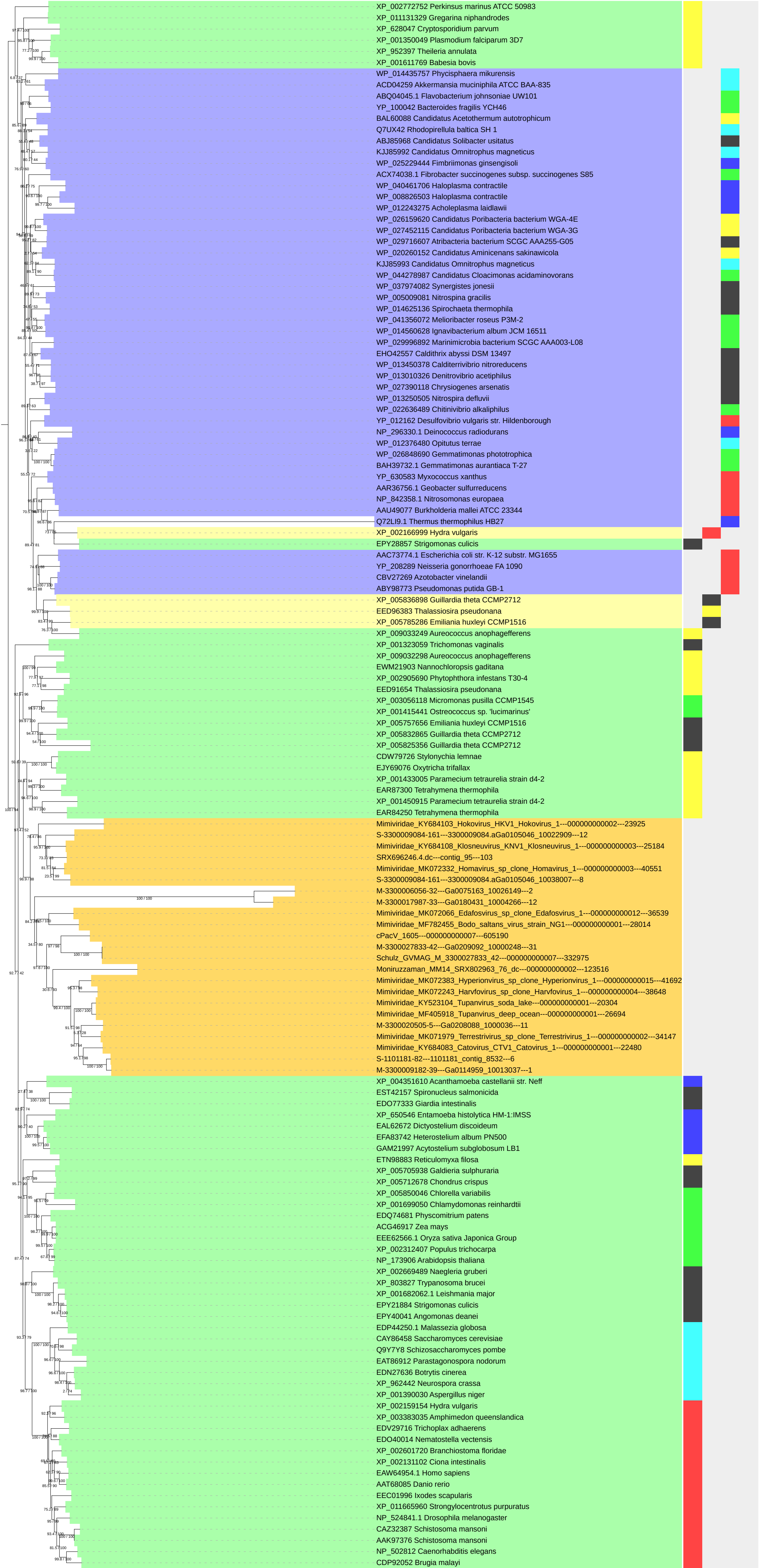
ProRS

substitution per site: 1



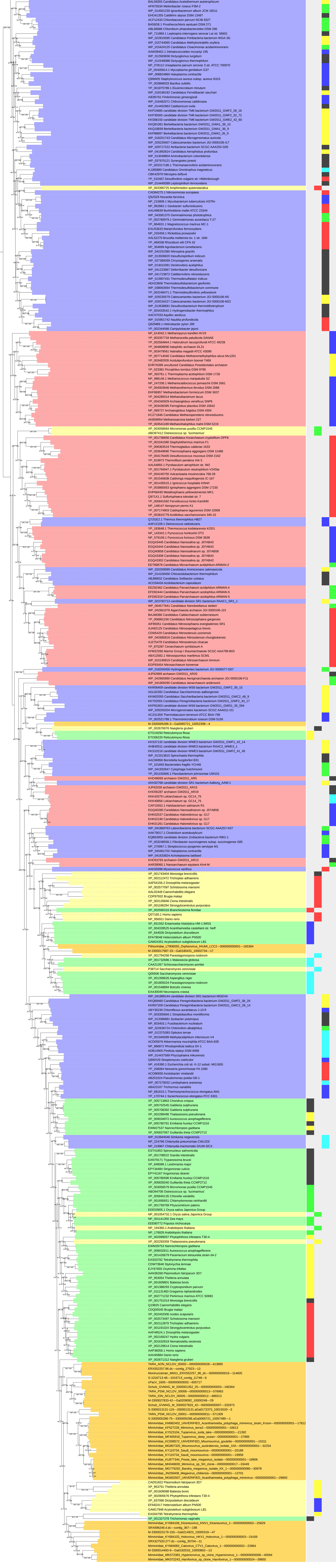
GlnRS

substitution per site: 1



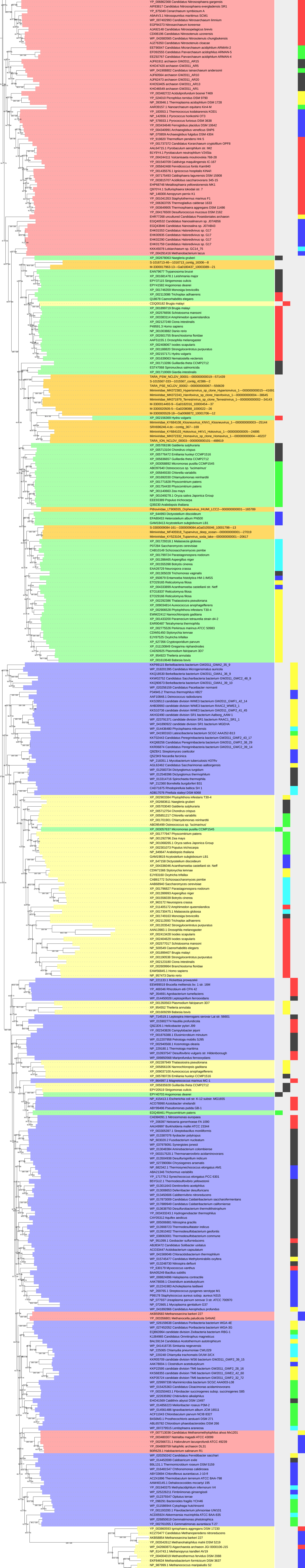
ArgRS

substitution per site: 1



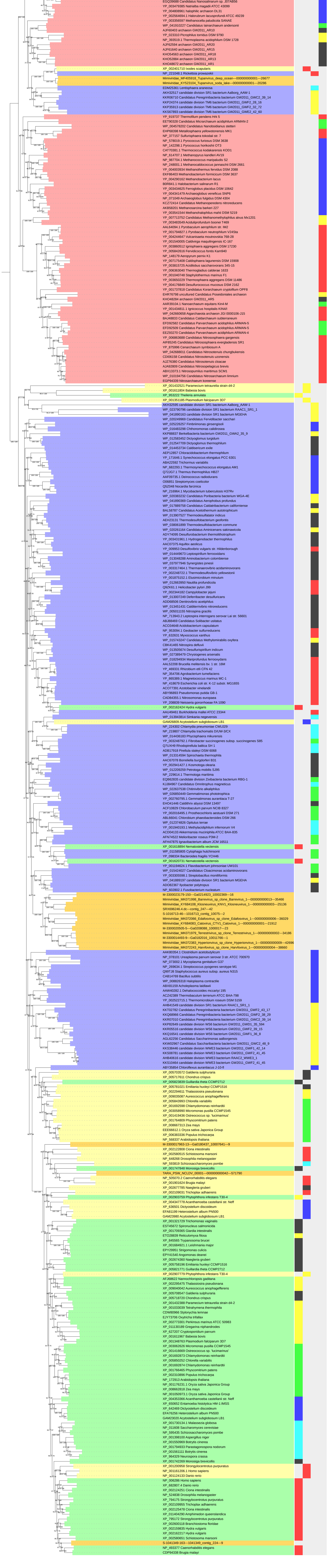
SerRS

substitution per site: 1



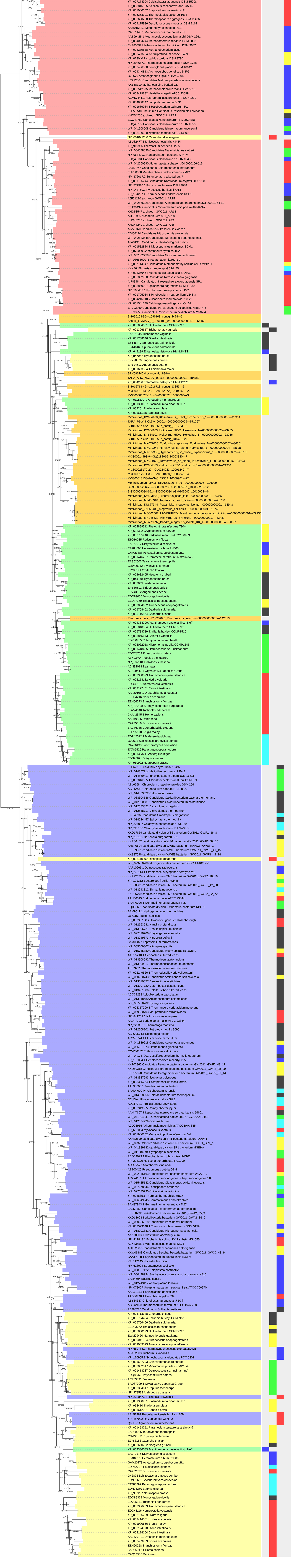
VaiRS

substitution per site: 1



TrpRS

substitution per site: 1



TyrRS

substitution per site: 1

