% deviation from pTRACA22 putative RelE for all sequences
% deviation from pTRACA22 putative RelE for human gut metagenome sequences
% deviation from pTRACA22 putative RelE for non-metagenomic sequences

- Residues conserved among all sequences examined
- Residues conserved only among sequences from human gut metagenomes
- Residues exhibiting conservative substitution in 98-100% of sequences
- Residues exhibiting conservative substitution in 96-97% of sequences
- Residues exhibiting conservative substitution in 94-95% of sequences
- Residues exhibiting conservative substitution in 92-93% of sequences