weekly report: amino acid seq

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Outline

- change alignment function
- generating core part given same information to see generation variety

requirement for alignment function

- not penalize similar a.a. as hard as totally wrong (customized similarity)
- want a.a to be more concentrated (exist a part without any gap)
- solution: pairwise2.align.globaldx

confusion about generation variety

- task: generating core part given same information to see generation variety
- how to check quality?
- possible solution: check BLAST