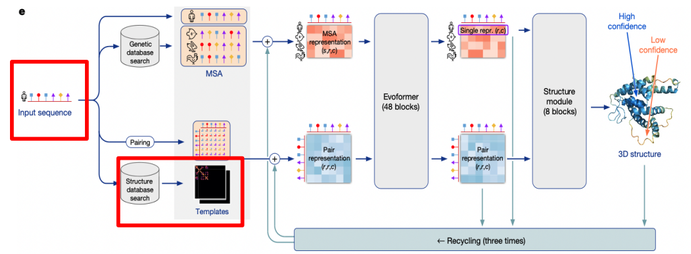
Input Protein sequence



Input protein sequence(s), then hit `Runtime` -> `Run all`

query_sequence: "ENFMDIECFMVLNPSQQLAIAVLSLTLGTFTVLENLLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFVYSFIDFHVFHRKDSRNVFLFKLGGVTASFTASVGSLFLAAIDRYISIH"

- Use `:` to specify inter-protein chainbreaks for **modeling complexes** (supports homo- and hetro-oligomers). For example **PI...SK:PI...SK** for a homodimer

jobname: "CB1"

num_relax: 5

- specify how many of the top ranked structures to relax using amber

template_mode: pdb100

- `none` = no template information is used. `pdb100` = detect templates in pdb100 (see notes). `custom` - upload and search own templates (PDB or mmCIF format, see notes)

코드 표시

Chain이 여러 개인 경우 각 chain 사이를 : 로 구분

jobname (ex. CB1)

Constrained relaxation of structures using Amber force field (stereochemical violation 제거)

Template_mode:

i) None - no template information is used

ii) pdb100 - detect templates in pdb100 (representative structure database based on the pairwise structure similarity by FoldSeek)

iii) custom - upload & search own templates

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