···MSA·····

·····A3M·query·····AlphaFold 3·····

·····MSA····· AlphaFold 3·AF3····· .a3m ·····
····· AF3 ·····
···

··· A3M ·····

A3M ····· query ·····
····· query ·····

··· | ···· | ·····

Query | ····· | ·····

A3M ·· | · query ···· | ·····query

···· | ····· | ·····

····· | ····· | ·····

·····

····· query.fa · A3M ·····
····· AF3 ·····

```
from pathlib import Path
import re

def read_fasta(path):
    records, name, parts = [], None, []
    for line in Path(path).read_text().splitlines():
        line = line.strip()
        if not line:
            continue
        if line.startswith('>'):
            if name is not None:
                records.append((name, ''.join(parts)))
            name, parts = line[1:].strip(), []
            if not name:
                raise ValueError('··FASTA··')
        else:
            if name is None:
                raise ValueError('·····FASTA··')
            parts.append(line)
    if name is not None:
        records.append((name, ''.join(parts)))
    if not records or any(not seq for _, seq in records):
        raise ValueError('FASTA·····')
    return records

query_records = read_fasta('query.fa')
if len(query_records) != 1:
    raise ValueError('query.fa·····')
query = query_records[0][1]
msa = read_fasta('external.a3m')
if msa[0][1] != query:
    raise ValueError('A3M·····query···')
for name, sequence in msa:
    aligned = re.sub(r'[a-z]', '', sequence)
    if len(aligned) != len(query):
        raise ValueError(f'{name}: ·····query')
print(f'·····{len(msa)}····query··{len(query)}')
```

····· A3M ·····
·····

· AF3 ···· MSA ··

AF3 ··· JSON · unpairedMsa · pairedMsa ·····/····· A3M·····
···· unpairedMsa··· pairedMsa ····· paired ····· MSA·····
·····

```
{
  "name": "one_protein_external_msa",
  "modelSeeds": [1],
  "dialect": "alphafold3",
  "version": 1,
  "sequences": [{
    "protein": {
      "id": "A",
      "sequence": "·····query··",
      "unpairedMsa": "·····A3M··",
      "pairedMsa": "",
      "templates": []
    }
  }]
}
```

····· JSON·····AF3 ··
····· AlphaFold Server ····· JSON ·····

·····

MSA ·····AF3 ····· paired MSA ·····
····· MSA ····· unpaired MSA ·····
·····

·····

····· query · A3M · SHA256·MSA ·····AF3 ·····JSON·····
····· PAE ·····
····· JSON/A3M ·····GPU···

····· A3M ····· AF3 · GPU ·····
·····

····

AlphaFold 3·····MSA·A3M····· https://github.com/google-deepmind/alphafold3/blob/main/docs/input.md

AlphaFold 3·····MSA·· https://github.com/google-deepmind/alphafold3/blob/main/docs/performance.md