fastx-utils之根据提供的序列ID，获取其序列：fetch

一、**fastx-utils fetch**介绍

功能描述：

`fastx-utils fetch` 根据提供的序列 `ID`，获取其序列。

命令行接口：

```
1  $ fastx-utils fetch
2
3  Usage: fastx-utils fetch <fa/fq> <id>
```

二、使用场景实例及其用法

示例演示：

示例文件：`protein.faa, annotation.txt`

```
1  $ cat protein.faa | head -n 6
```

```
1  >AGE80385.1
2  MKKIIIISATTIVIGITSFAYFGSKTPLHNEAKAVESQKHNNHKKEEIPAFPKADHNAKKIDNDFSVVTNPKSNLVL
   INKHRKLPDGYIPEDLTRPNVPFISPKDKEKTLLRKDAAEALENMFKAAKKEGLDLTAVSGYRSYKRQKSLHDTYVR
   RQGKAEANSVSAIPGTSEHQTGLAMDISSKSAKFQLEPIFGETAEGKWVAEHAHEFGFVIRYLEDKTDTTEYAYEPW
   HLRYVGNPYATYLYKHHLTLEEAMEDKK
3  >AGE79558.1
4  MINHELVERINFLAKKAKAEGLTEEEQRERQSLREQYLKGFRQNMLNELKGIKVVNEEGTDVTPTKLKALKKQDNAK
   LN
5  >AGE81073.1
6  MDKVISNEILQQFKDRMRLGDDEDANLRRILFASNKDLTRVCGNYDLNIDEVFKELVFERSRYVYNDALEYFDKNFL
   SQINSLSIGKALEAIKLDGD
```

运行命令：

```
1  $ fastx-utils  fetch protein.faa AGE78977.1
```

```
1  >AGE78977.1
2  MQIGSNIHTLSQPTKITSSTLEHNTISSTKLESKKINDPIKFDIRSSEKEMKQPEHKFNELDLWKMLKDKGVPLWII
   LEMLQKARKEKEAQNNSVQNSNAIEETSETRLNEVM
```

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