

A

Input

Do you already have a template? ☒ Yes ☐ NoAtomic structure used as template `import structure 3bp5.outputPdb.`Chain `("model": 0, "chain": "A", "residues": 114)`Target sequence `import aminoacid seq, Q15116 from UniProtKB.outputSequence.`Options to improve the alignment: Provide your own sequence alignmentSequence alignment input `Runs/000791_ChimeraModelFromTemplate/extra/aligned_1.fasta`Additional target sequence to include? ☒ Yes ☐ NoChain `("model": 0, "chain": "B", "residues": 191)`Target sequence `import aminoacid seq, Q12LC89 from UniProtKB.outputSequence.`Options to improve the alignment: Provide your own sequence alignmentSequence alignment input `Runs/000791_ChimeraModelFromTemplate/extra/aligned_2.fasta`

B

&gt;3bp5\_\_0\_B

```
-----MLFTVTAPKEVYTVDVGSSVSLECDFDRRECTELEGIRASLQ
-----KVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQYRCLVIC
GAAWDYKYLTVKVKASYMRIDTRILEV-PGTGEVQLTCQARGYPLAEVSWQNVSV-----
PANTSHIRTPEGLYQVTSVLRLKPQPSRNFSCMFNAHMKELTSA-----IIDP-----
```

&gt;Q2LC89

```
-----LQLHQIAALFTVTPKELYIEHGSNVTLECNFDTGSHVNLGAITASLQ
-----KVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIY
GVAWDYKYLTLKVKASYRKINTHILKV-PETDEVELTCQATGYPLAEVSWPNVSV-----
PANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFNTHVRELTLA-----SIDLQSQMEP
RTHPTWLLHIFIPSCII-AFIFIATVIALRKQLCQ--KLYSSKDTTKRPVTTTKREVNSA
I
```

&gt;Q9BQ51

```
MIFLLMLSLLEQLHQIAALFTVTPKELYIEHGSNVTLECNFDTGSHVNLGAITASLQ
-----KVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQYQCIIY
GVAWDYKYLTLKVKASYRKINTHILKV-PETDEVELTCQATGYPLAEVSWPNVSV-----
PANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFNTHVRELTLA-----SIDLQSQMEP
RTHPTWLLHIFIPFCII-AFIFIATVIALRKQLCQ--KLYSSKDTTKRPVTTTKREVNSA
I
```

&gt;Q9NZQ7

```
--MRIFAVFIFMTYWHLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQLDLAALIVYWE
MEDKNIIQFVHGEECLKVQHSSYRQARLLKDQLSLGNAALQITDVKLQDAGVYRCMISY
GGA-DYKRITVKVNAPYNKINQRILVDPVTSEHELTCQAEYGPKAIEVIWTSSDHQVLSG
KTTTTNSKREEKLFNVTSTLRINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPNE
RTHLVILGAI--LLCLGVALTFI--FRLRKGRMMDVKKCGIQDTNSKKQSDTHLEET--
-
```