

**A**

Input

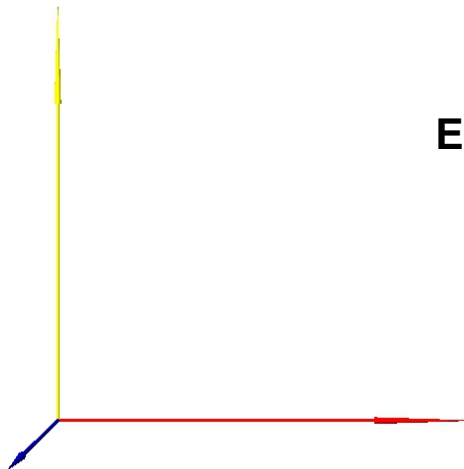
Do you already have a template? ☐ Yes ☒ NoTarget sequence `import aminoacid seq, Q15116 from UniProtKB.outputSequence.`

Protein sequence database: PDB

Similarity matrix: BLOSUM62

cutoff evalule: 0.001

Maximum number of sequences: 100

**C****B**

Modeller Comparative

Sequence alignments

aligned\_1.fasta  
bp1 [1]

Target sequences

aligned\_1.fasta Q15116

**D**

Seqview [ID: aligned\_1.fasta]

Q15116 MQ I PQAPWPV VWAV LQLGWRPGWFLDSPDRPWNPTTFSPALLVVTEGDNATFTCS  
 Q15116 FSNTSESFVLNWMYRMSPSNQTDKLAAPFEDRSQPGQDCRFRTVQLPNGRDFHMSV  
 Q15116 VRARRNDSGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPSPRPAGQ  
 Q15116 FQTLVGVGVGGLLGSLLVLLVWVLAVICSRARGTIGARRTGQPLKEDPSAVPVFS  
 Q15116 VDYGELDFQWREKTPPEPPVPCVPEQTEYATIVFPSGMGTTSSPARRGSADGPRSAQ  
 Q15116 PLRPEDGHCSWPL

**E**

BlastProtein [name: bp1]

Blast Protein (an [RBLI](#) web service)

Search Parameters

Chain: ▾

Database: PDB ▾

# Sequences: 100

Matrix: BLOSUM62 ▾

Cutoff: 1e-3

Blast

Results for: chain: null, database: pdb, cutoff: 0.001, maxSeqs: 100, matrix: BLOSUM62

Show in sequence viewer

Q Search

10 ▾

<input type="checkbox"/>	ID	Name	E-Value	Score	Title
<input type="checkbox"/>	1	5WT9_G	3.14716e-121	345	Complex structure of PD-1 and nivolumab-Fab
<input type="checkbox"/>	2	6JBT_F	1.27984e-107	310	Complex structure of toripalimab-Fab and PD-1
<input type="checkbox"/>	3	6JJ_P_C	4.1605e-105	303	Crystal structure of Fab of a PD-1 monoclonal antibody MW11-h317 in complex with PD-1