










A


Input

Do you already have a template? ☒ Yes ☐ No

Atomic structure used as template   


Chain   

Target sequence   




Options to improve the alignment: 




Other sequences to align


Object	Info
import aminoacid seq, from 3rrq amino acid	Sequence (name = User,
import aminoacid seq, P01832 from UniP	Sequence (name = User,

Multiple alignment tool: 

Additional target sequence to include? ☒ Yes ☐ No


Chain   

Target sequence   

Options to improve the alignment: 

Other sequences to align

Object	Info
import aminoacid seq, Q9BQ51 from Unif	Sequence (name = User,
import aminoacid seq, Q9NZQ7 from Unif	Sequence (name = User,

Multiple alignment tool: 

B

Modeller Comparative Sequence alignments

aligned_1.fasta
aligned_2.fasta

Target sequences

aligned_1.fasta

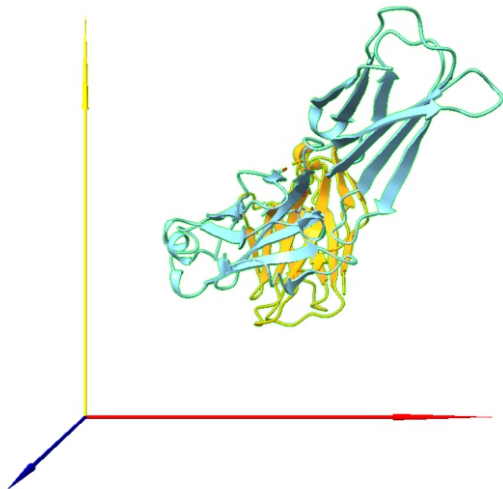
aligned_2.fasta

Options

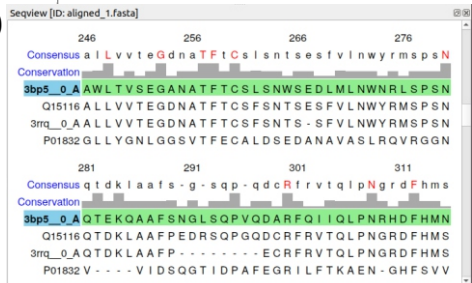
Basic ☒ Advanced

Make multichain model from multichain template ☒

C



D



E

