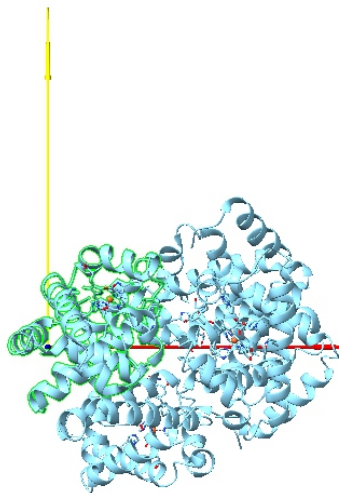


A

Input

Do you already have a template? ☒ Yes ☐ NoAtomic structure used as template `import structure 3lqd.outputPdb.`Chain `{"model": 0, "chain": "B", "residues": 146}`Target sequence `import aminoacid seq, 3lqd_B_mutated from file.outputSequence.`Options to improve the alignment: NoneAlignment tool for two sequences: Bio.pairwise2Additional target sequence to include? ☐ Yes ☒ No**B****C**

Seqview [ID: aligned_1.fasta]

1	11
Consensus	VHLSGEEKSAVT a l wGKVN V
Conservation	
3lqd_0_B	VHLSGEEKSAVTALWGKVN V
Seq_3lqd_B_mutated	VHLSGEEKSAVTESAGKVN V
21	31
Consensus	EEVGGETLGRLLVVPWTQR
Conservation	
3lqd_0_B	EEVGGETLGRLLVVPWTQR
Seq_3lqd_B_mutated	EEVGGETLGRLLVVPWTQR
41	51
Consensus	FFE s f G d l STASAVMGNPKV

D

Modeller Comparative
Sequence alignments

aligned_1.fasta

Target sequences

aligned_1.fasta	Seq_3lqd_B_mutated
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