



Nov 12, 2023

Version 1

Multiple Sequence Alignment V.1

DOI

<https://dx.doi.org/10.17504/protocols.io.eq2lyj14wlx9/v1>

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Protocol Citation: Leonardo Parra-Rivas 2023. Multiple Sequence Alignment. **protocols.io**

<https://dx.doi.org/10.17504/protocols.io.eq2lyj14wlx9/v1>

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Protocol status: Working

We use this protocol and it's working

Created: November 12, 2023



Last Modified: November 12, 2023

Protocol Integer ID: 90823

Keywords: sequence

Abstract

Multiple Sequence Alignment



- 1 Protein sequences were retrieved from Uniprot or NCBI via Jalview's sequence fetcher Jalview (RRID:SCR_006459)(<https://www.jalview.org/help/html/features/seqfetch.html>).

- 2 Then, the sequences were aligned with the Clustal Omega Webserver [(RRID:SCR_001591) <http://www.ebi.ac.uk/Tools/msa/clustalo/>] with default parameters.

- 3 For the α -synuclein alignment human (uniprot OP37840), chimpanzee (uniprot P61145), baboons (uniprot A0A2I3N0Z9), marmoset (uniprot F7GY62), rat (uniprot P37377), mouse (uniprot O55042), rabbit (uniprot G1U0V2), cow (uniprot Q3T0G8), bat (uniprot A0A6J2L5S3), shrew (uniprot J7H0X3), armadillo (NCBI XP_004480597), elephant (uniprot G3T7Z3), tenrec (NCBI XP_004703317.1), chicken (uniprot Q9I9H1), zebra finch (uniprot Q4JHT6), frog (uniprot Q7SZ02), and fish (uniprot A0A090D865) sequences were used.