Multiple sequence alignment of erythrocytic α-spectrin sequences from 58 different species

Sequences of erythrocytic α -spectrin were collected from the UniProtKB database at uniprot.org. 58 sequences with "erythrocytic α -spectrin" annotation were selected with an additional criterium being a comparable sequence length to human erythrocytic α -spectrin (2,419 residues). Multiple sequence alignment was performed with Clustal Omega (webserver version accessed at https://www.ebi.ac.uk/Tools/msa/clustalo/ on 04.30.2020) with default parameters. The result is given in the file with the ending .clustal_num.

In addition, the sequence alignment is displayed as a .tif file, with colored residues indicating high identity according to the 'identity' coloring option of Mview; colors vary according to physicochemical properties as specified in the MView documentation (Madeira, Park et al. 2019).

Multiple sequence alignment of erythrocytic β-spectrin sequences from 11 different species

Sequences of erythrocytic β -spectrin were collected from the UniProtKB database at uniprot.org. 11 sequences with "erythrocytic β -spectrin" annotation were selected with an additional criterium being a comparable sequence length to human erythrocytic β -spectrin (2,137 residues). Multiple sequence alignment was performed with Clustal Omega (webserver version accessed at https://www.ebi.ac.uk/Tools/msa/clustalo/ on 04.30.2020) with default parameters. The result is given in the file with the ending .clustal_num.

In addition, the sequence alignment is displayed as a .tif file, with colored residues indicating high identity according to the 'identity' coloring option of Mview; colors vary according to physicochemical properties as specified in the MView documentation (Madeira, Park et al. 2019).

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