

Each neighbour is shown in the pairwise Dali-alignment to 2nxfa. Inserted segments relative to the top structure are hidden. You can check the 'Expand gaps' option in the summary page to see the complete sequence of the matched proteins. Uppercase means structurally equivalent positions with 2nxfa. Lowercase means insertions relative to 2nxfa. The first part shows the amino acid sequences of the selected neighbours. The second part shows the secondary structure assignments by DSSP (H/h: helix, E/e: strand, L/l: coil). The most frequent amino acid type is coloured in each column.

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