

Molecular Cell, Volume 65

Supplemental Information

Tardigrades Use Intrinsically Disordered

Proteins to Survive Desiccation

Thomas C. Boothby, Hugo Tapia, Alexandra H. Brozena, Samantha Piskiewicz, Austin E. Smith, Ilaria Giovannini, Lorena Rebecchi, Gary J. Pielak, Doug Koshland, and Bob Goldstein

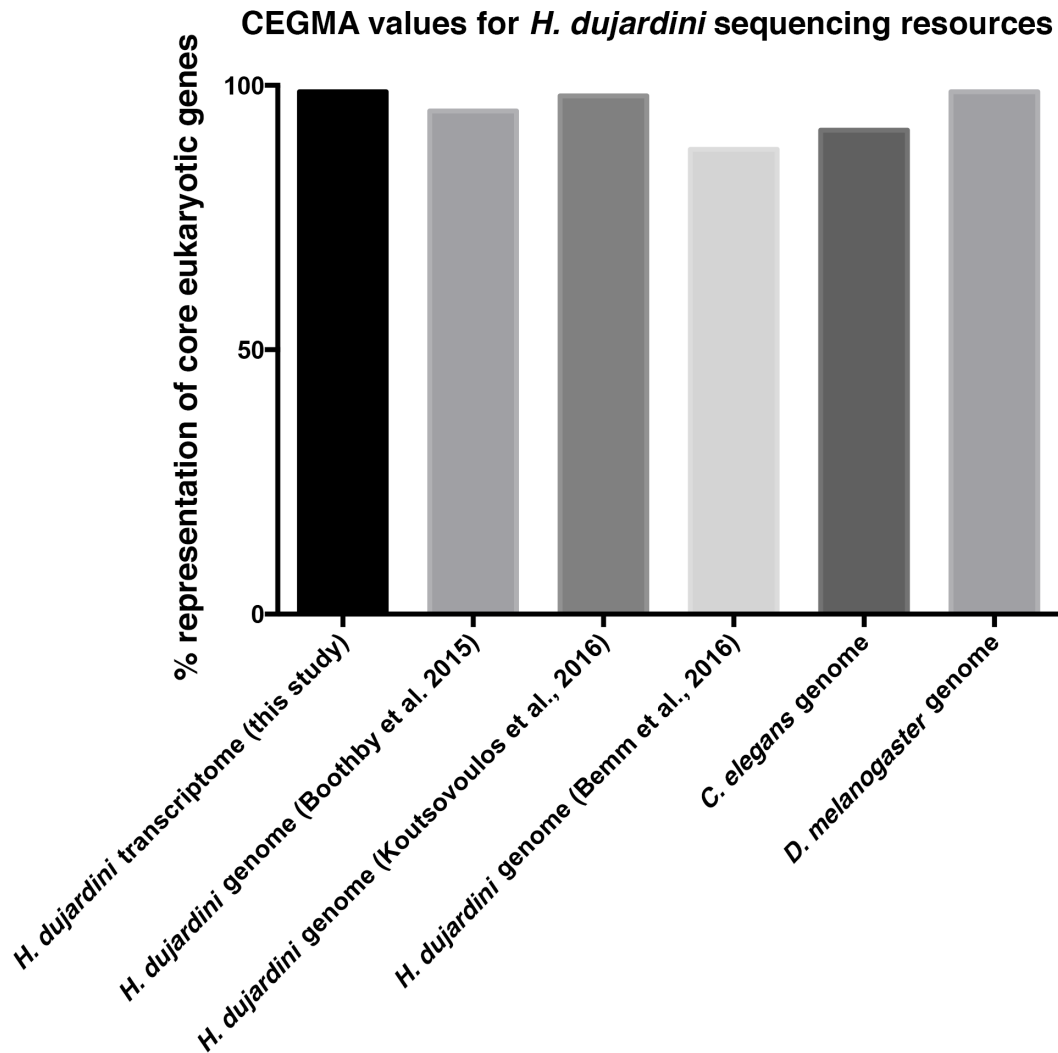


Figure S1. Related to Figure 1 Assessment of Core Eukaryotic genes within Our Transcriptome Assembly

Graph showing the percent of core eukaryotic genes (partial) contained within our *H. dujardini* transcriptome assembly, an independent *H. dujardini* transcriptome assembly(Levin et al., 2016), multiple *H. dujardini* genome assemblies(Bemm et al., 2016; Boothby et al., 2015; Koutsovoulos et al., 2016), and genome assemblies from well sequenced model invertebrates (*C. elegans* and *D. melanogaster*). CEMGA values for *C. elegans* and *D. melanogaster* were obtained from (Wang et al., 2014).

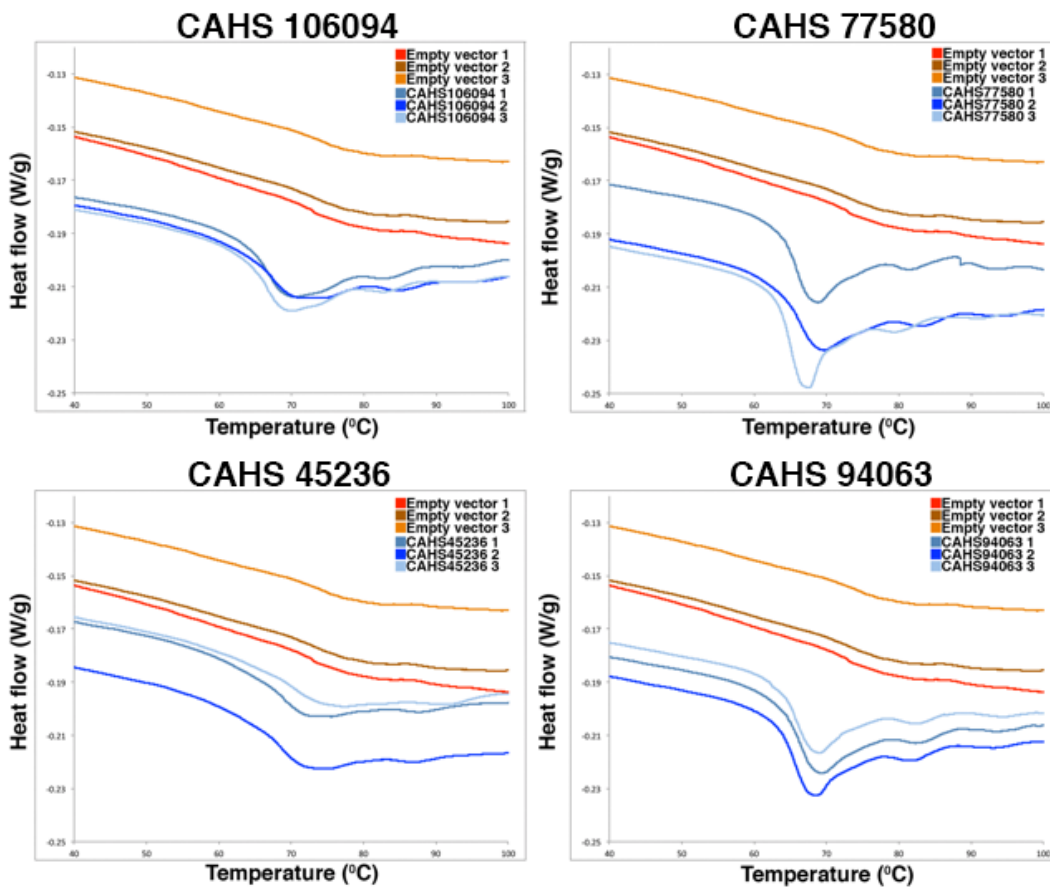


Figure S2. Related to Figure 7 Additional Differential Scanning Calorimetry Thermograms for Yeast Heterologously Expressing Different CAHS Proteins.

CAHS proteins

IUPRED^{1,2} Disordered Protein Predictions

1. The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins

Zsuzsanna Dosztányi, Veronika Csizmók, Péter Tompa and István Simon

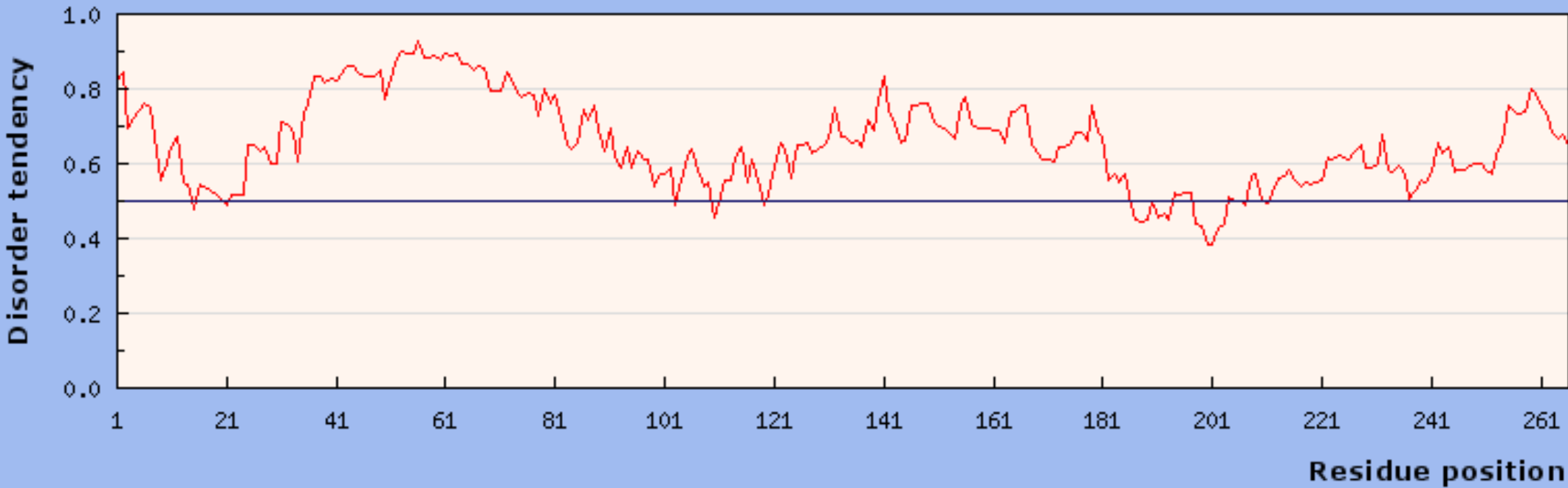
J. Mol. Biol. (2005) 347, 827-839.

2. IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content

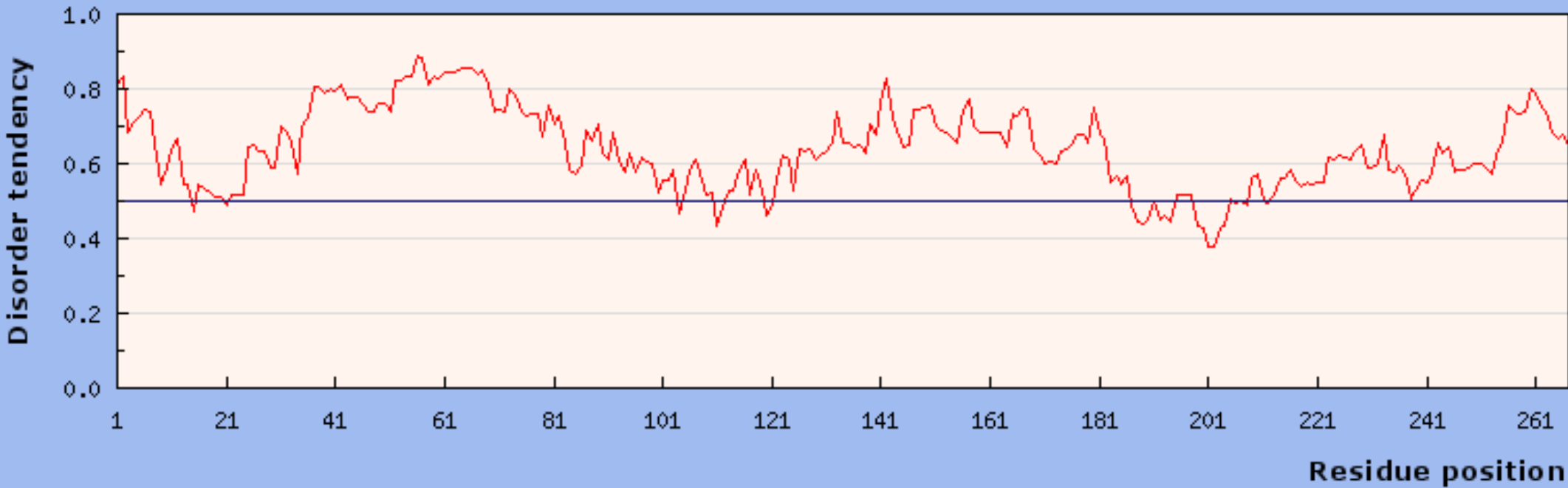
Zsuzsanna Dosztányi, Veronika Csizmók, Péter Tompa and István Simon

Bioinformatics (2005) 21, 3433-3434.

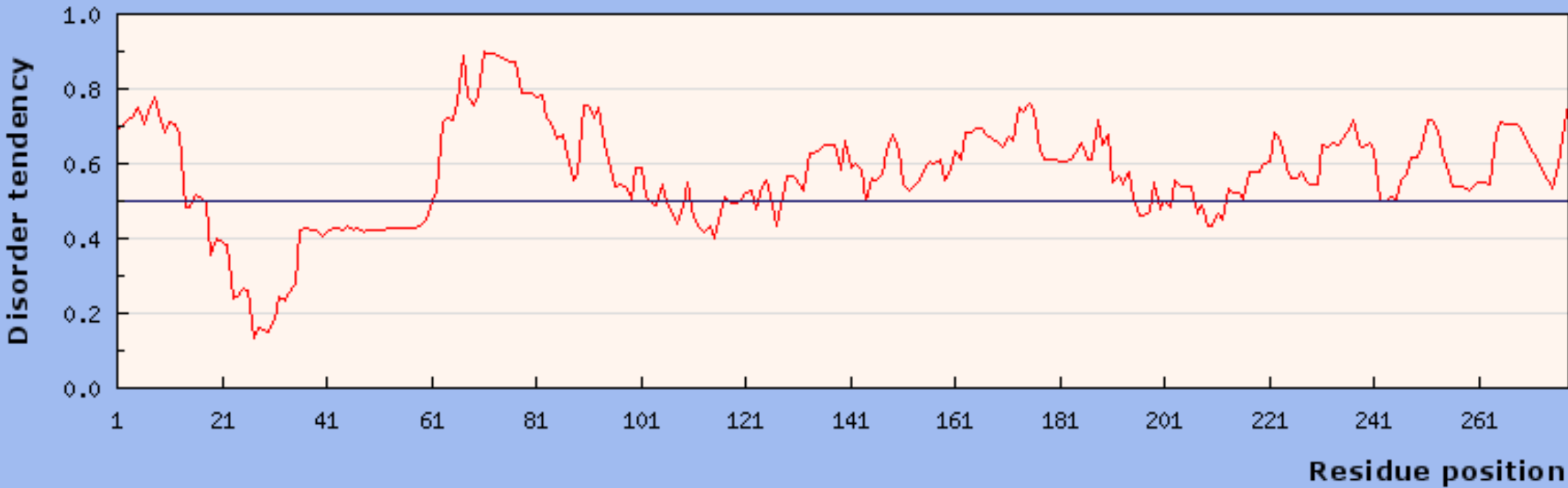
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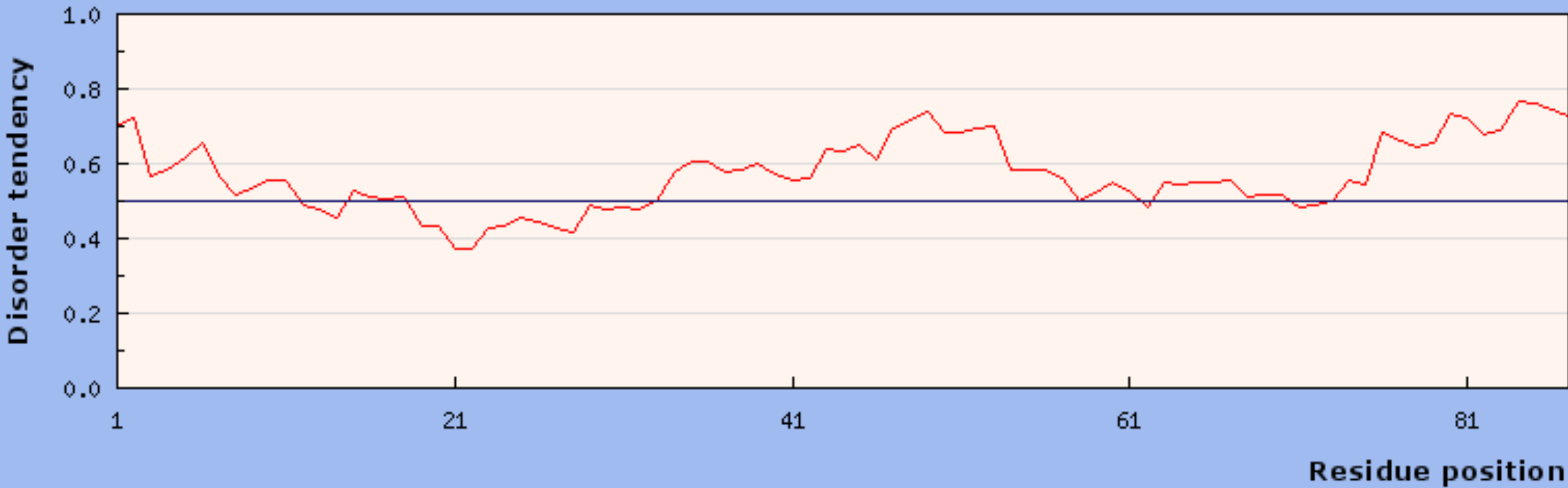
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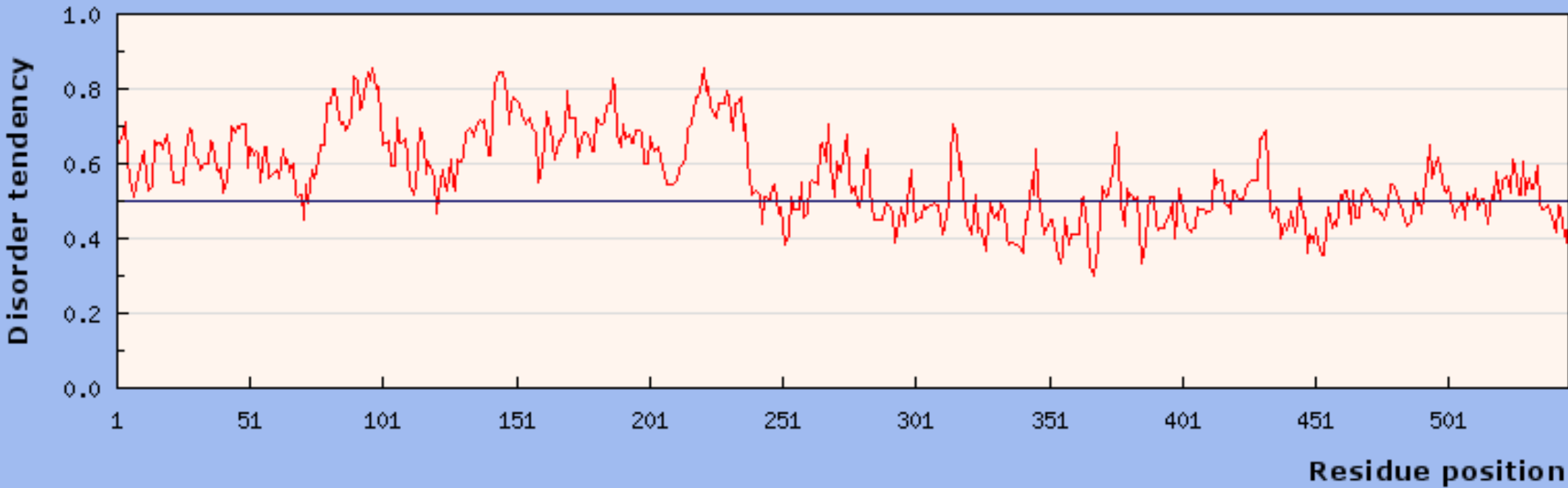
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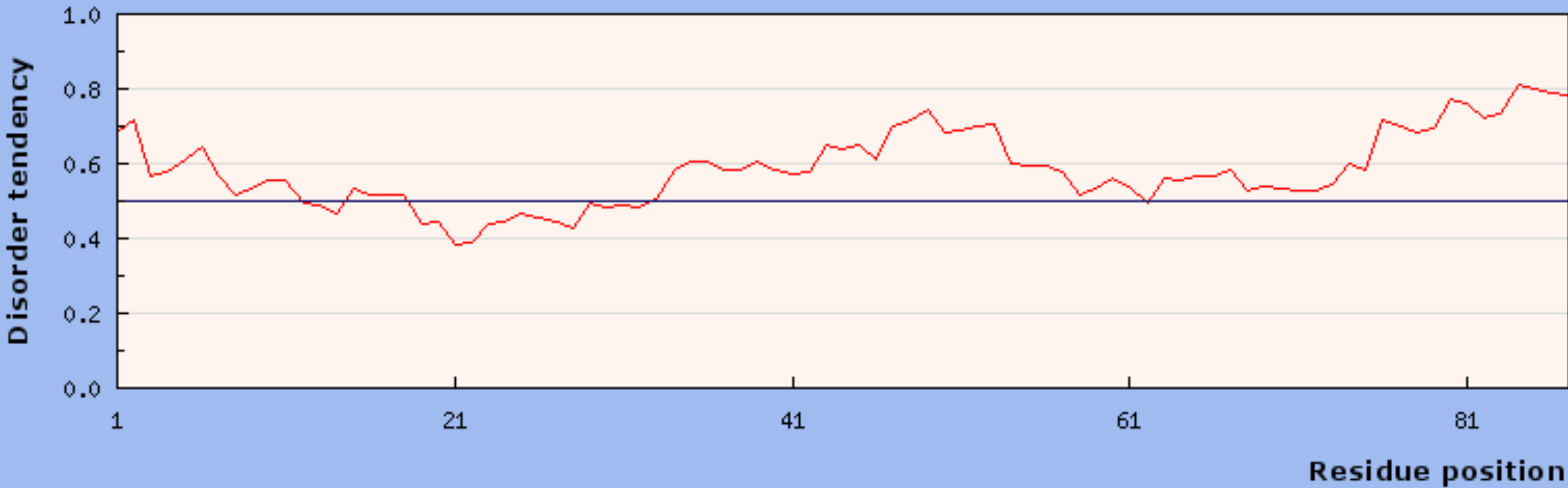
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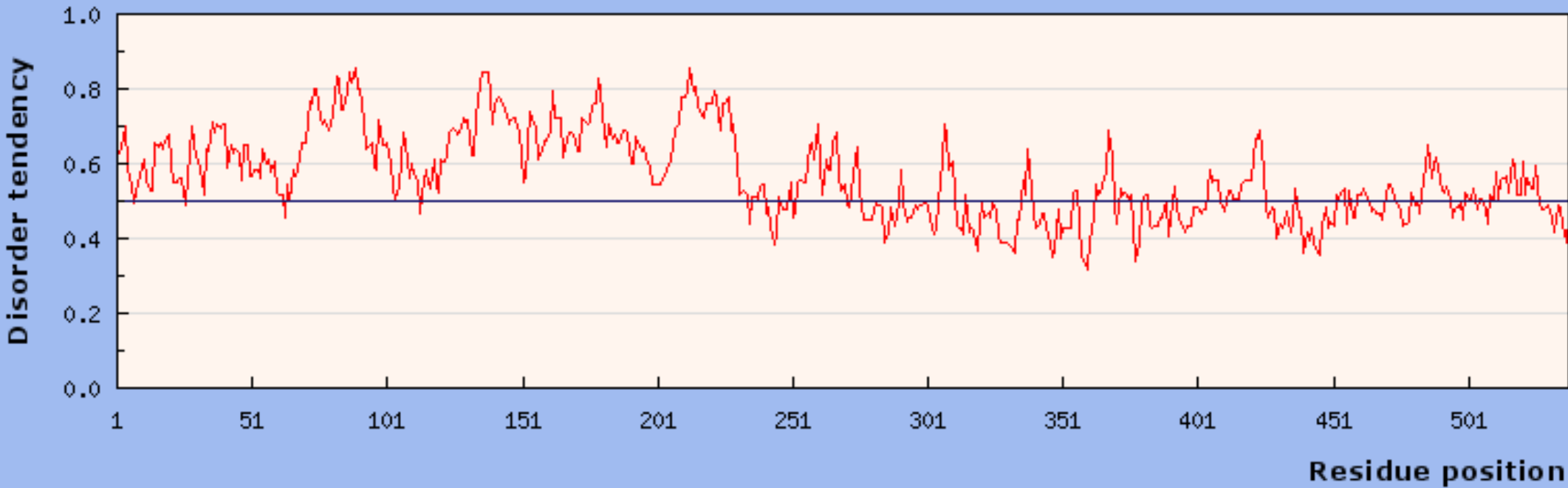
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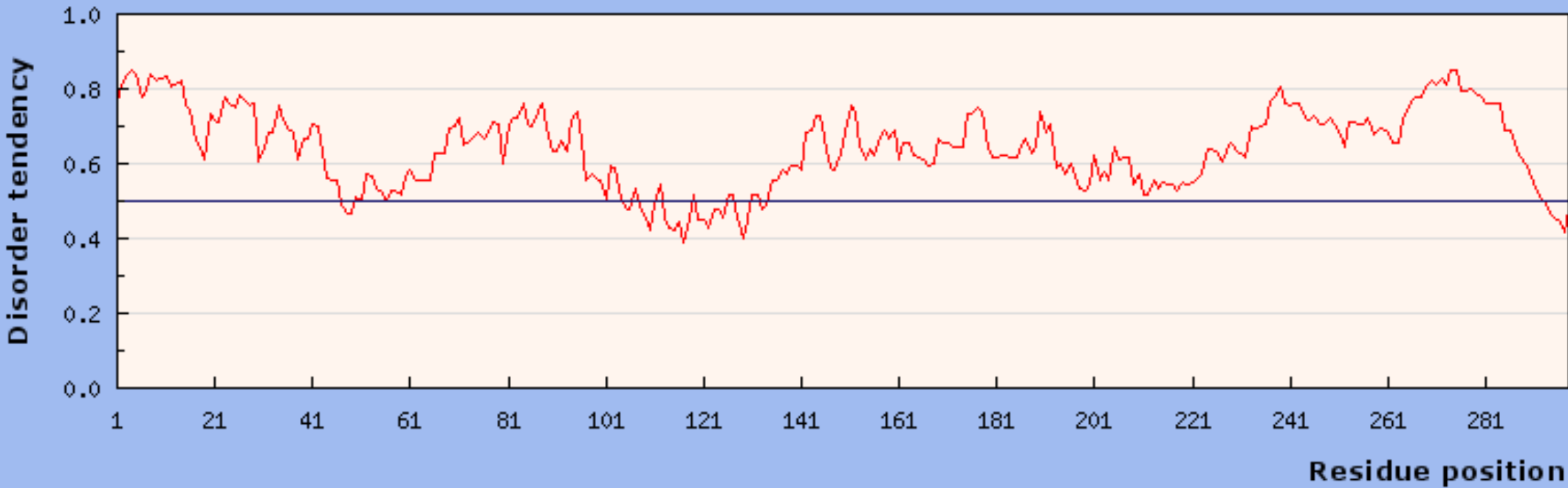
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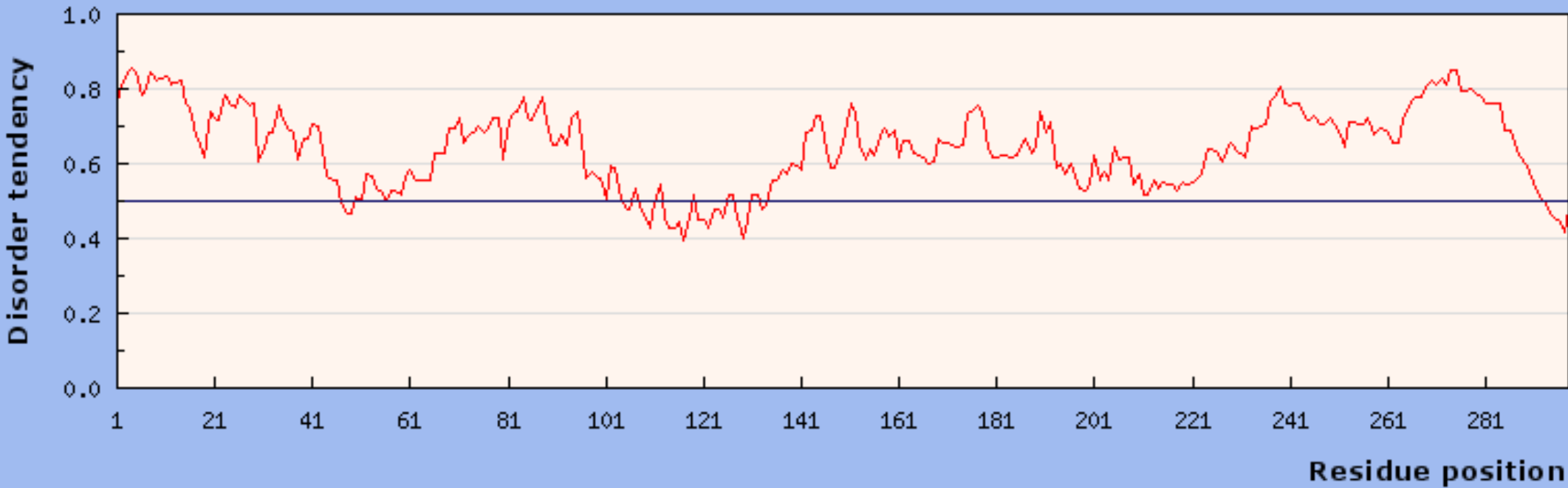
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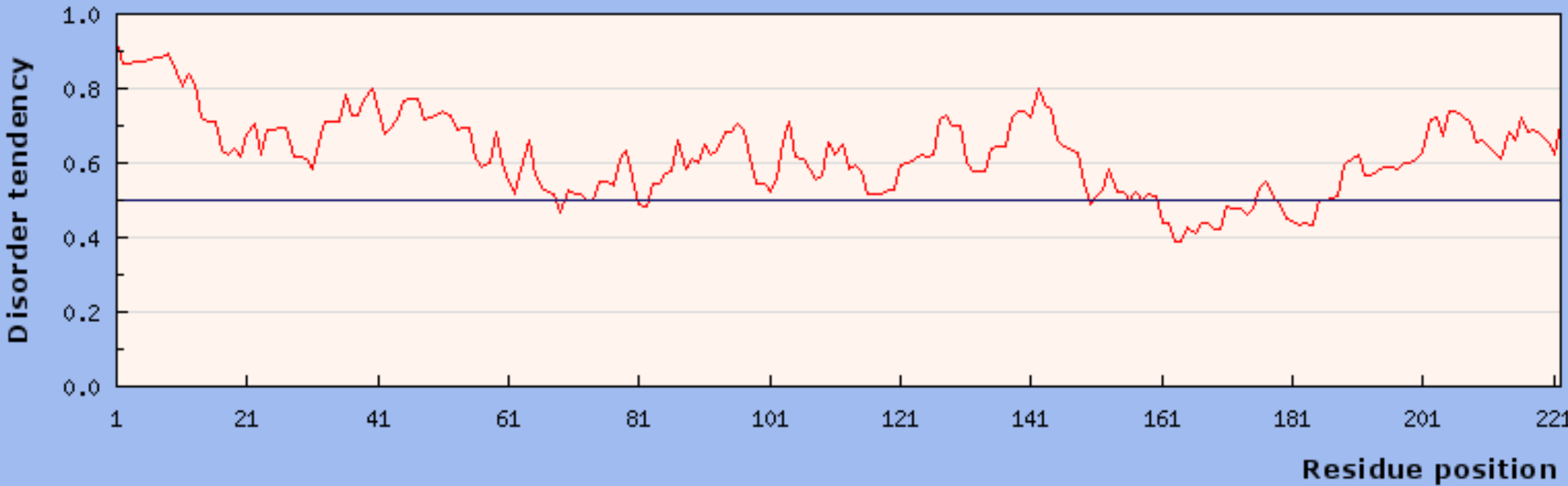
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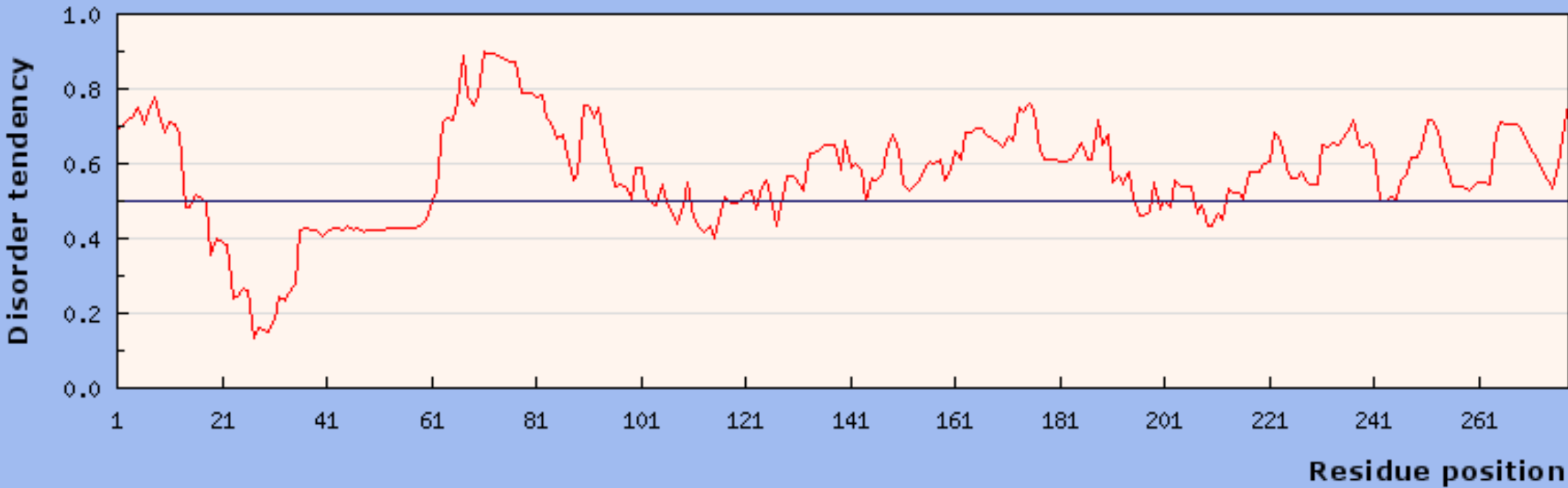
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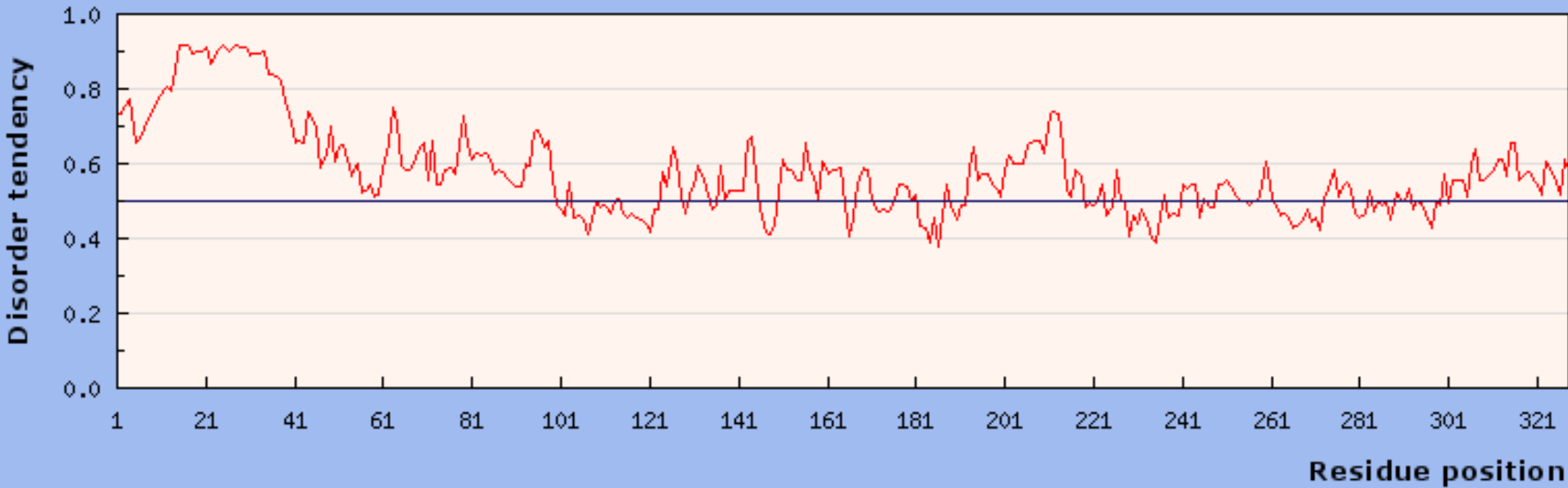
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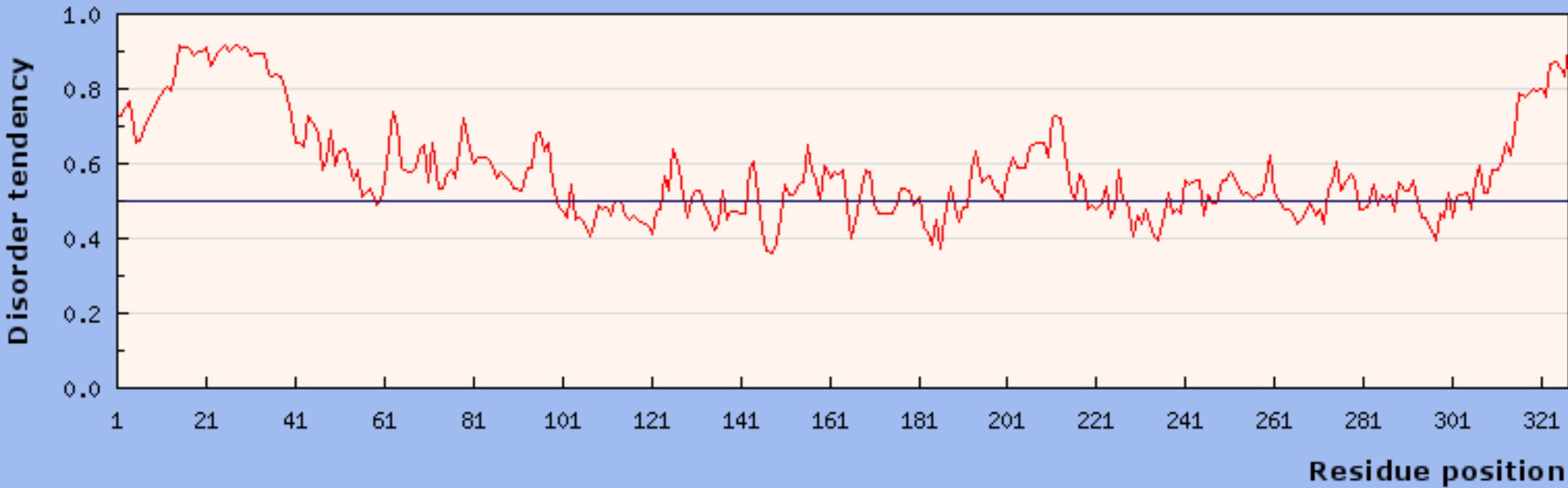
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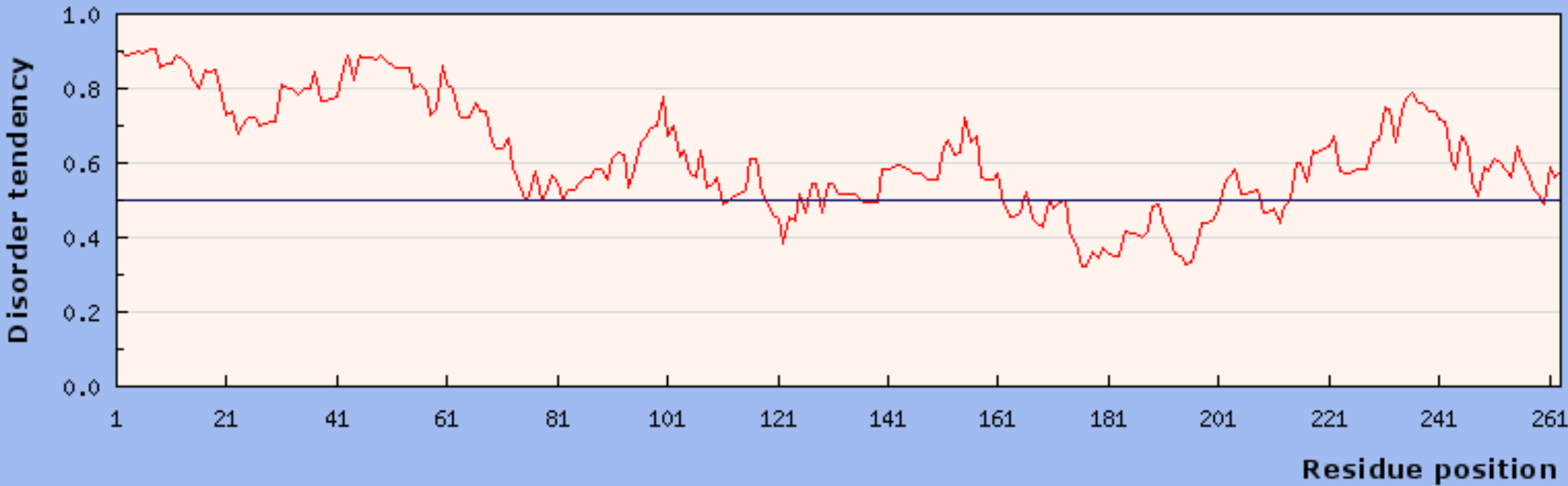
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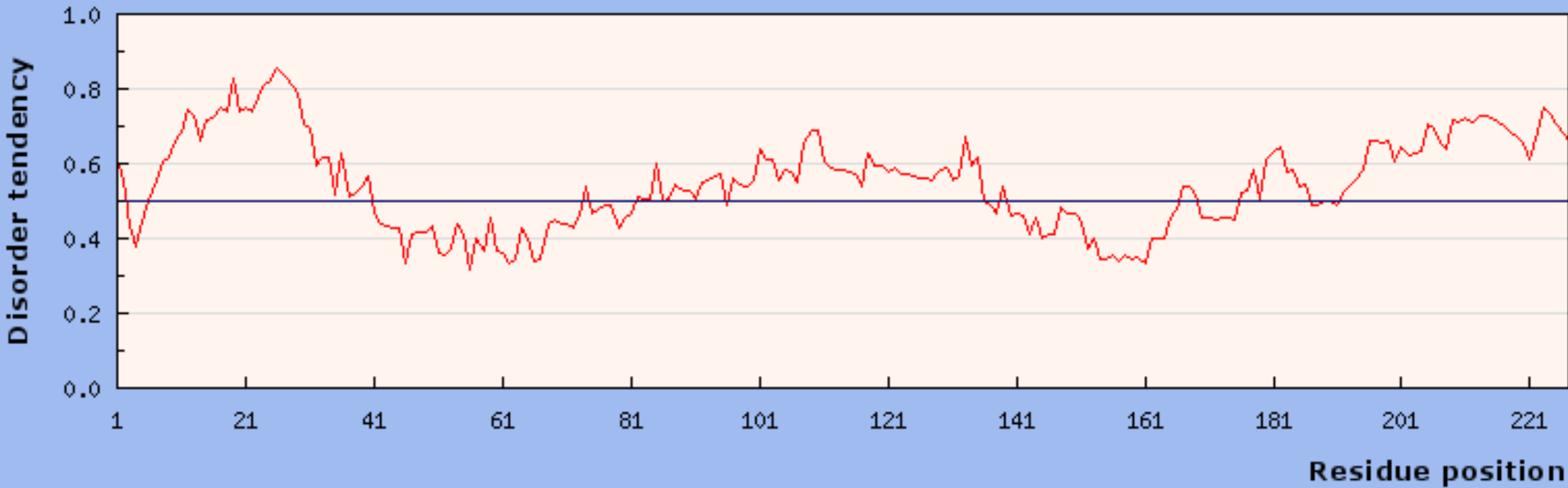
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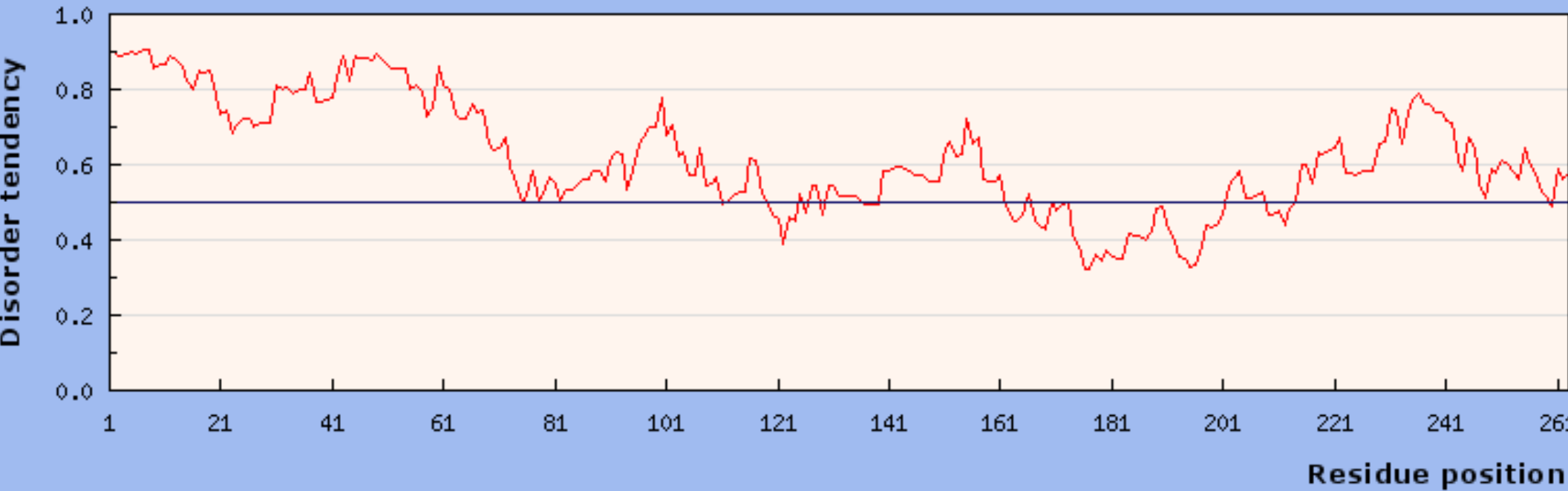
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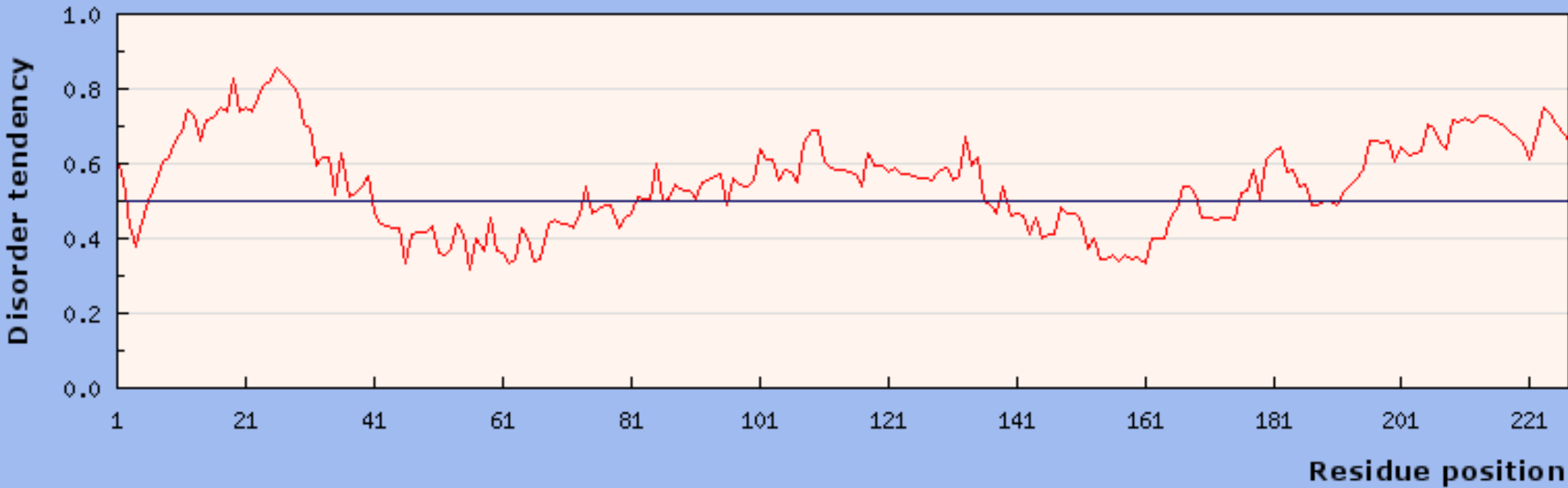
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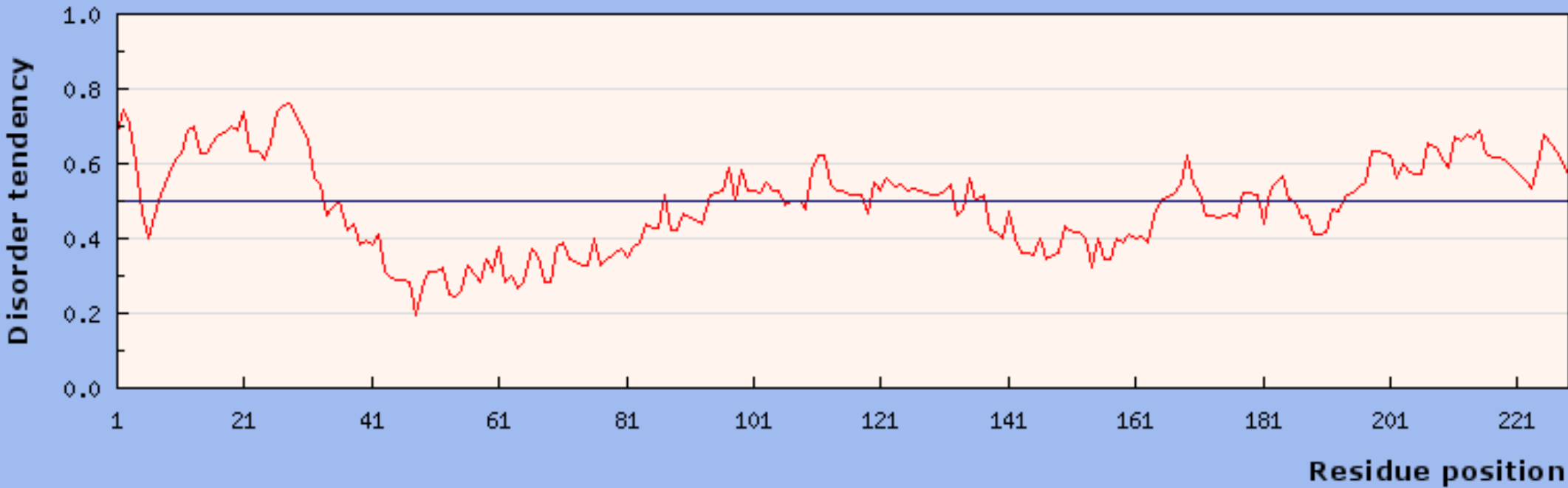
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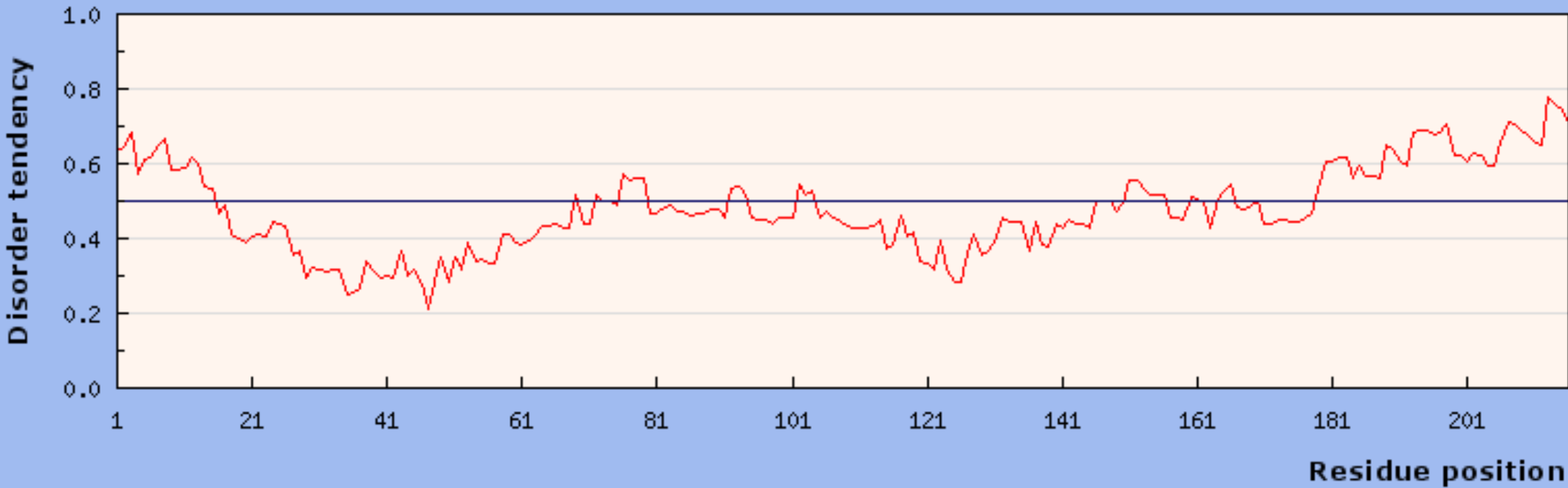
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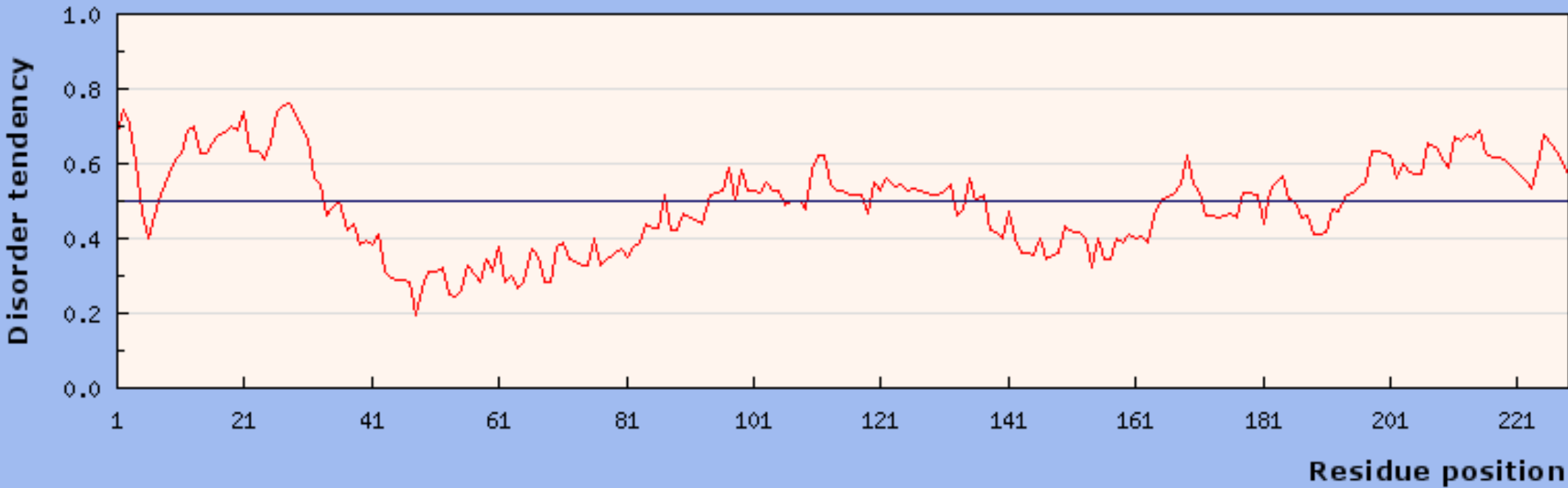
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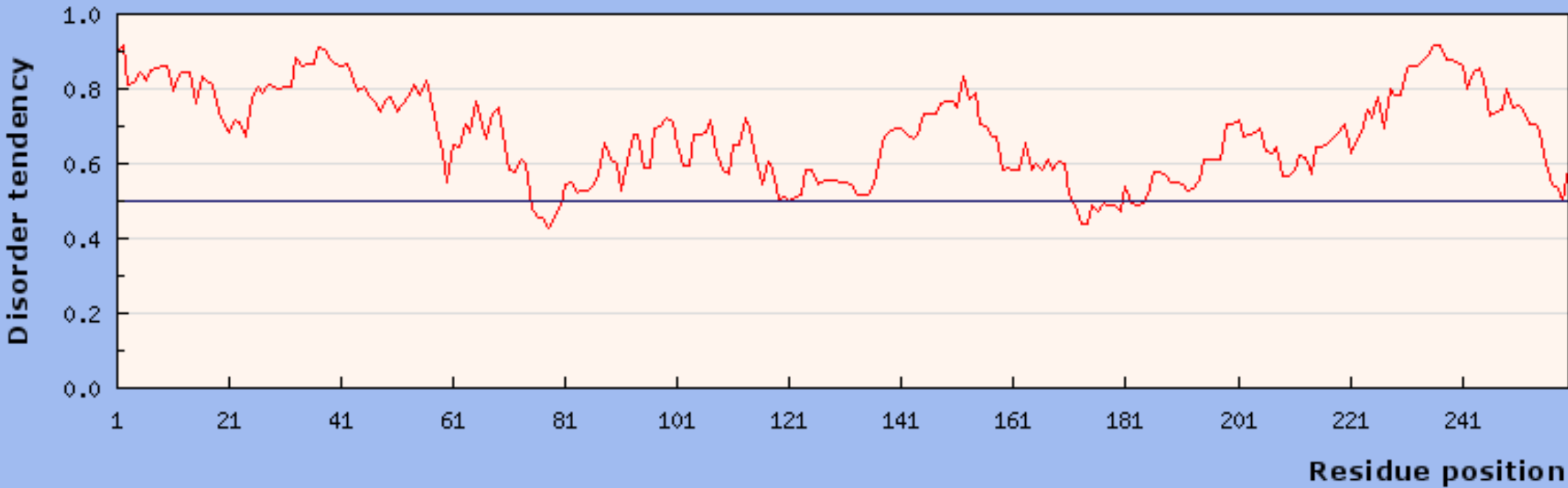
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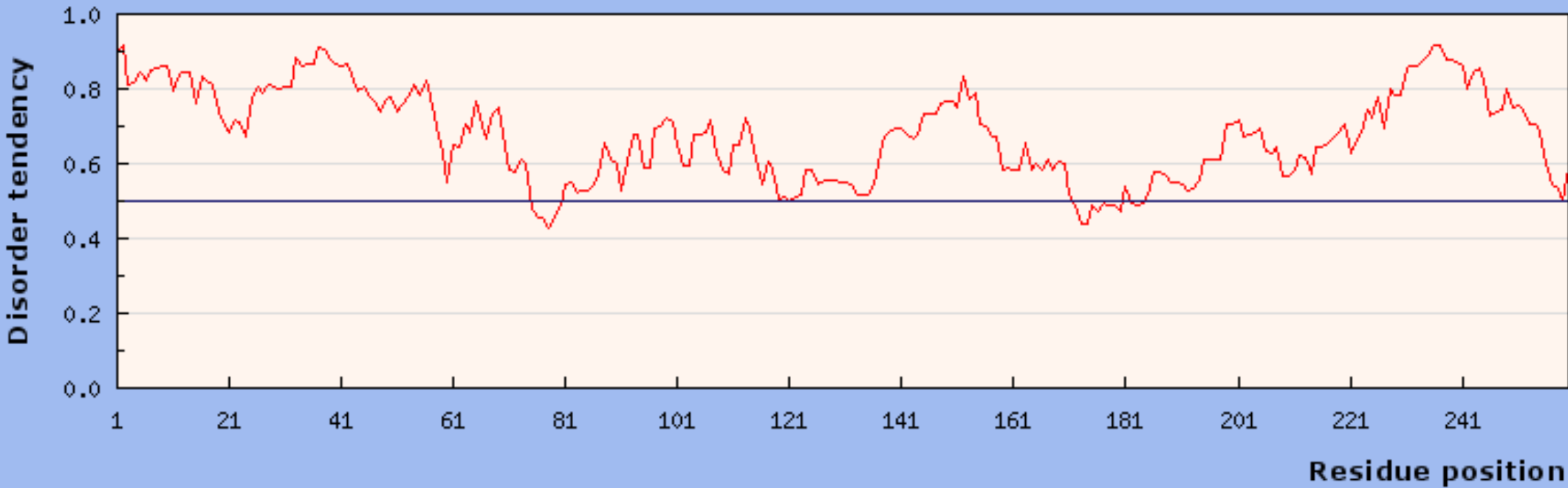
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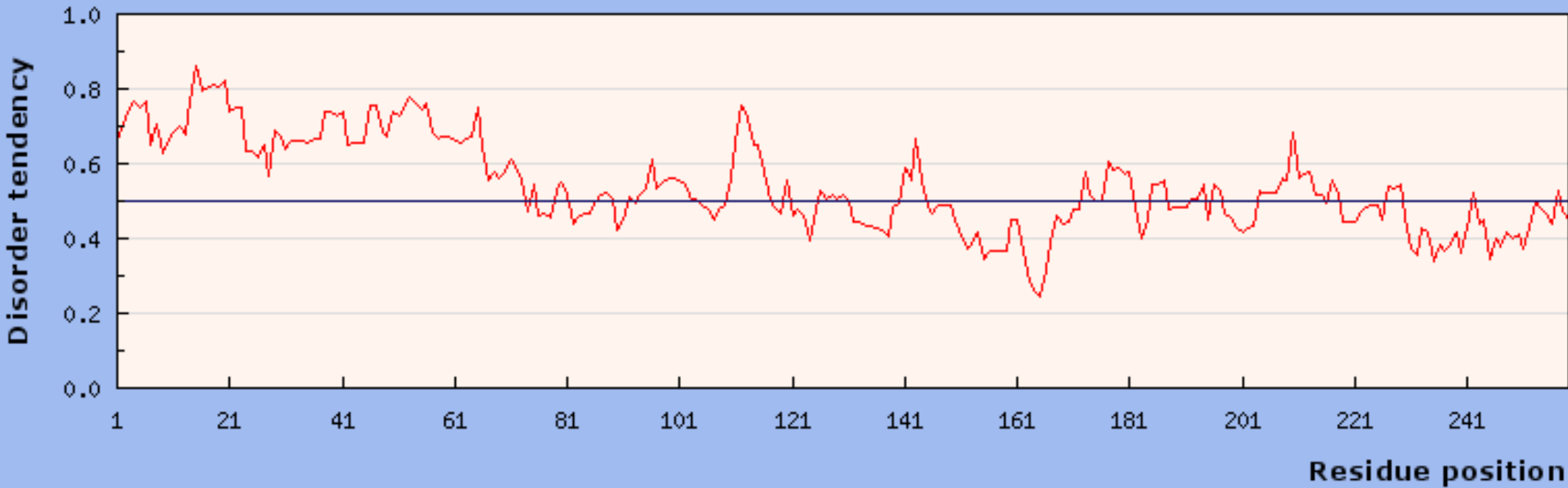
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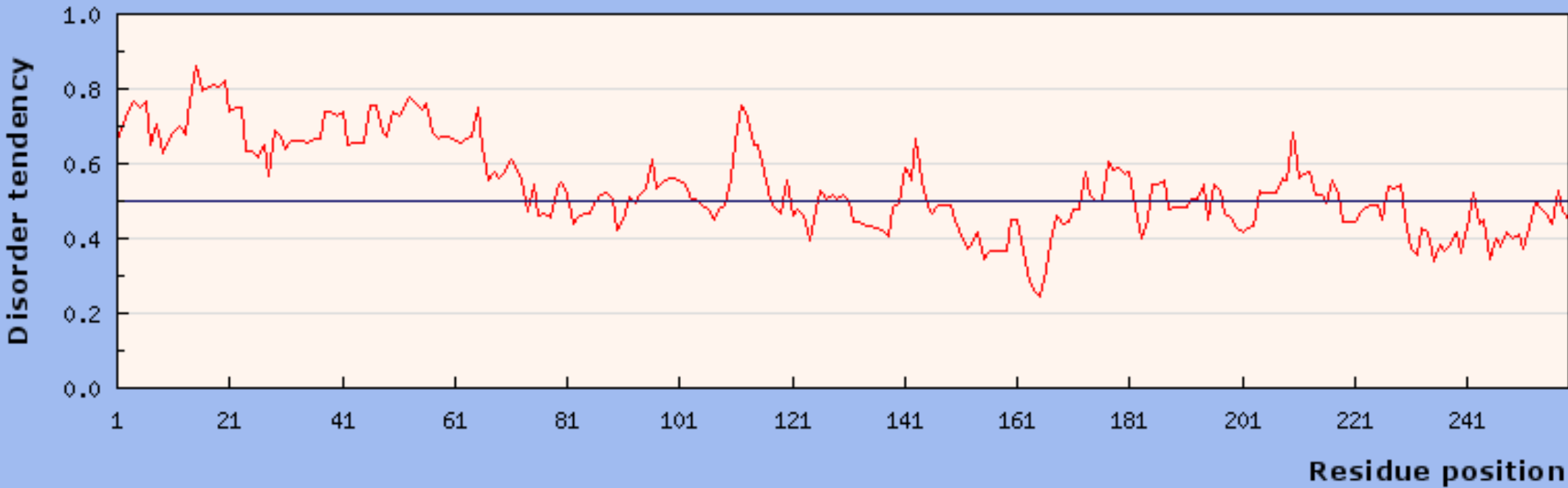
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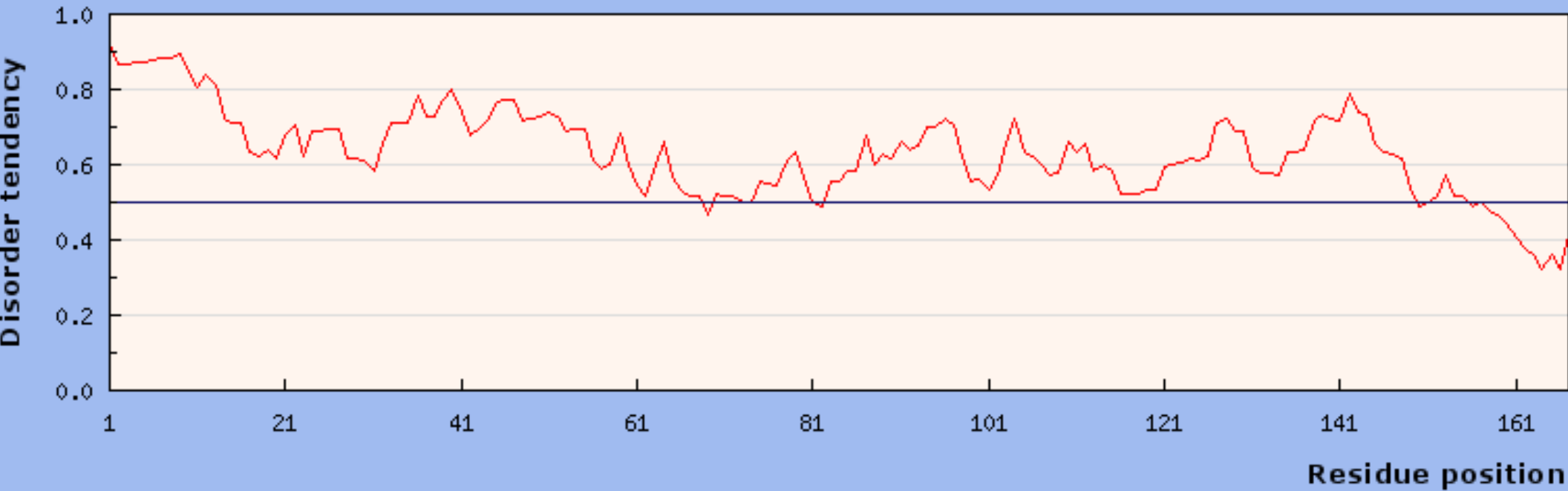
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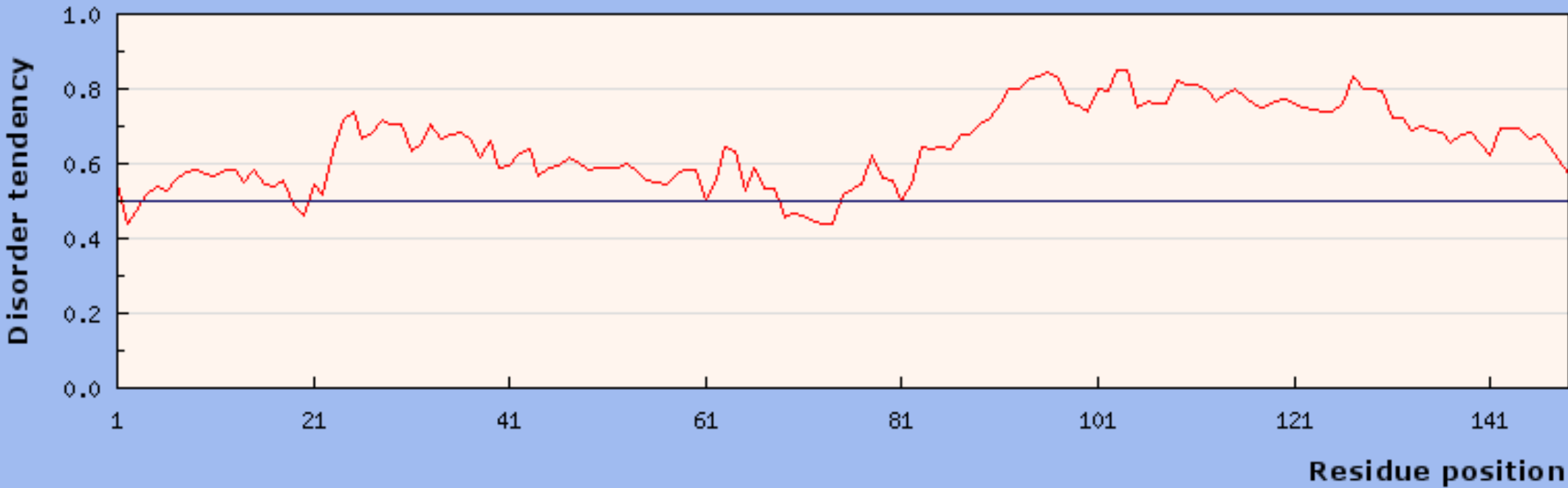
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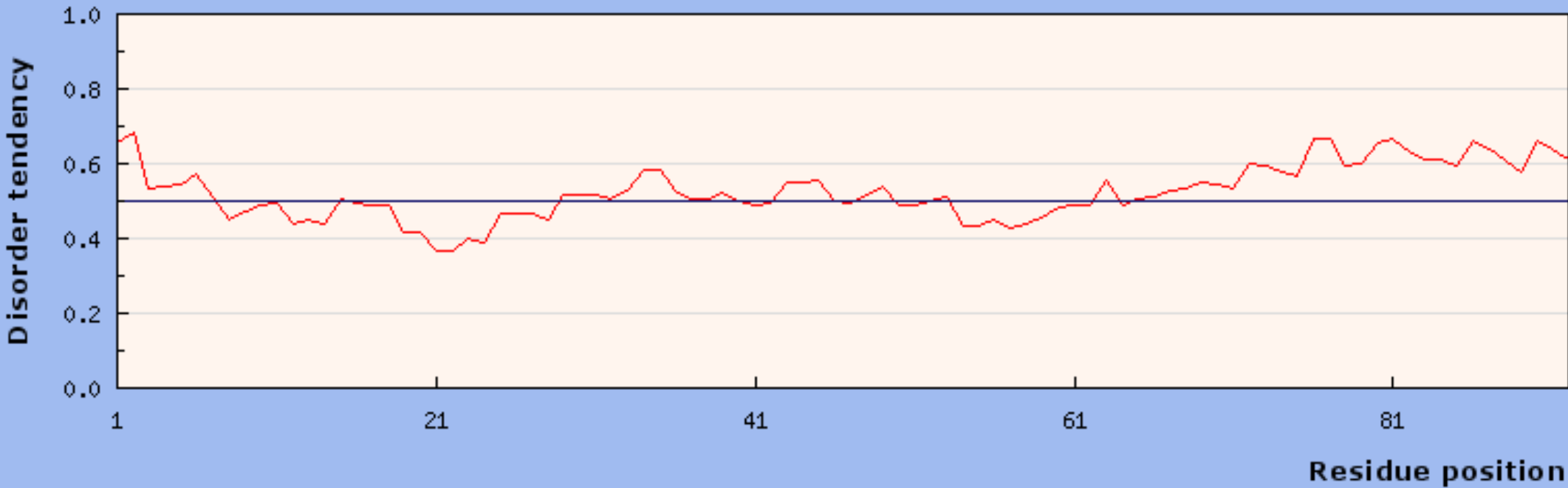
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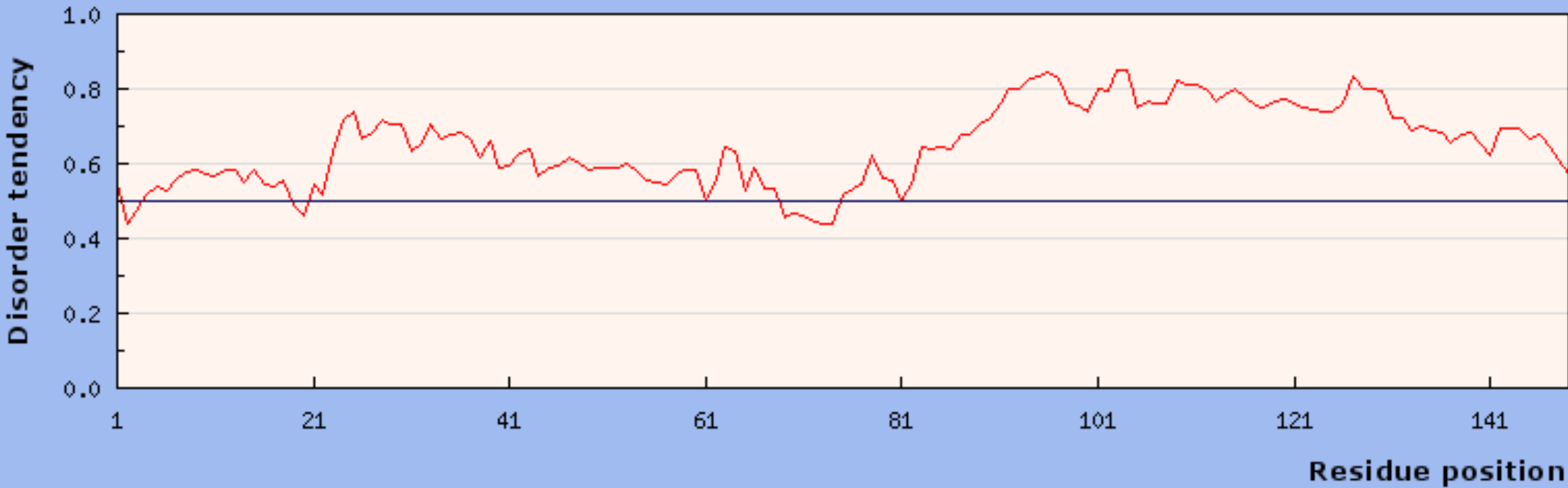
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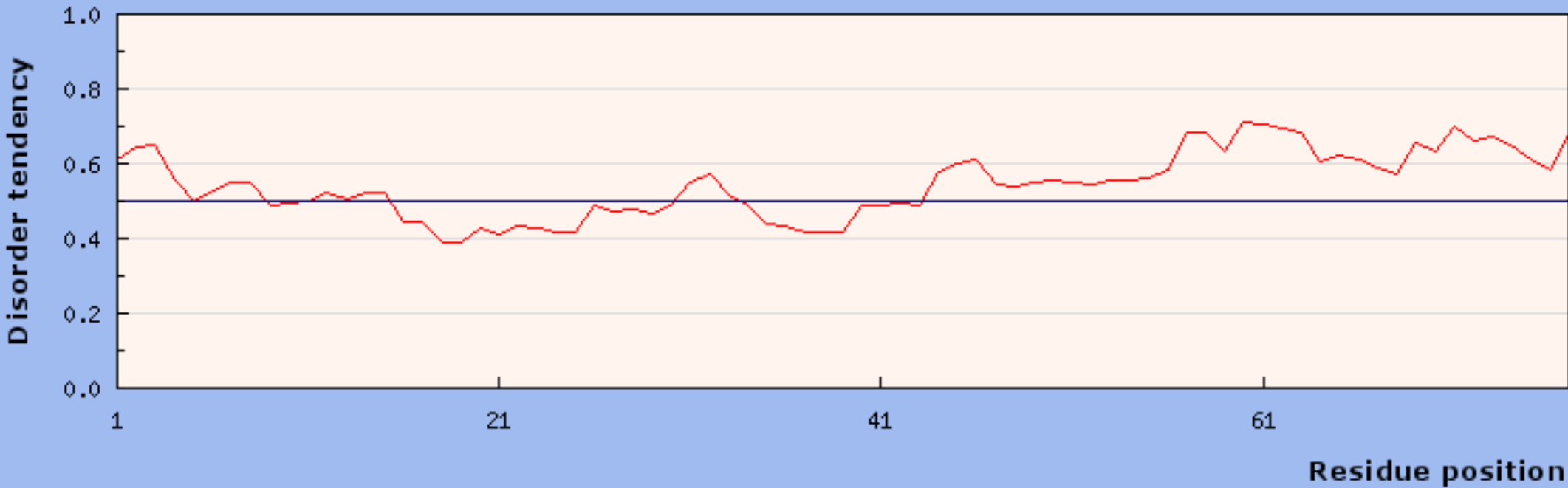
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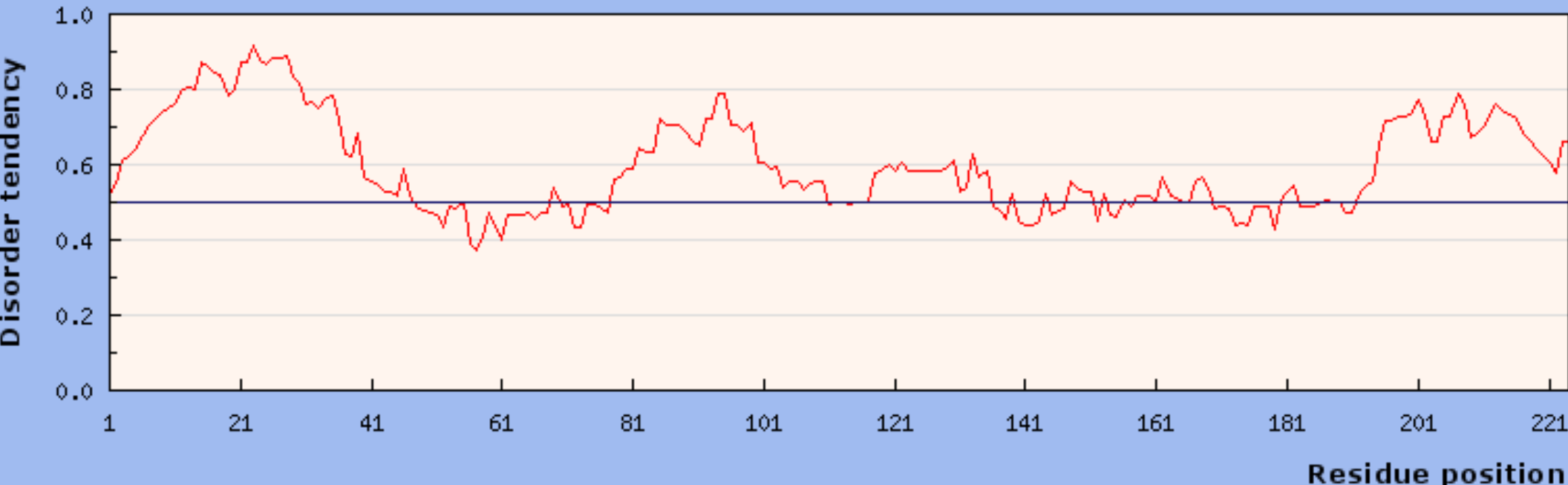
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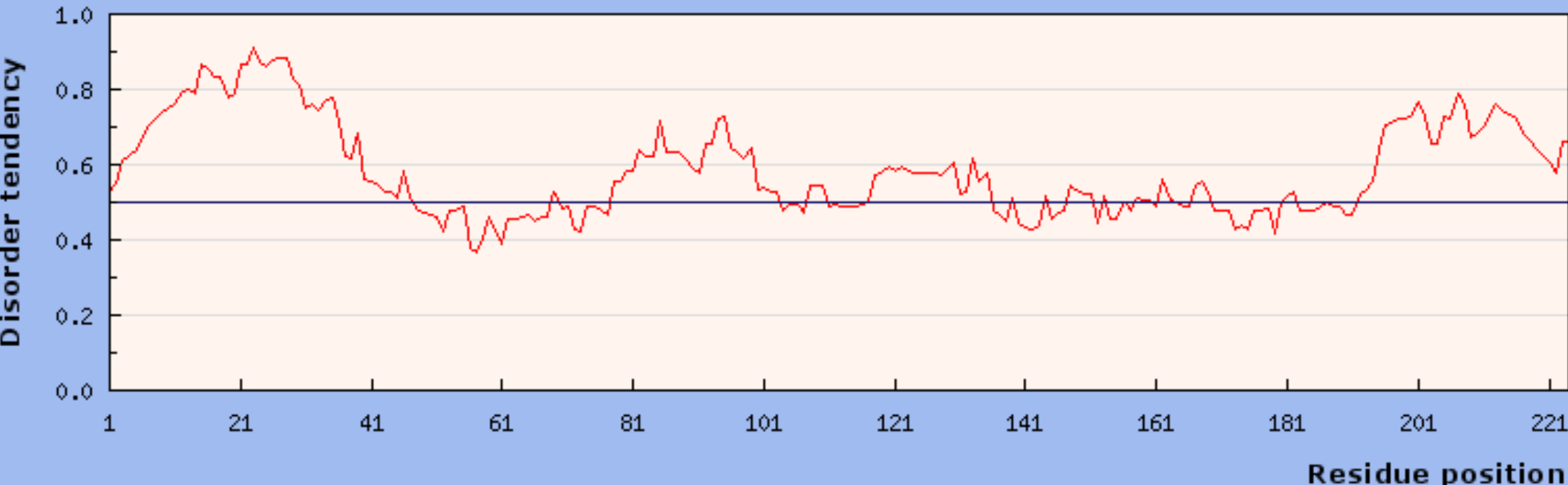
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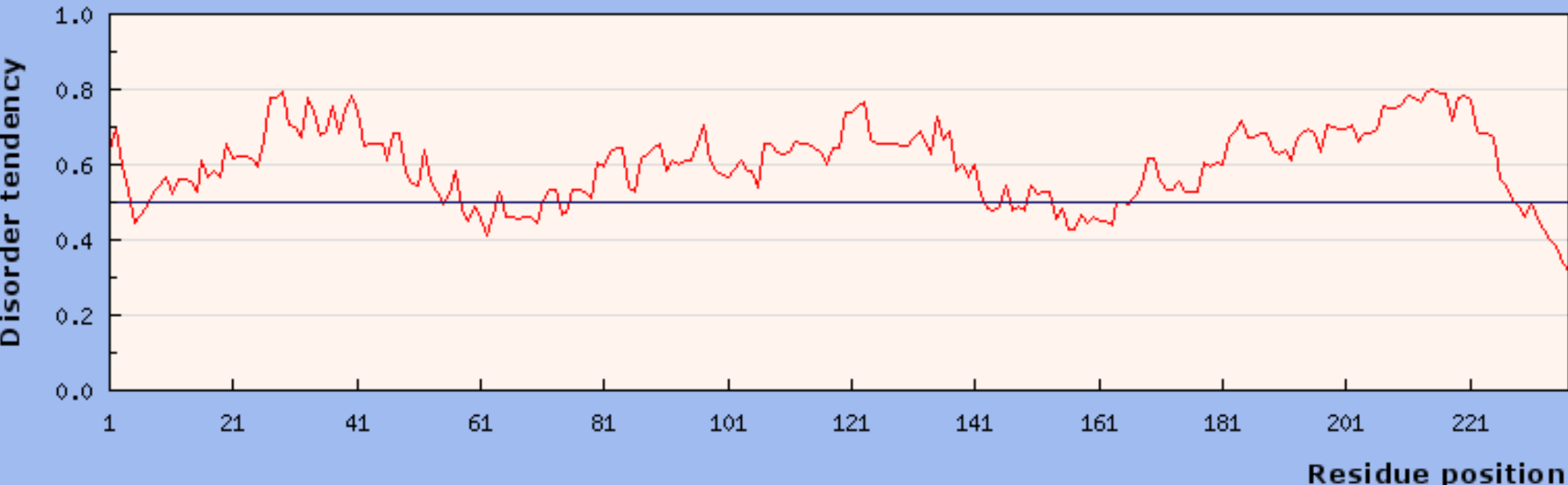
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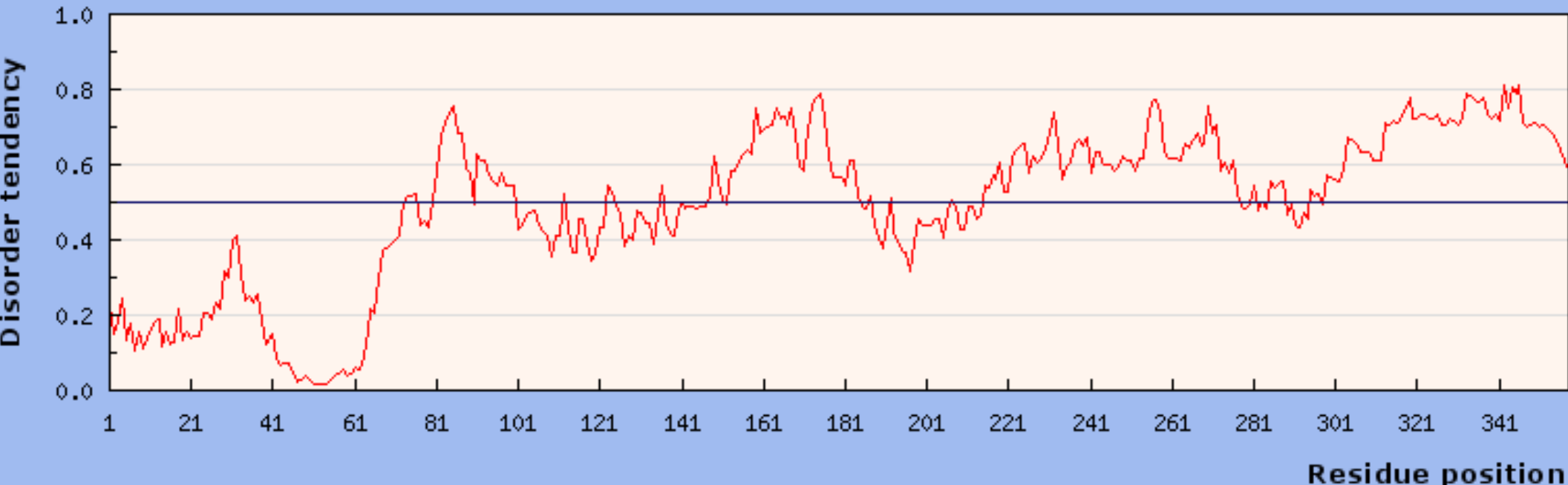
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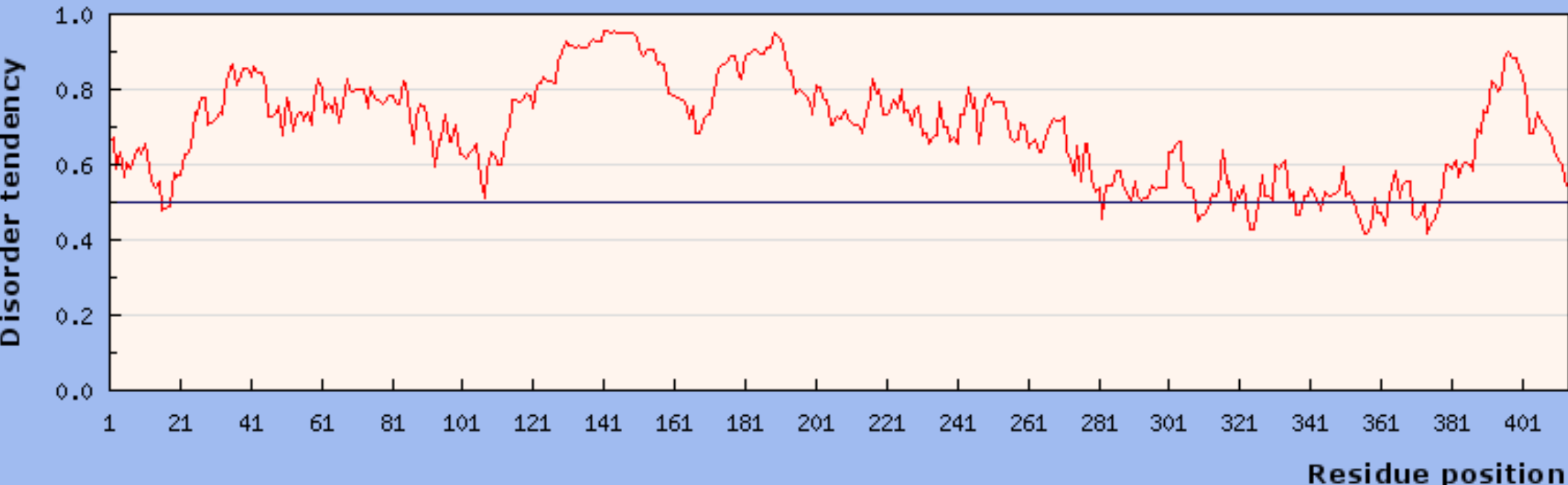
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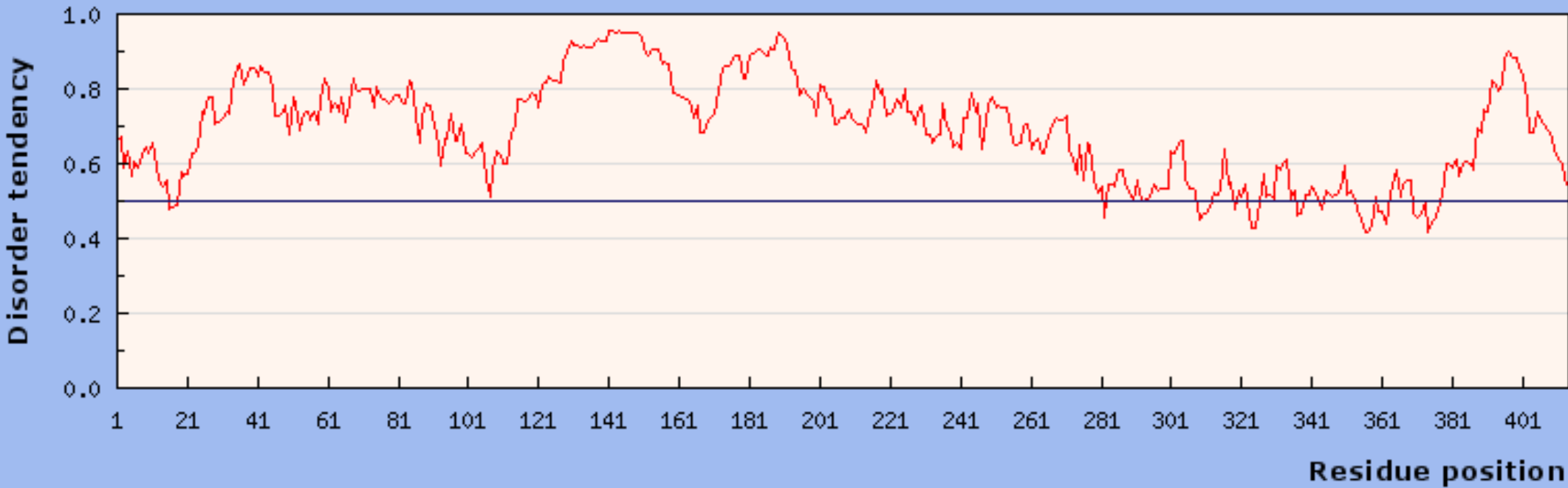
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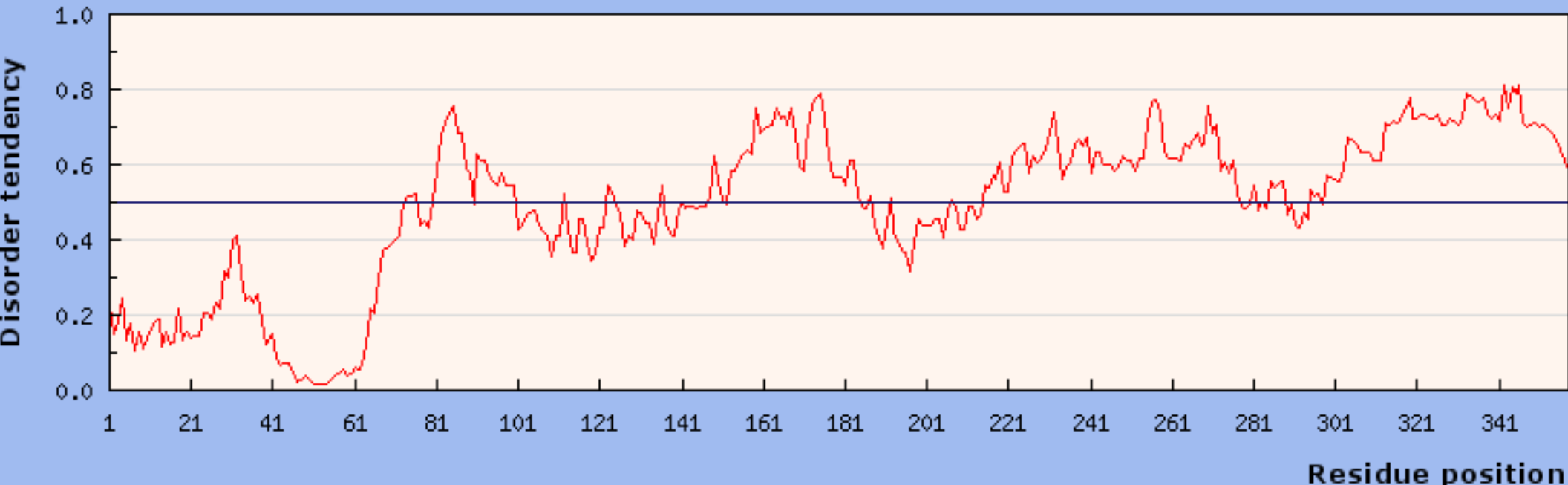
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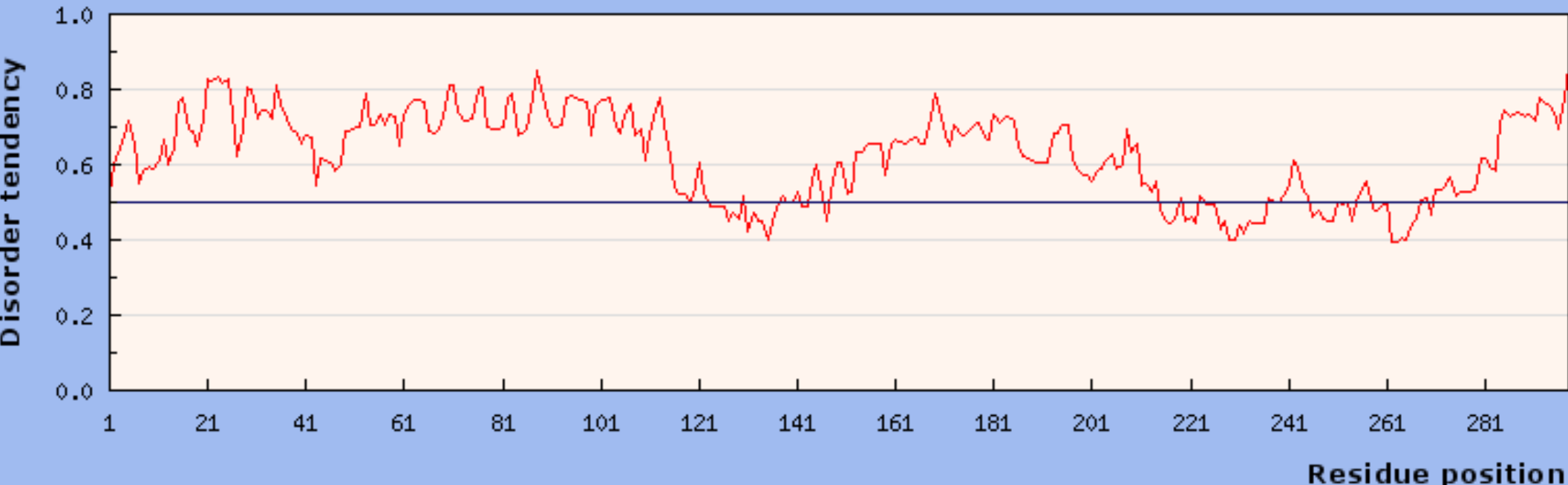
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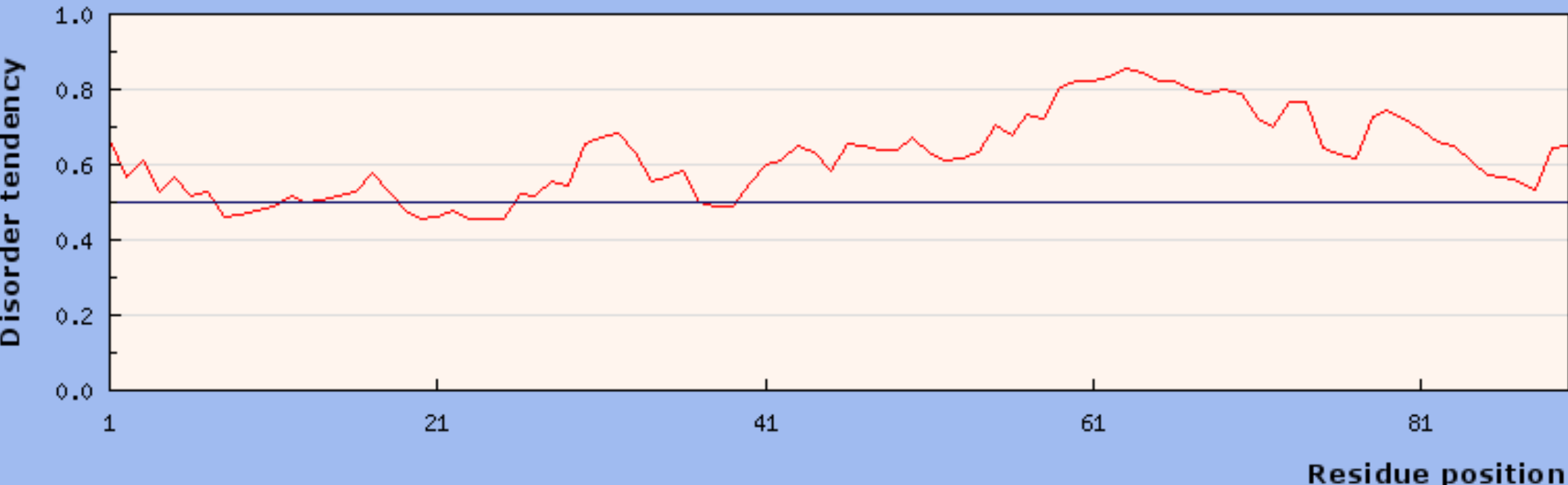
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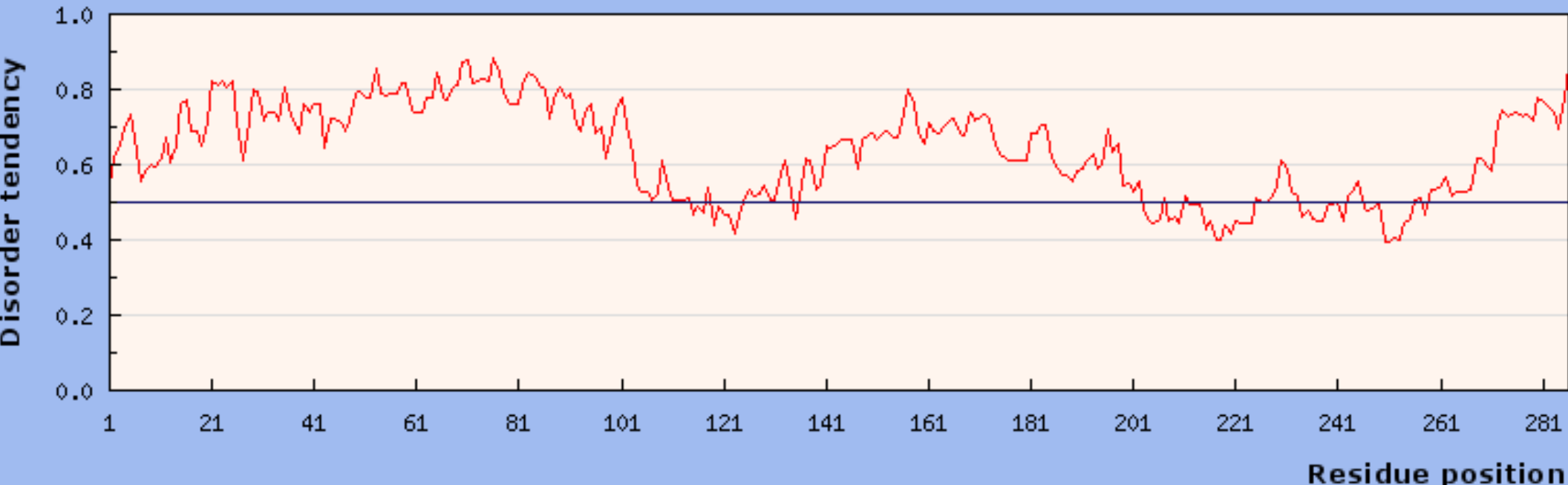
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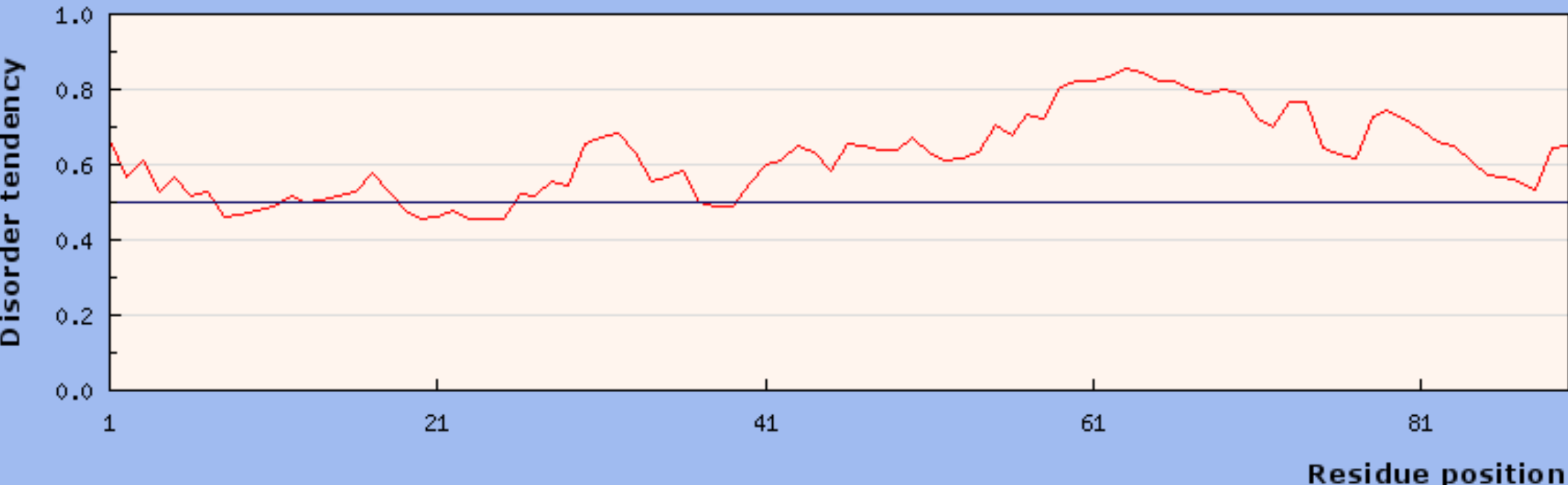
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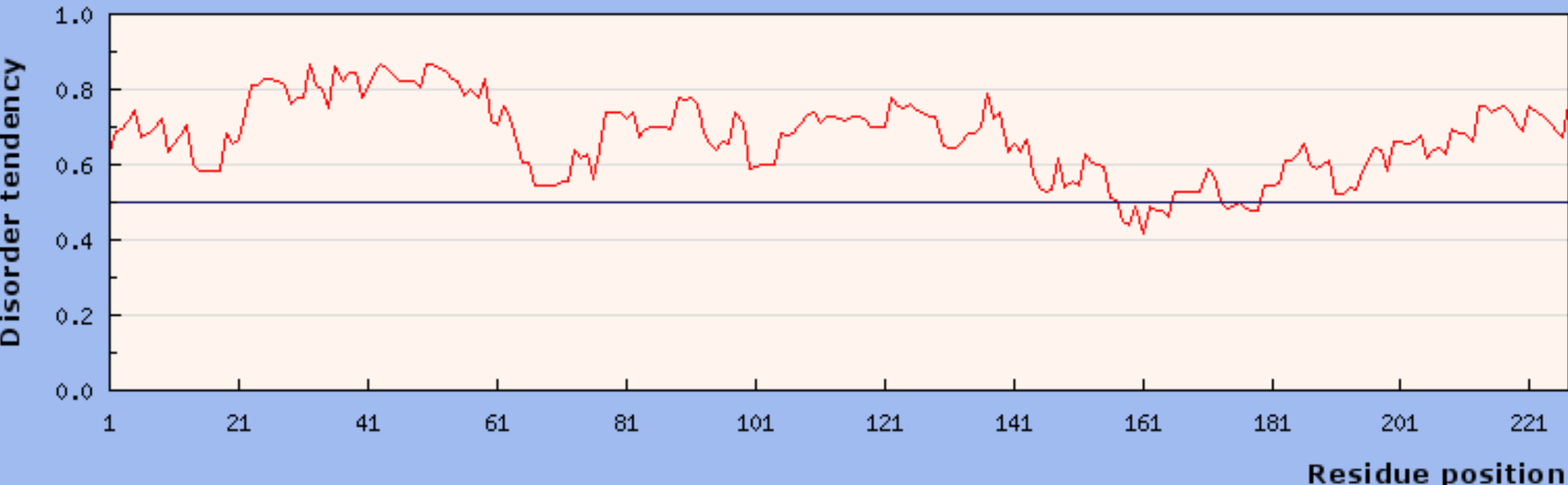
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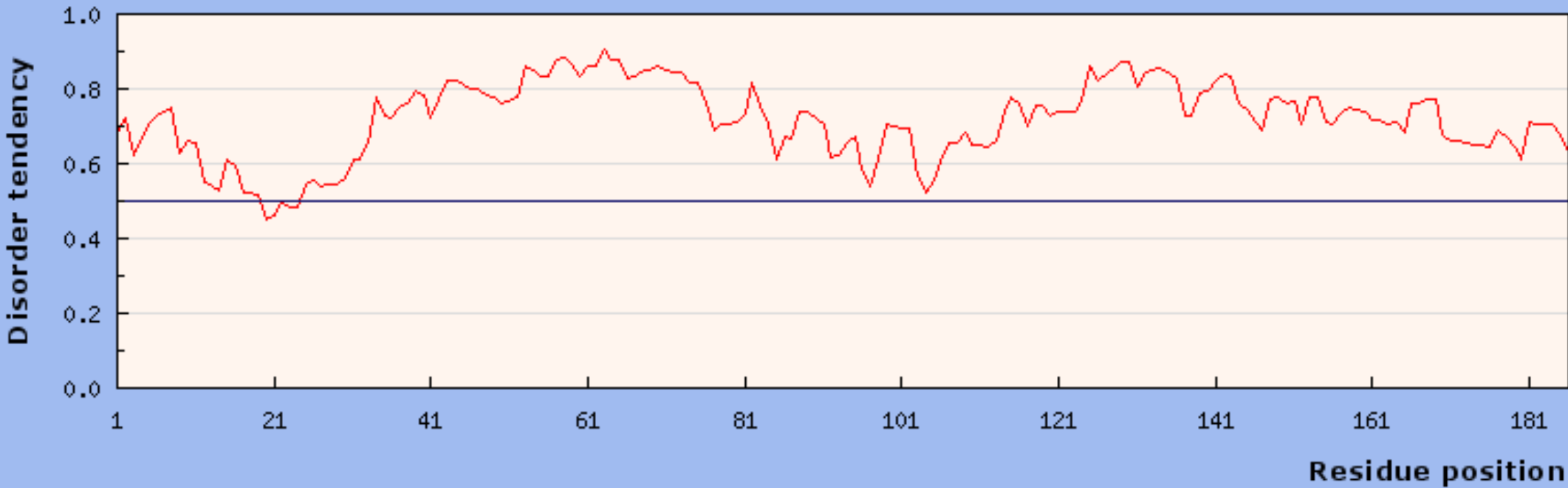
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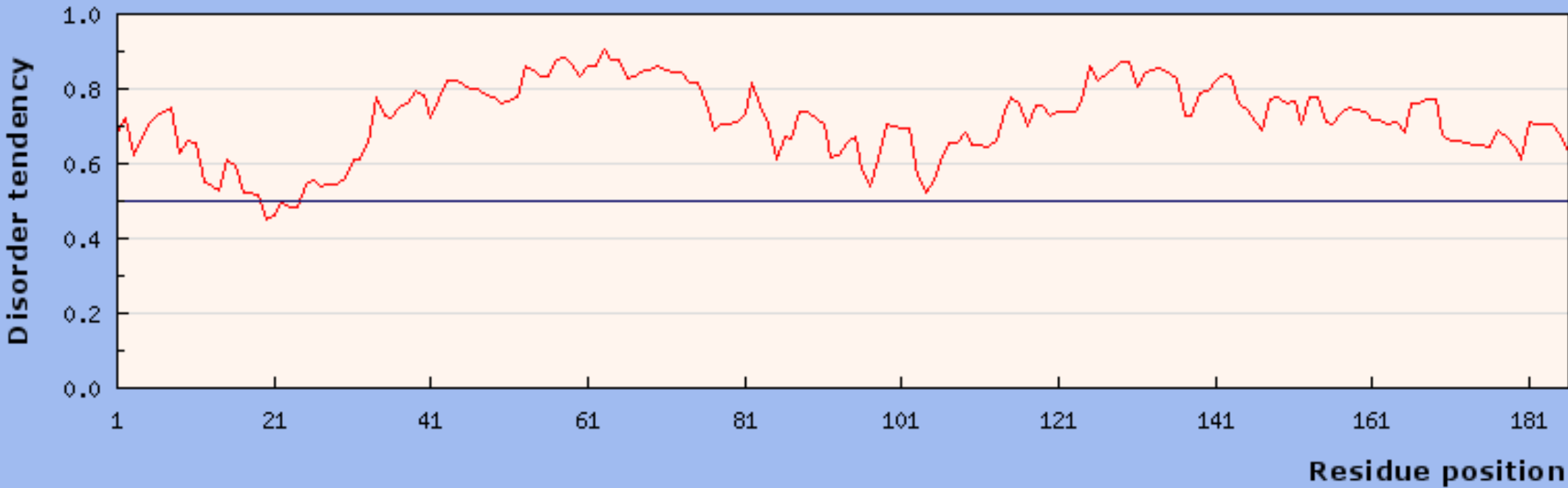
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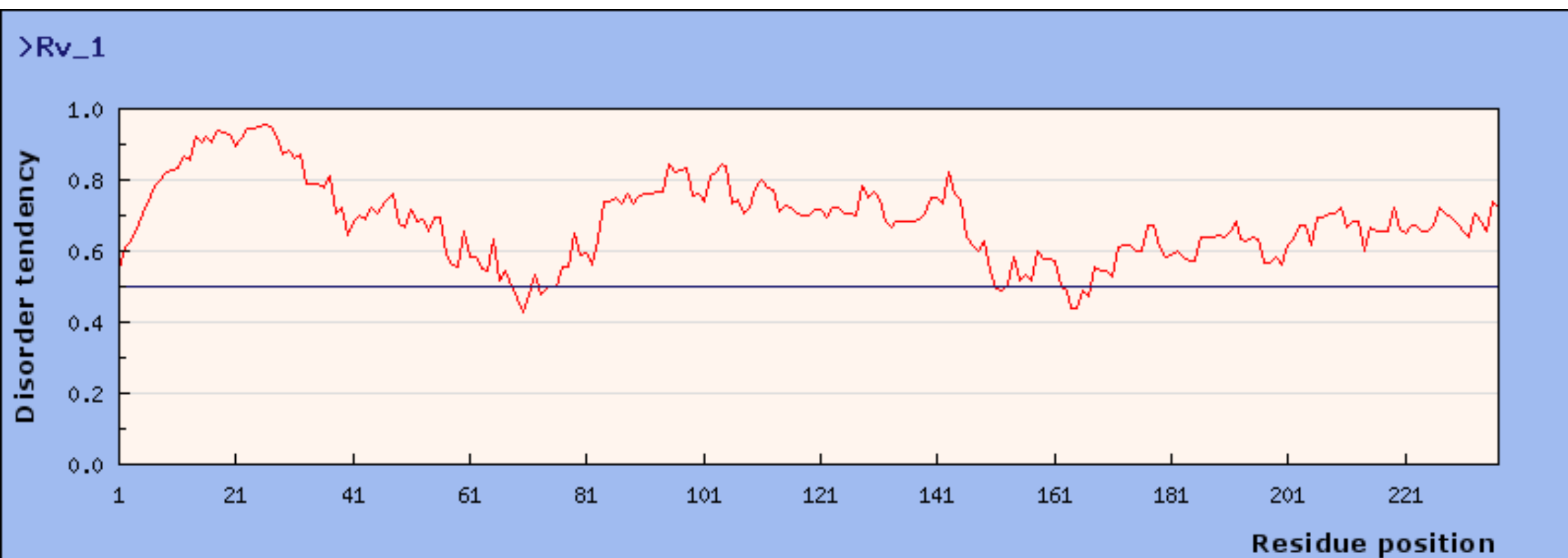


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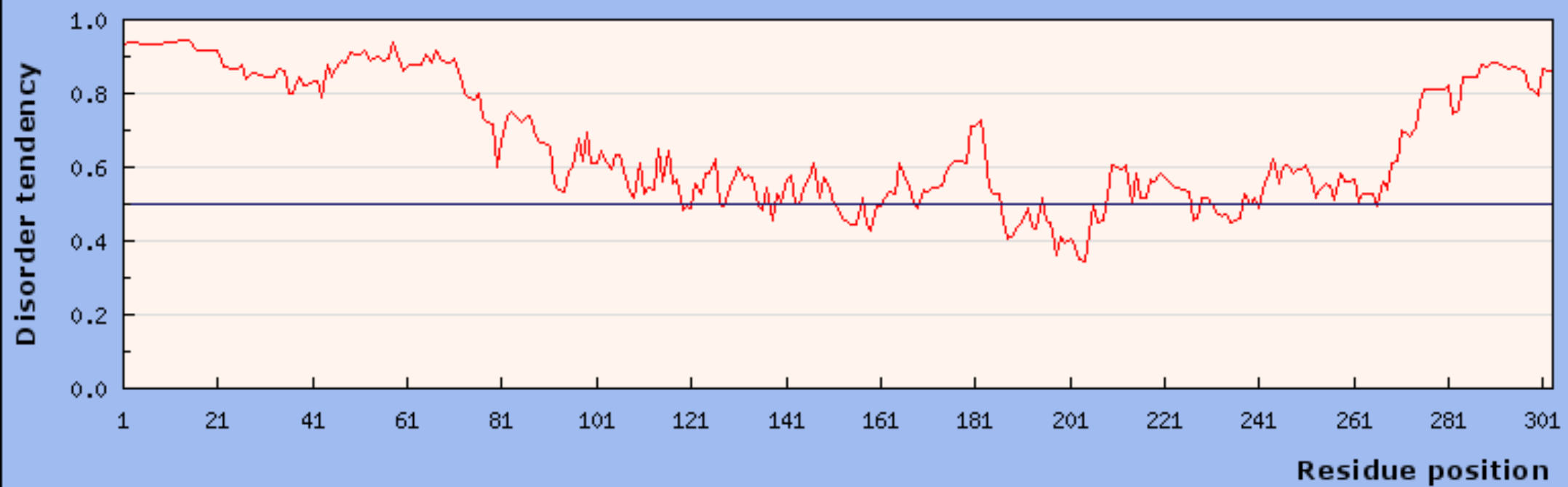


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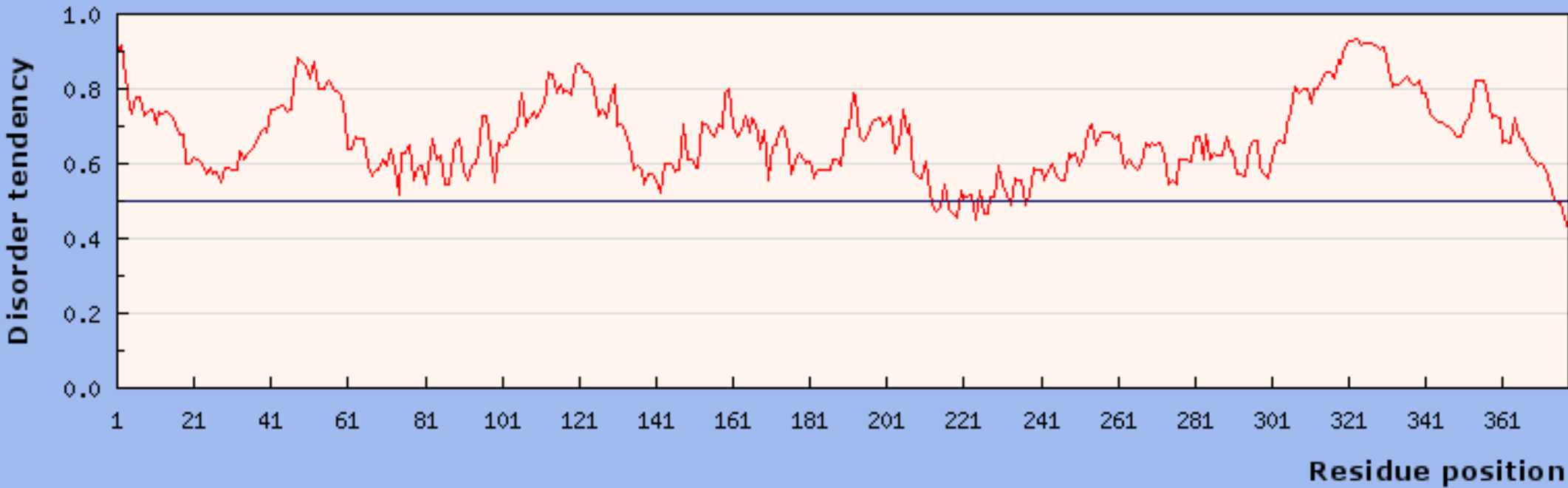




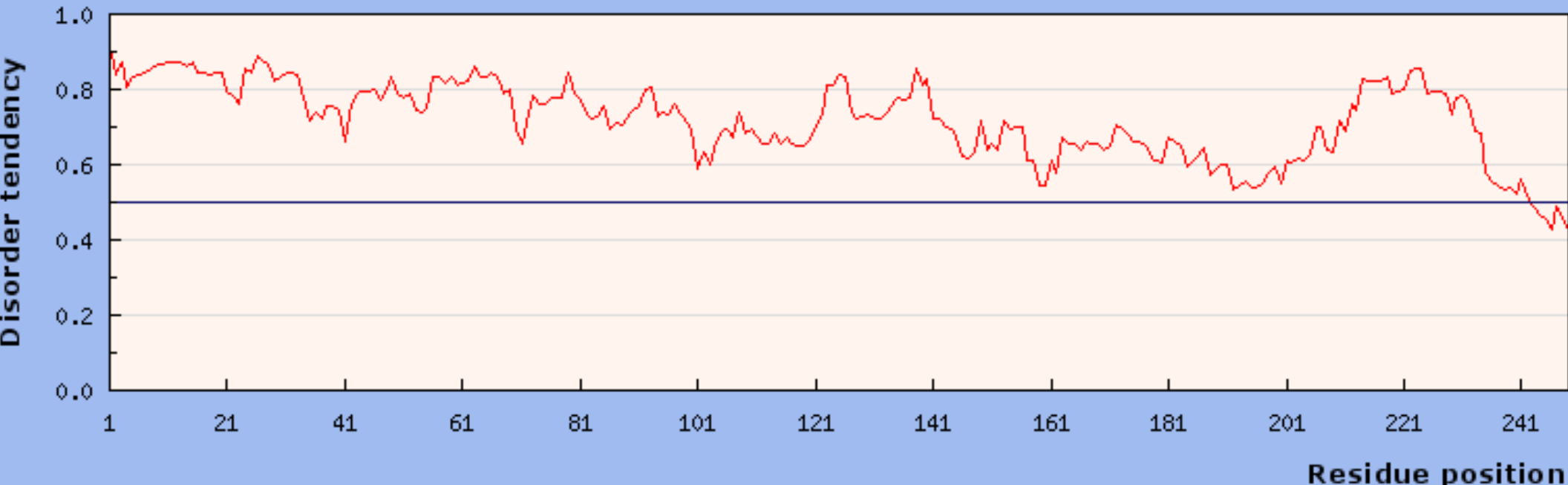
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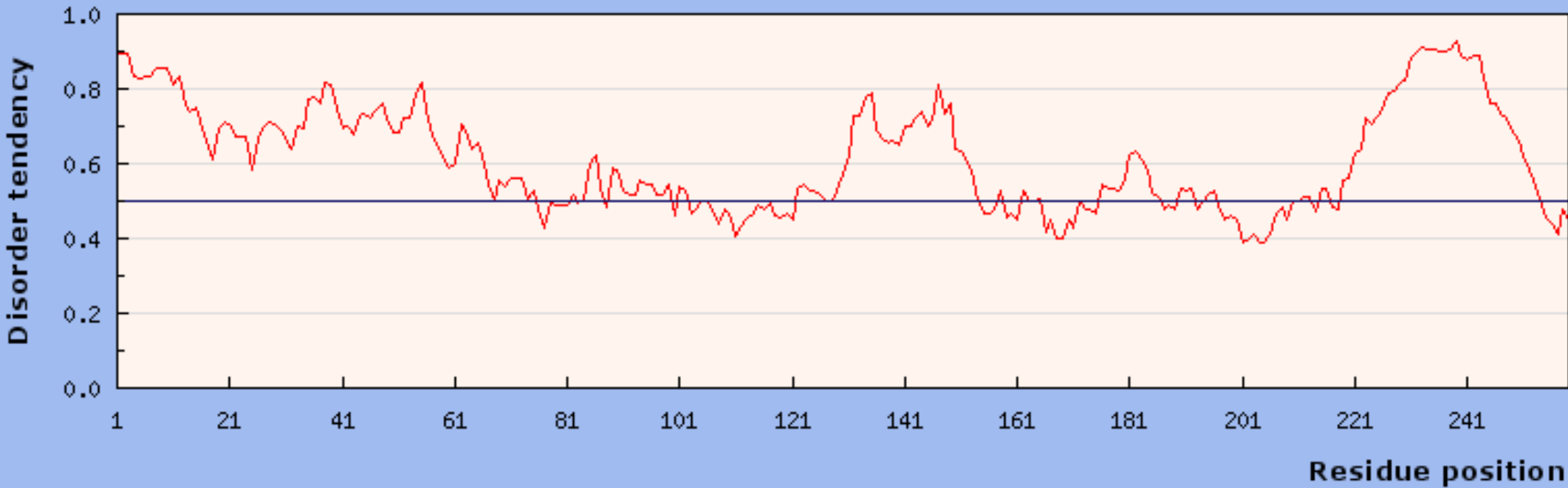
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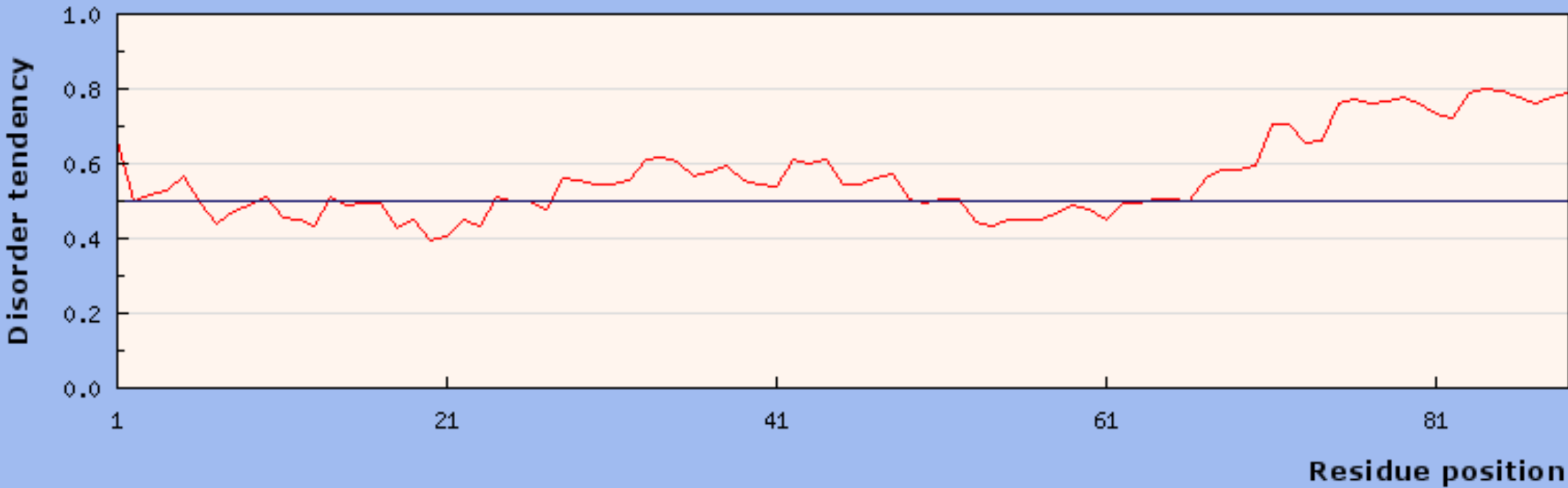
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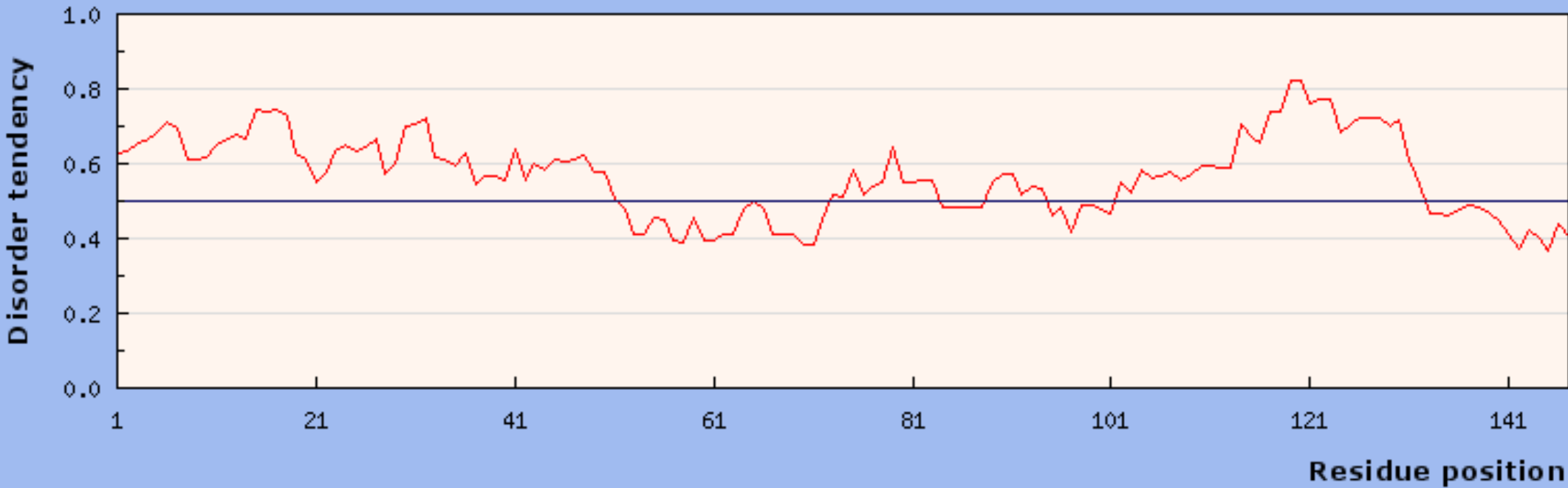
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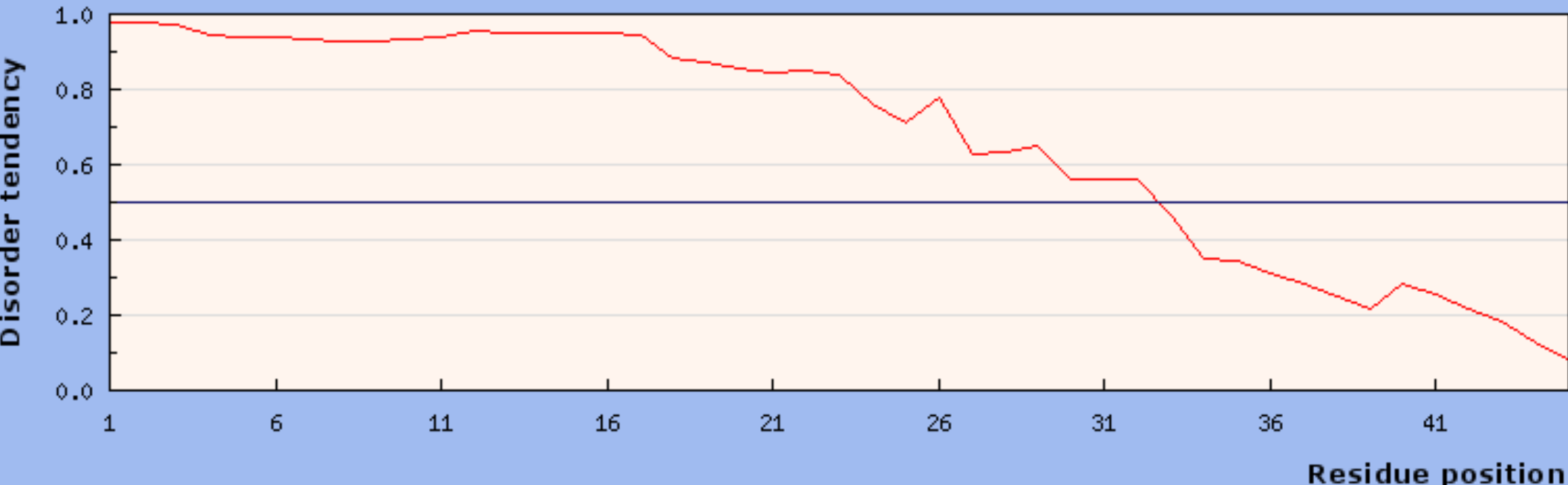
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MAHS proteins

IUPRED^{1,2} Disordered Protein Predictions

1. The Pairwise Energy Content Estimated from Amino Acid Composition Discriminates between Folded and Intrinsically Unstructured Proteins

Zsuzsanna Dosztányi, Veronika Csizmók, Péter Tompa and István Simon

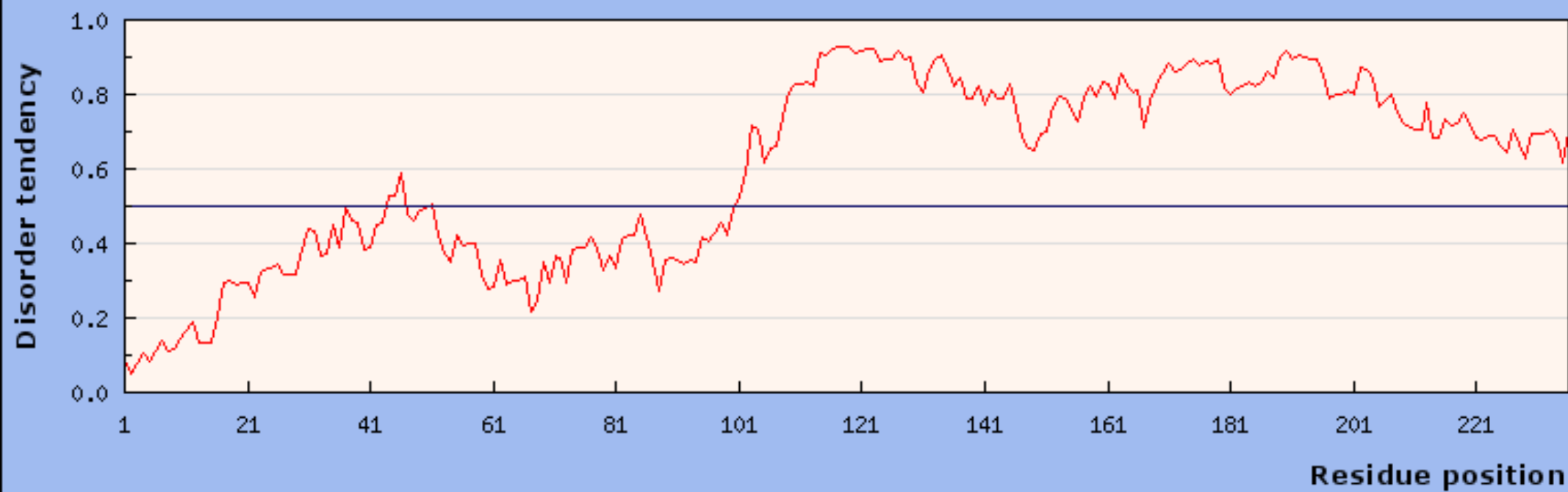
J. Mol. Biol. (2005) 347, 827-839.

2. IUPred: web server for the prediction of intrinsically unstructured regions of proteins based on estimated energy content

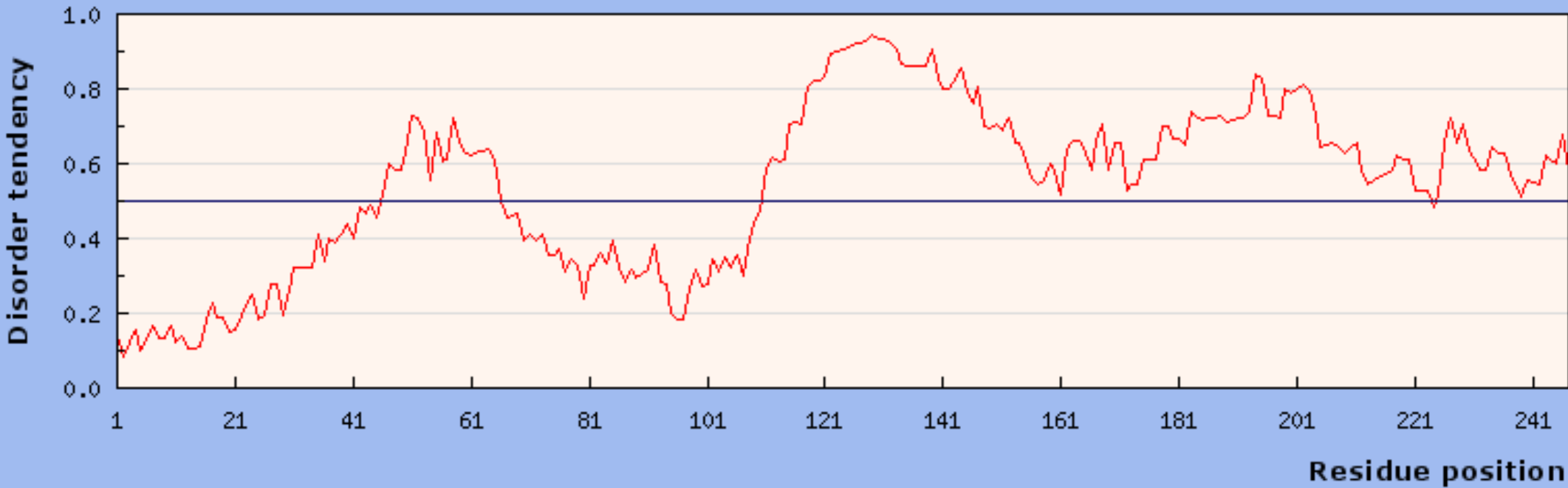
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Bioinformatics (2005) 21, 3433-3434.

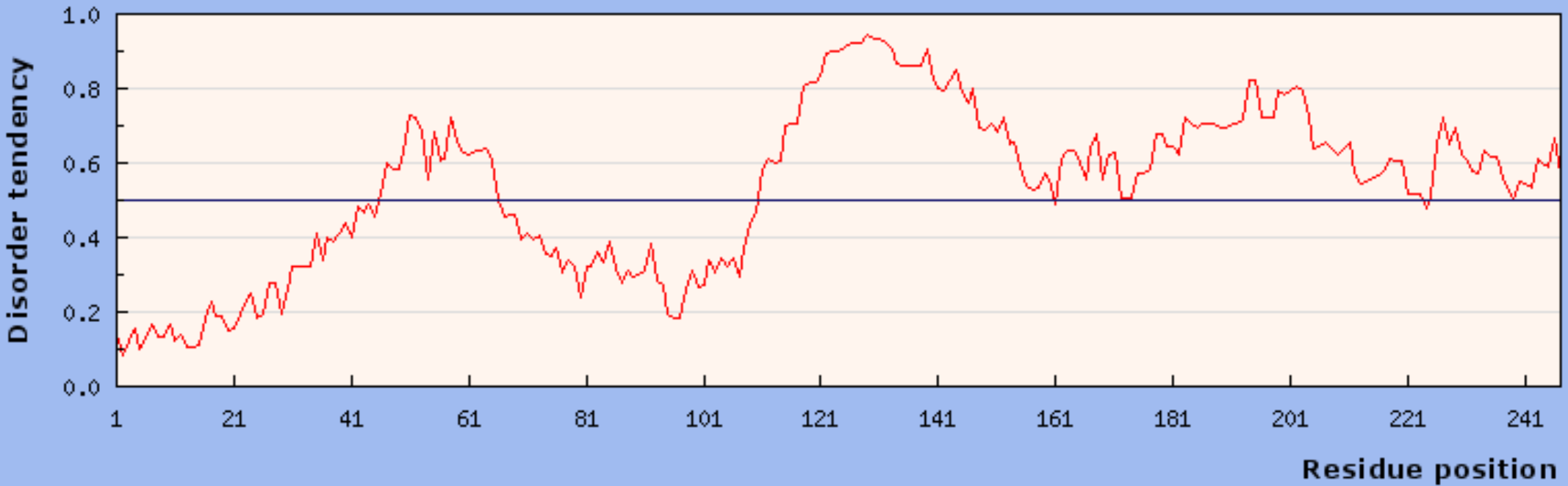
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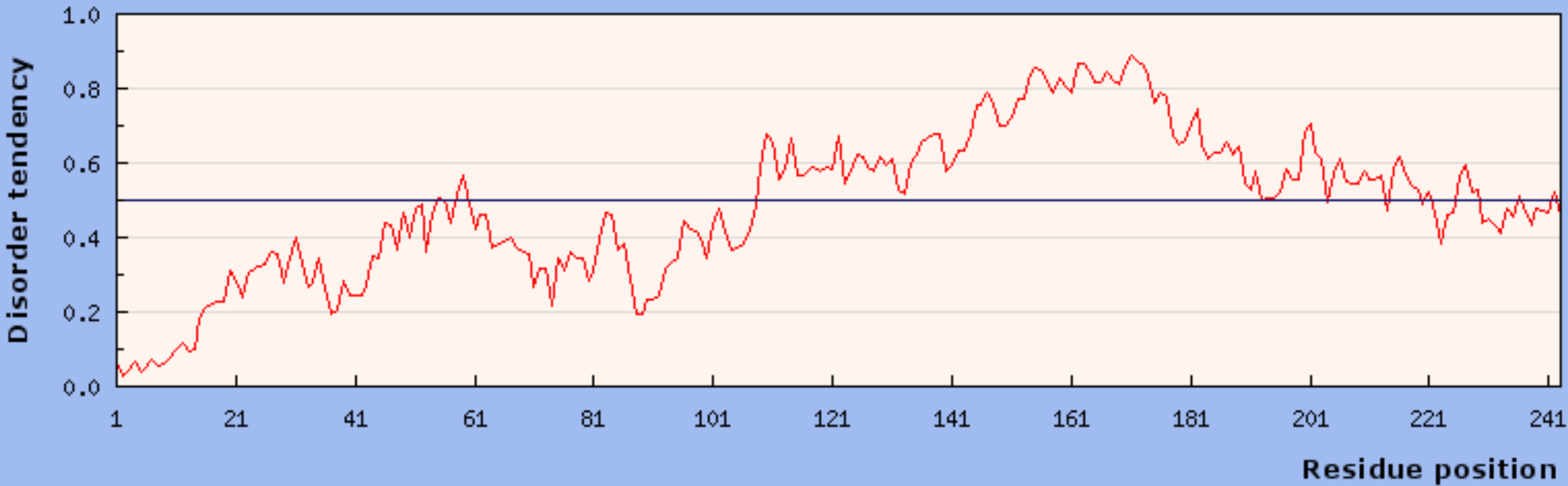
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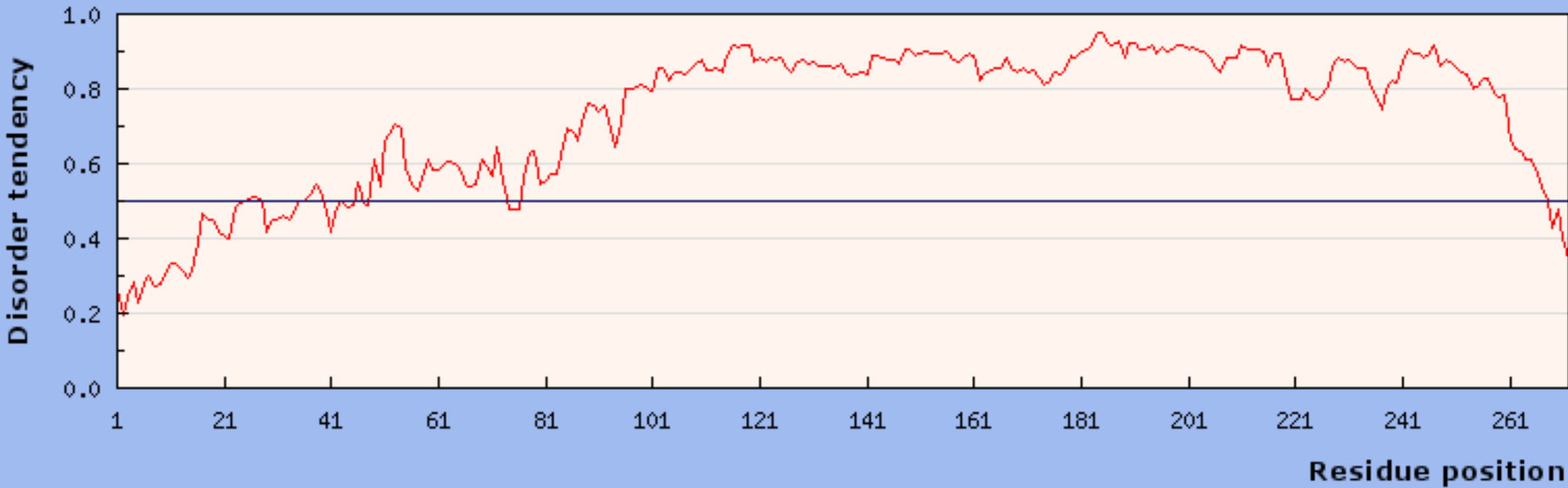
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SAHS proteins

IUPRED^{1,2} Disordered Protein Predictions

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Zsuzsanna Dosztányi, Veronika Csizmók, Péter Tompa and István Simon

J. Mol. Biol. (2005) 347, 827-839.

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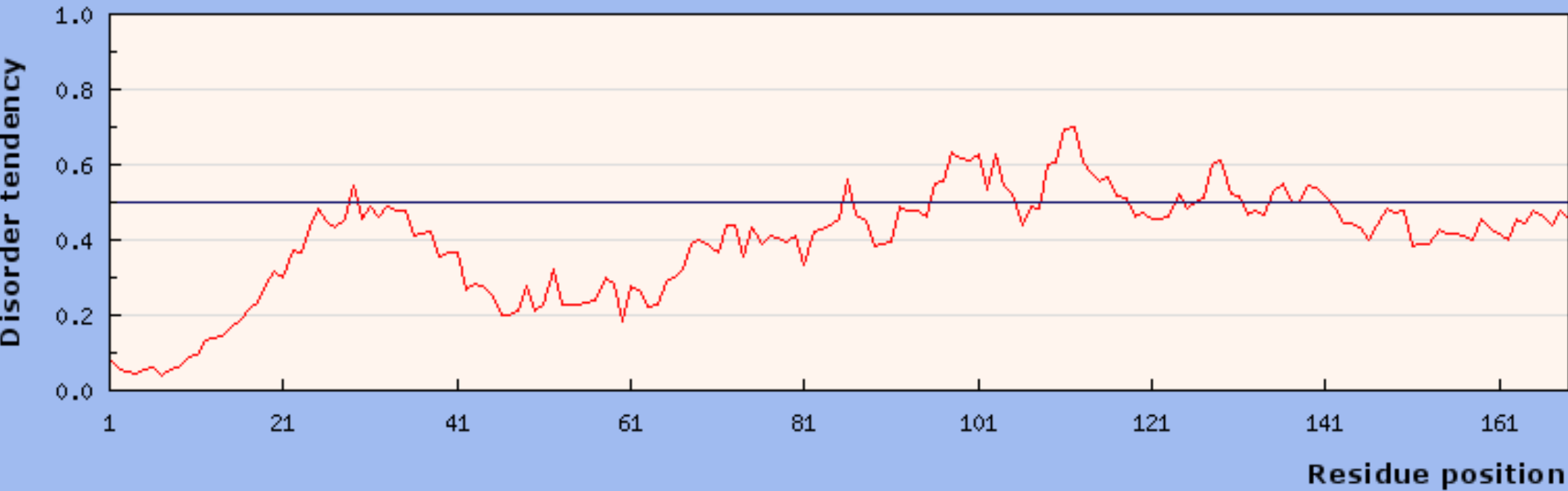
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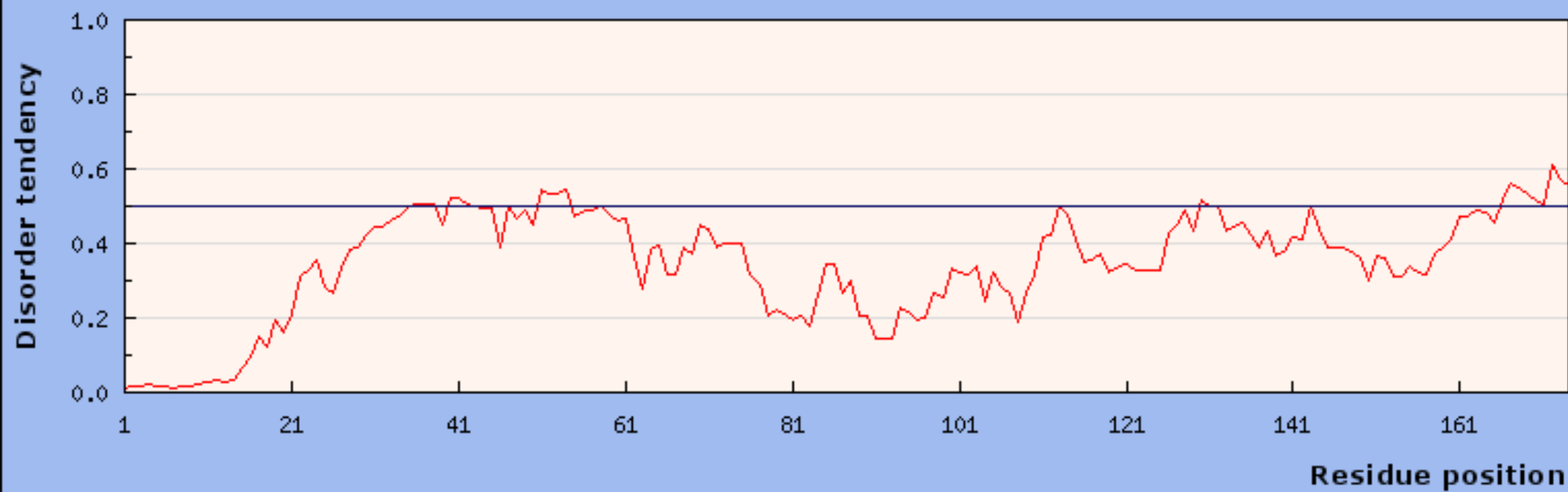
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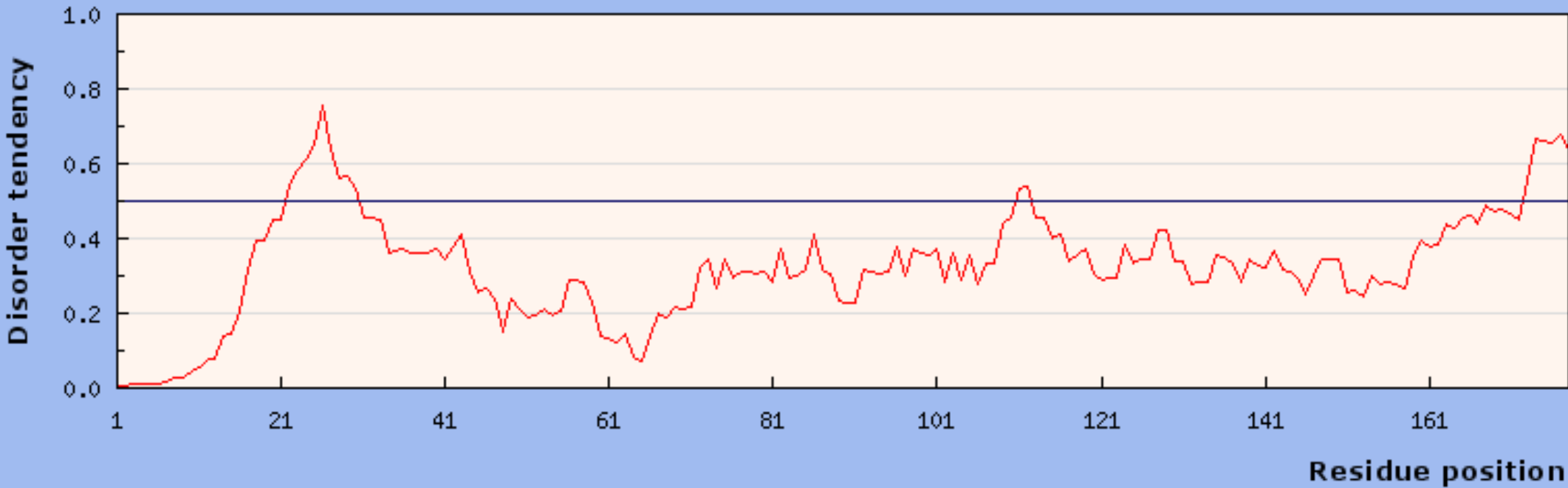
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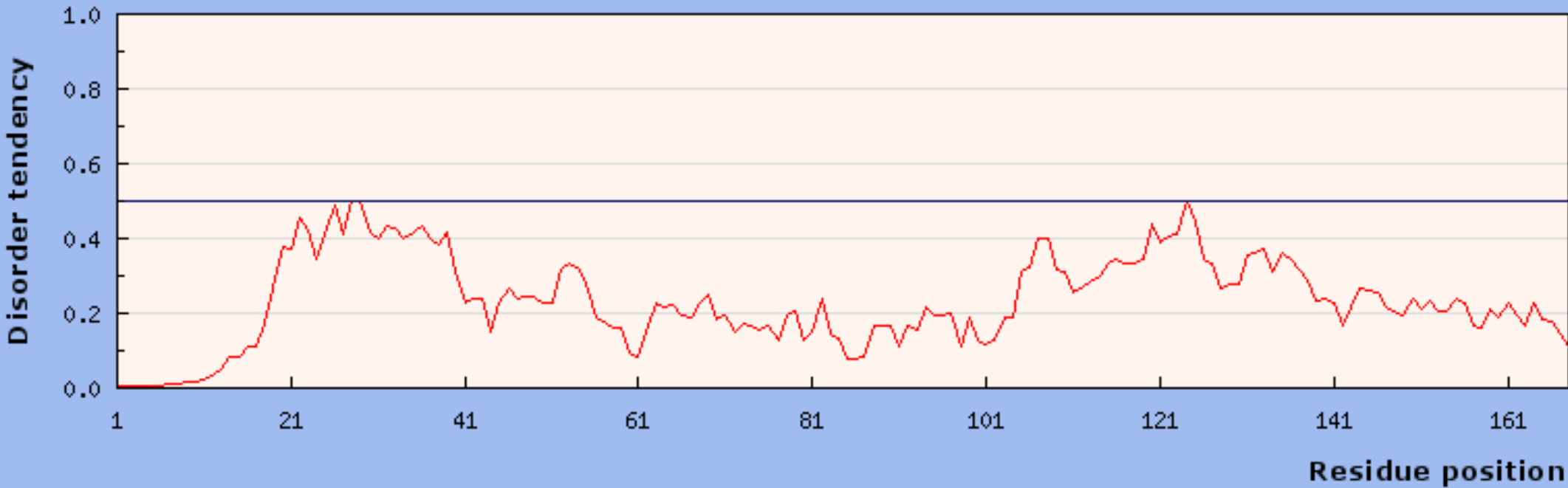
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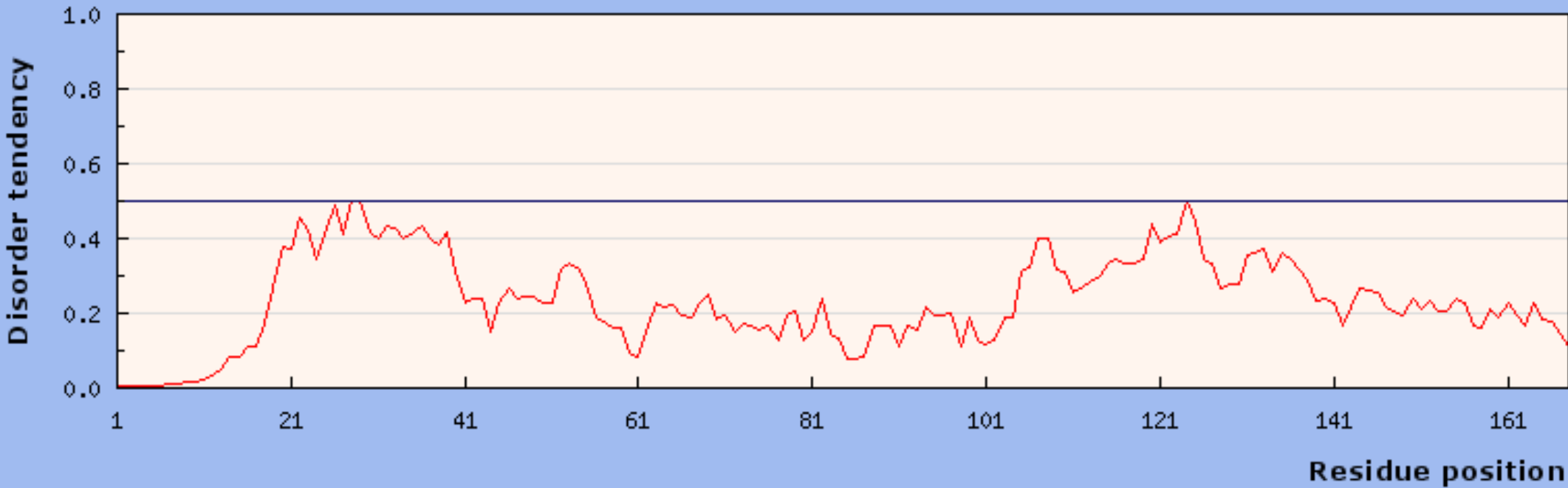
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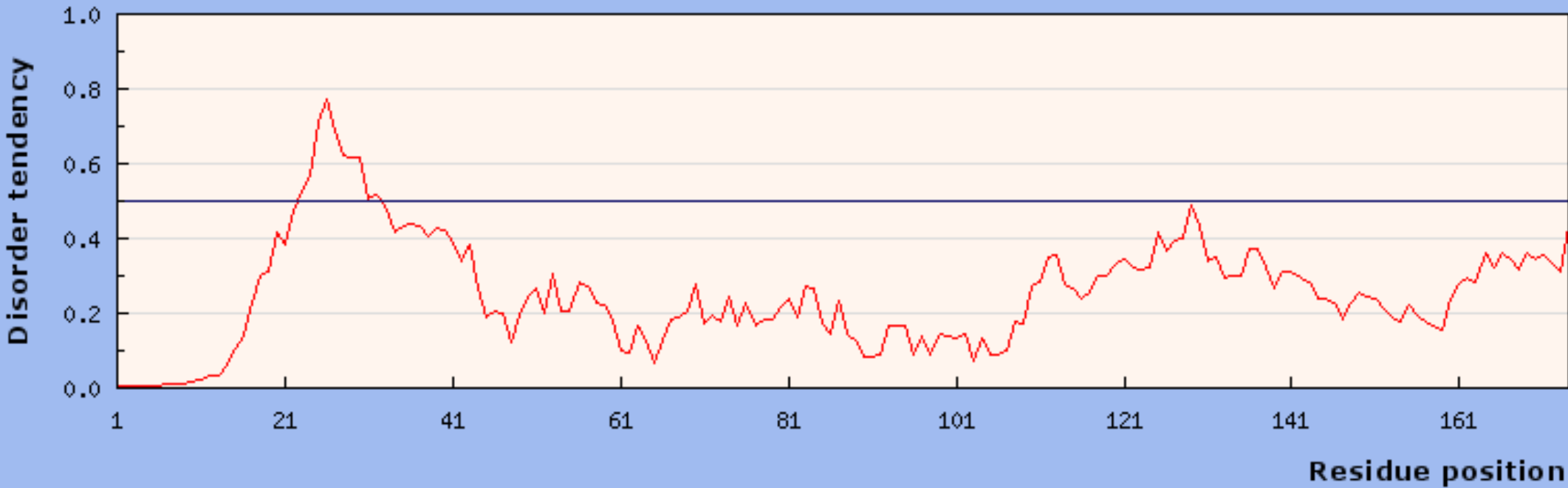
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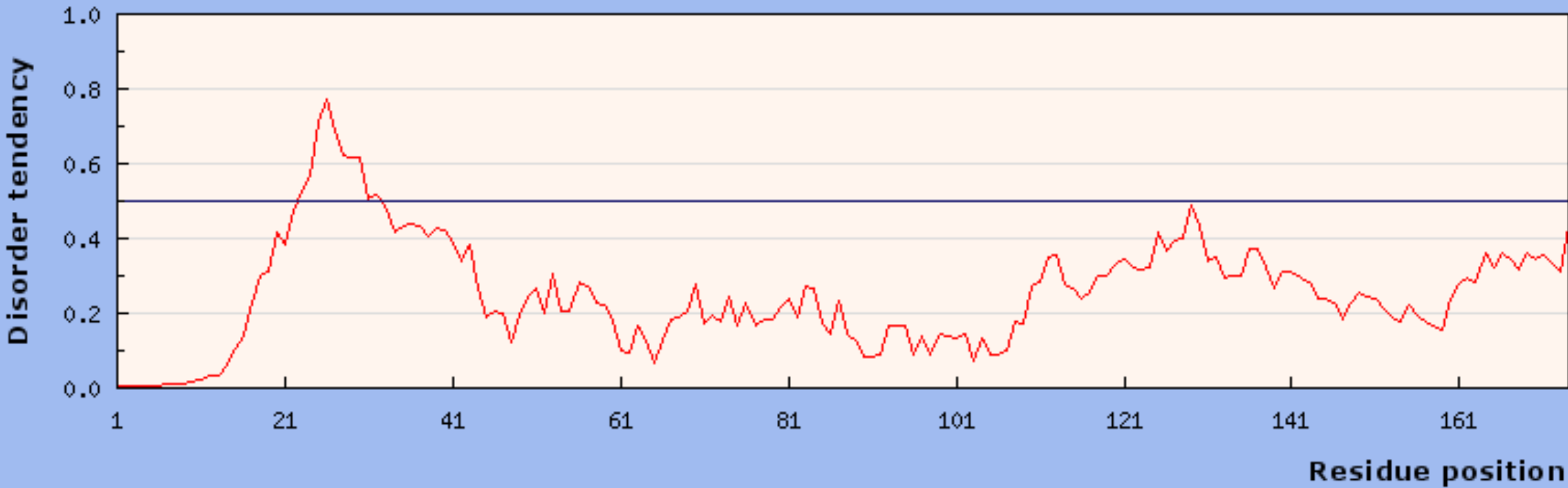
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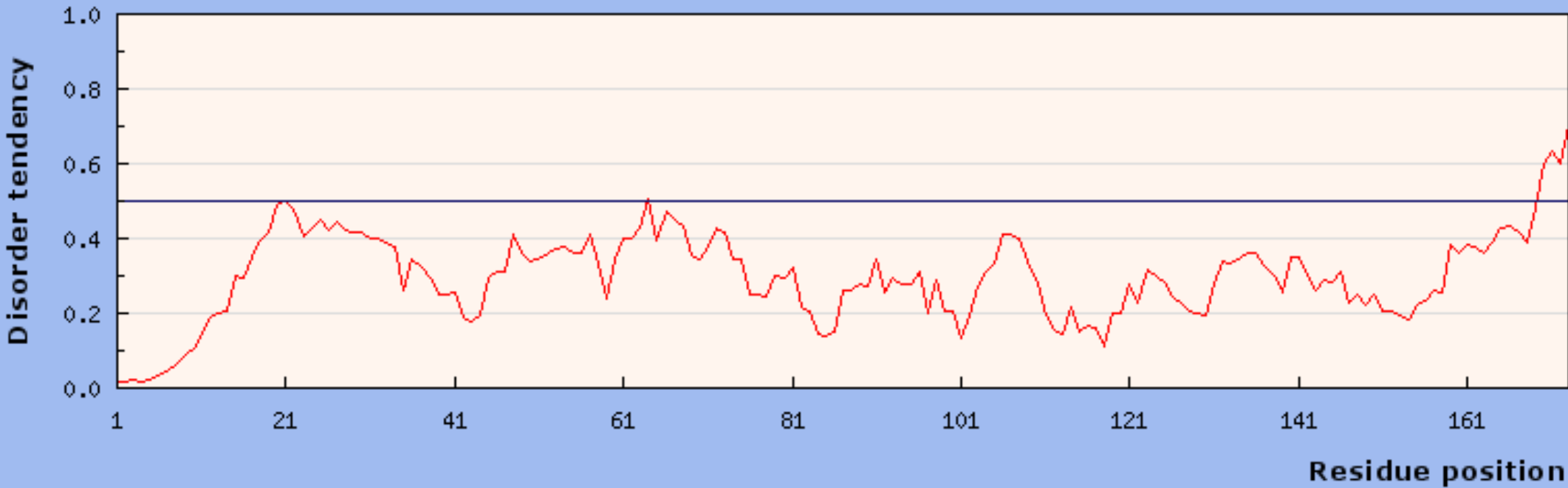
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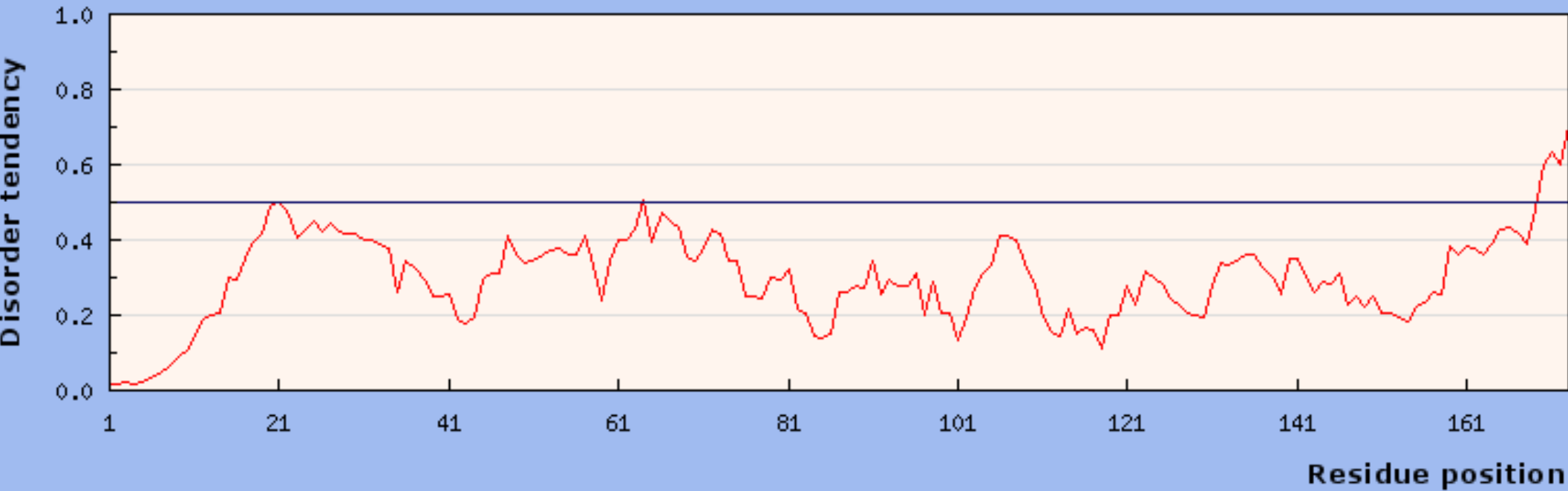
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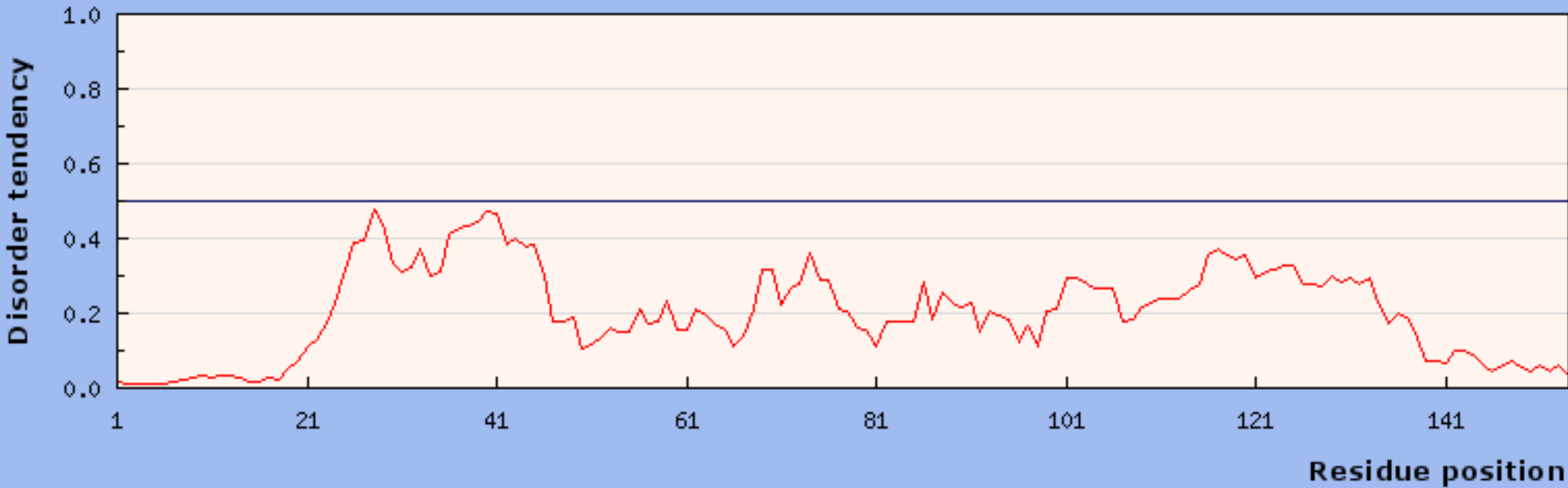
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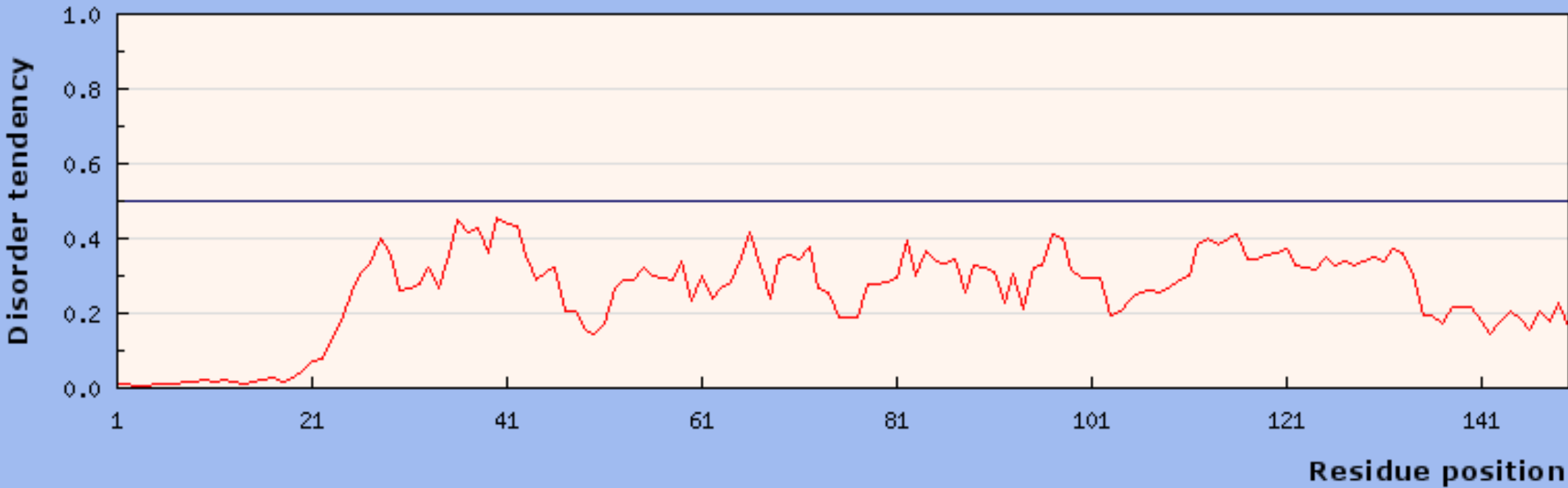
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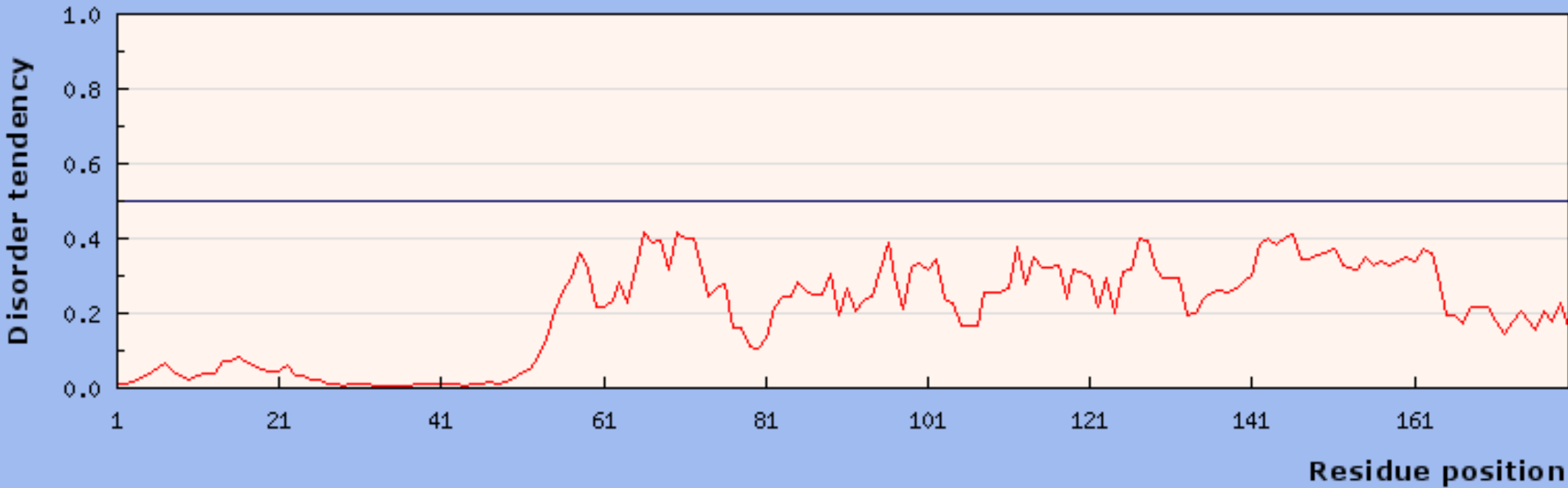
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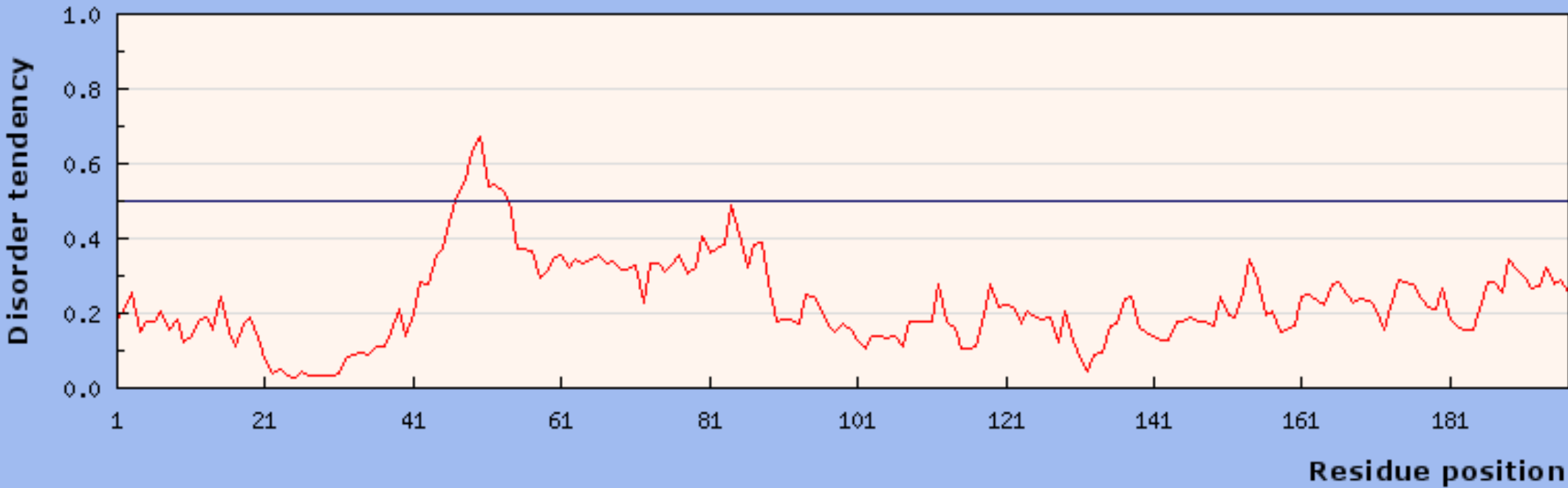
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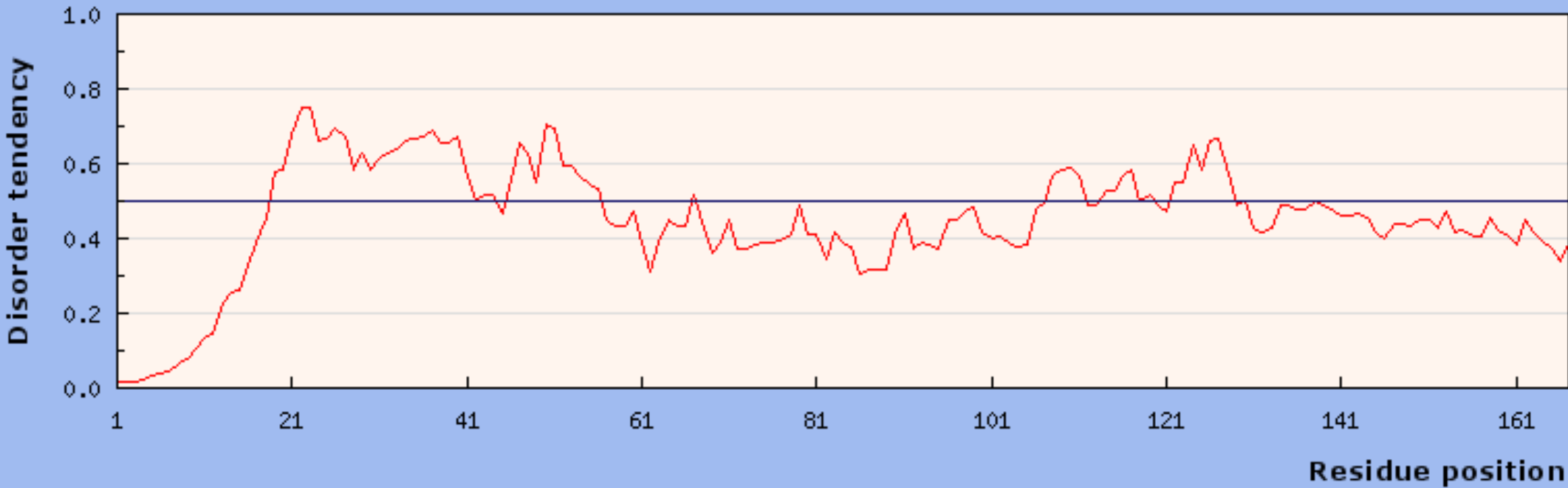
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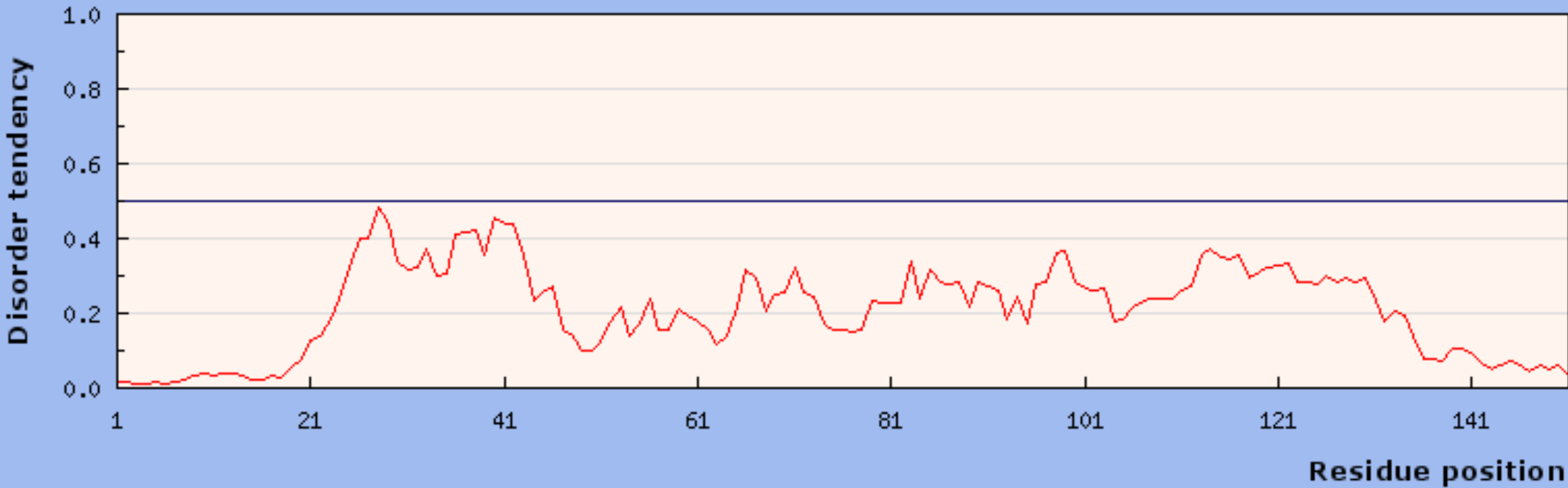
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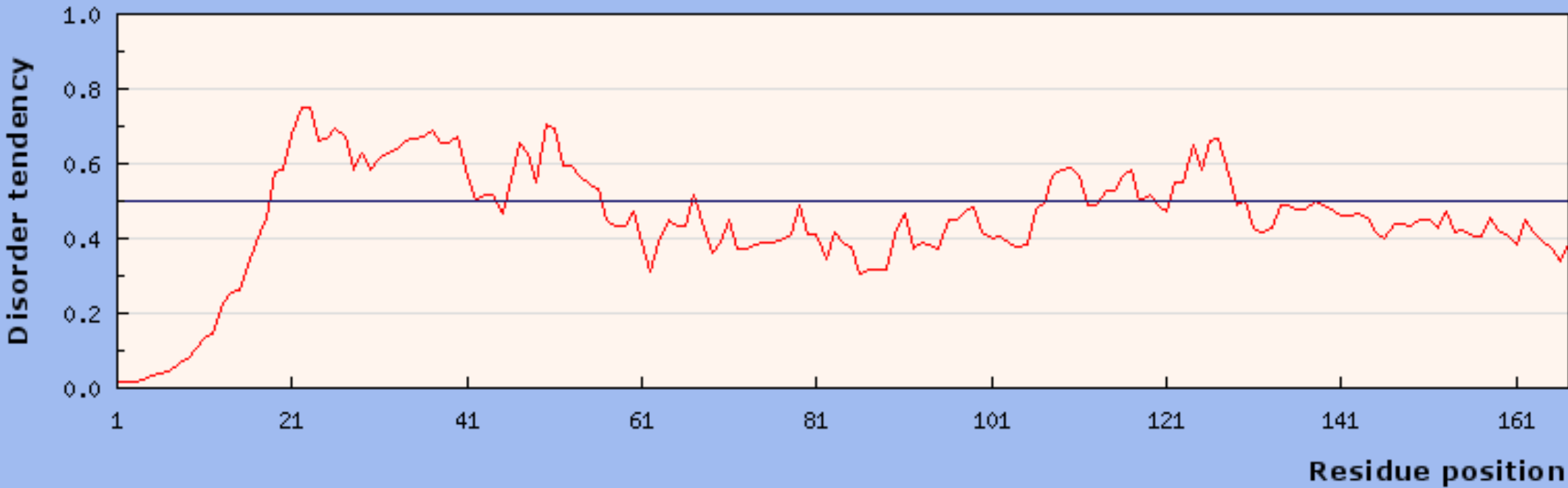
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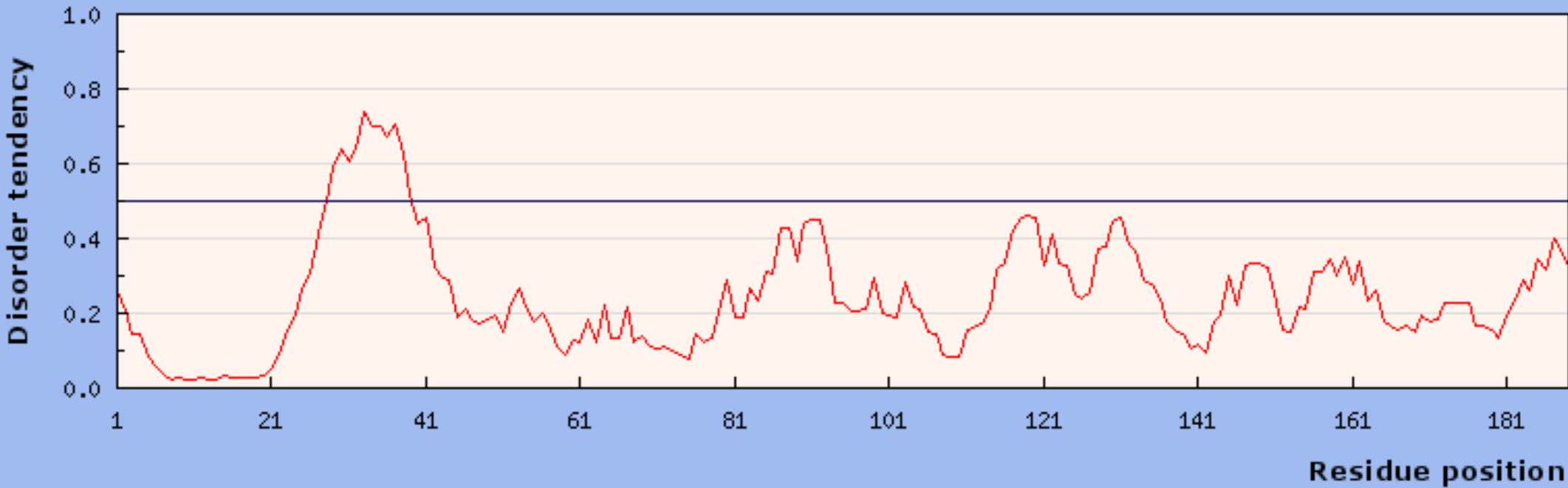
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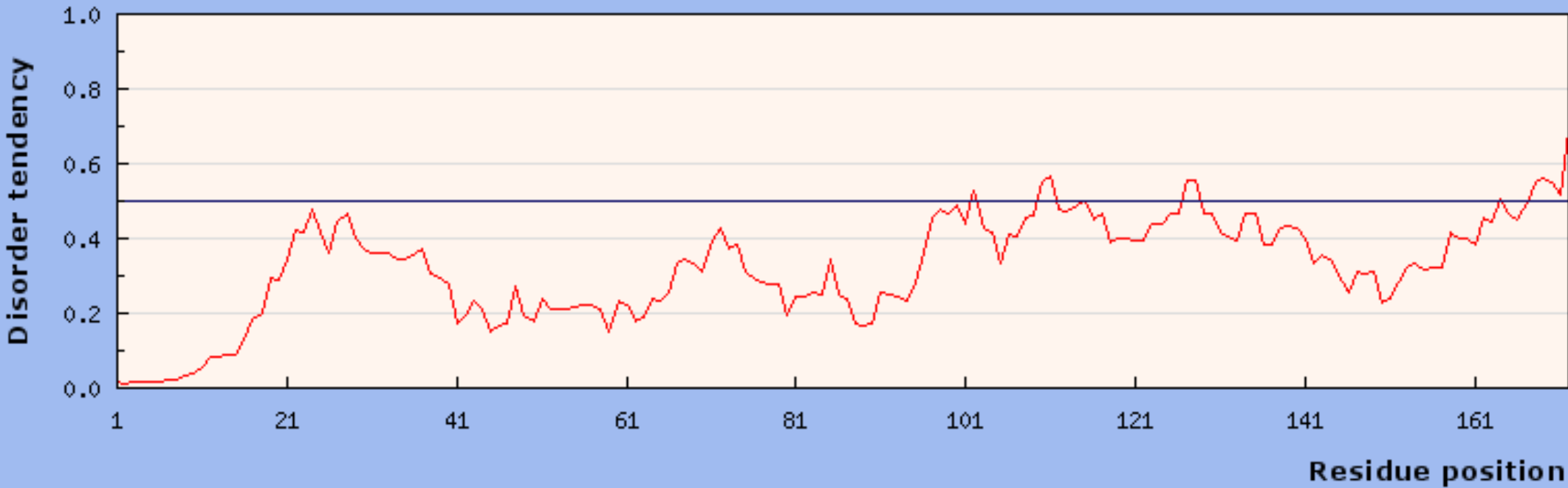
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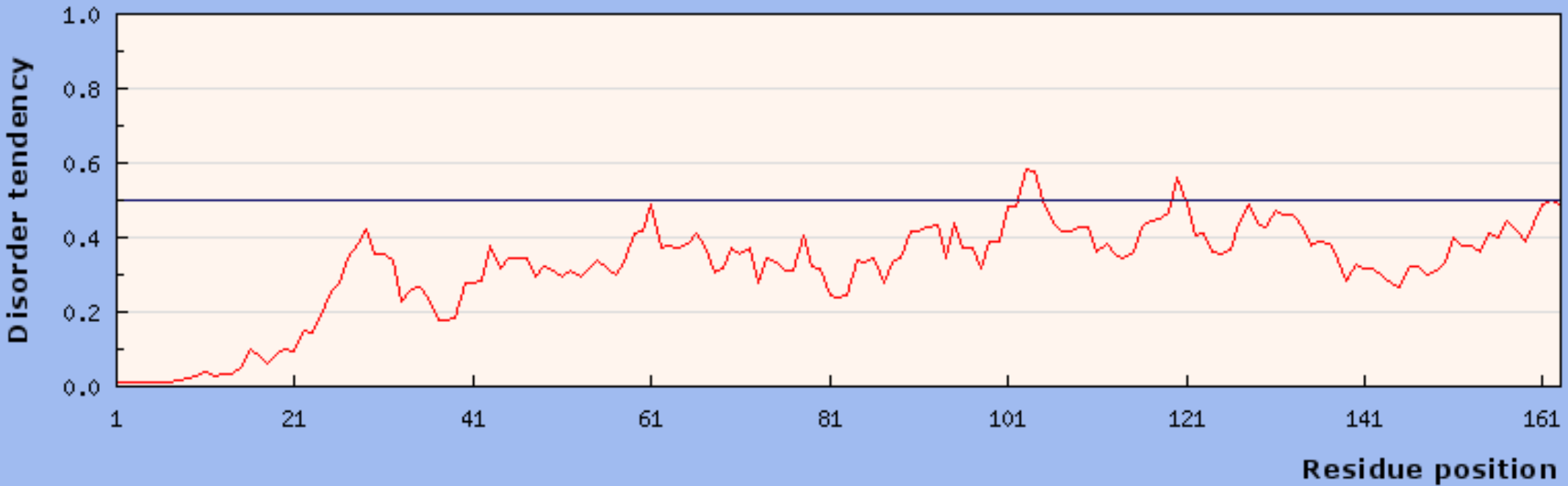
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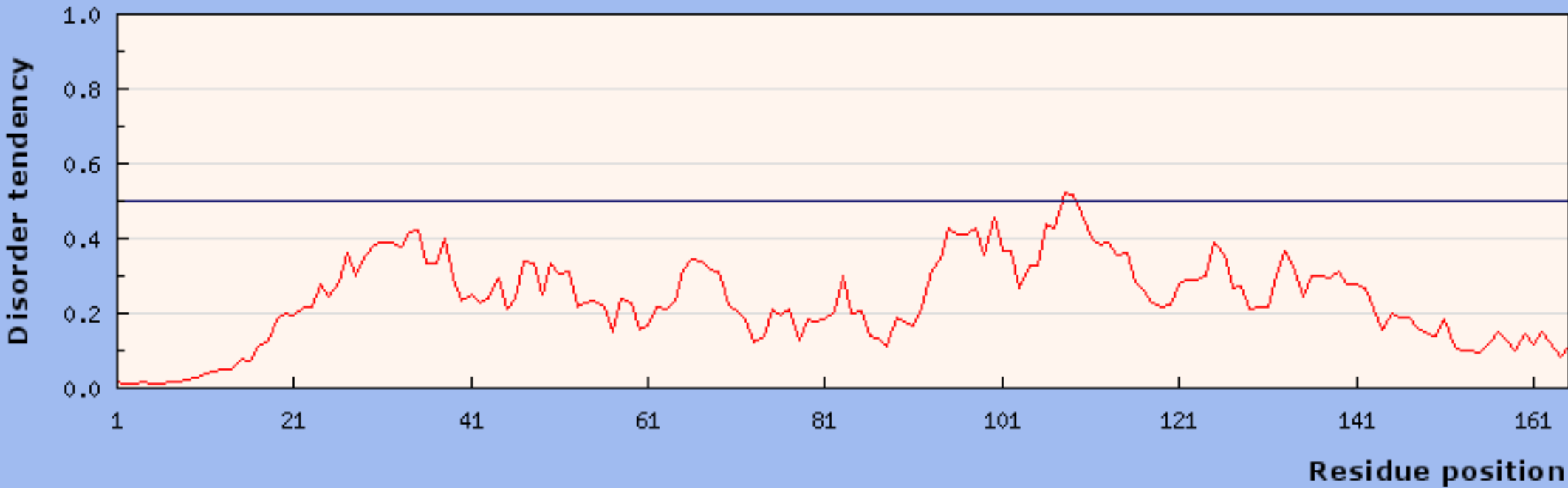
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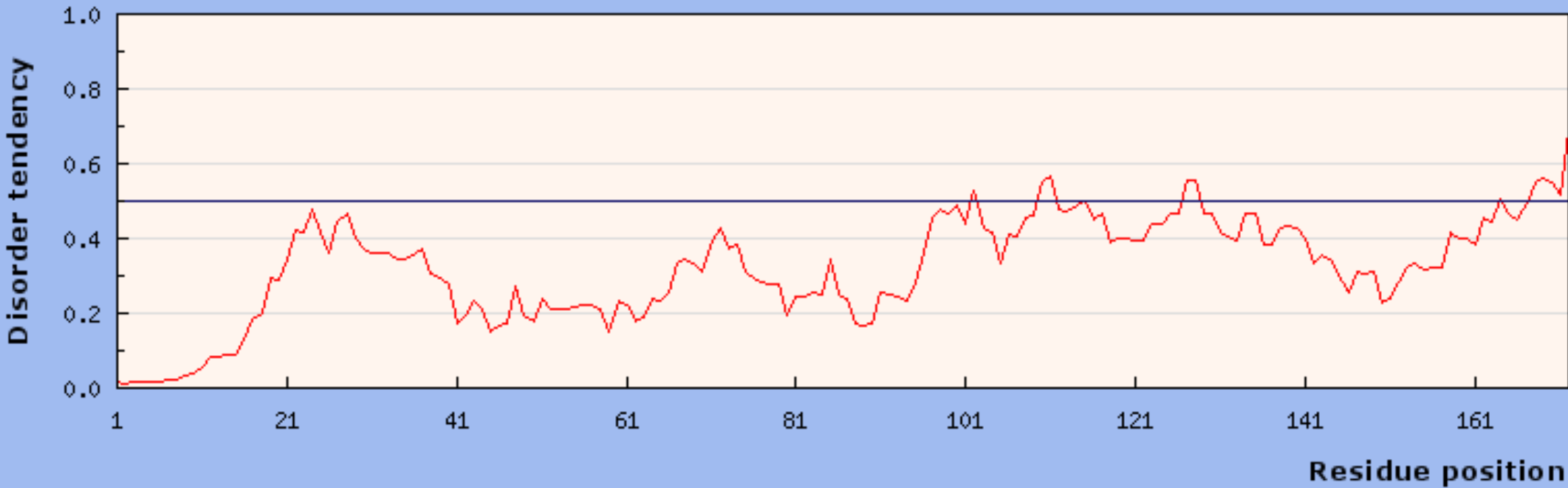
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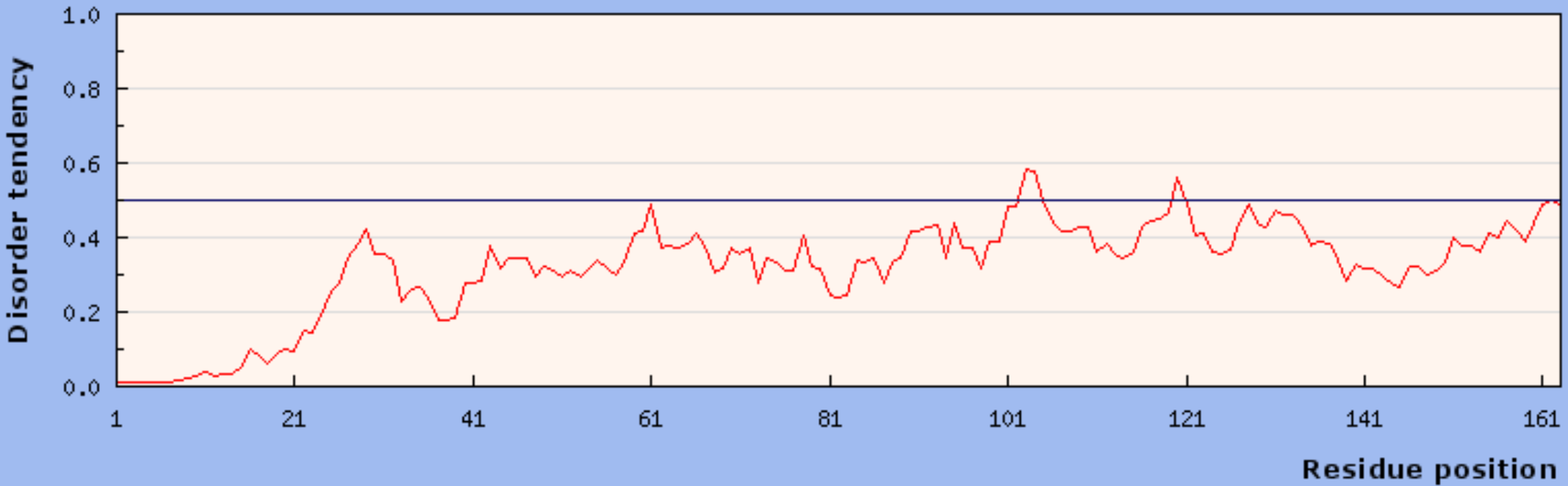
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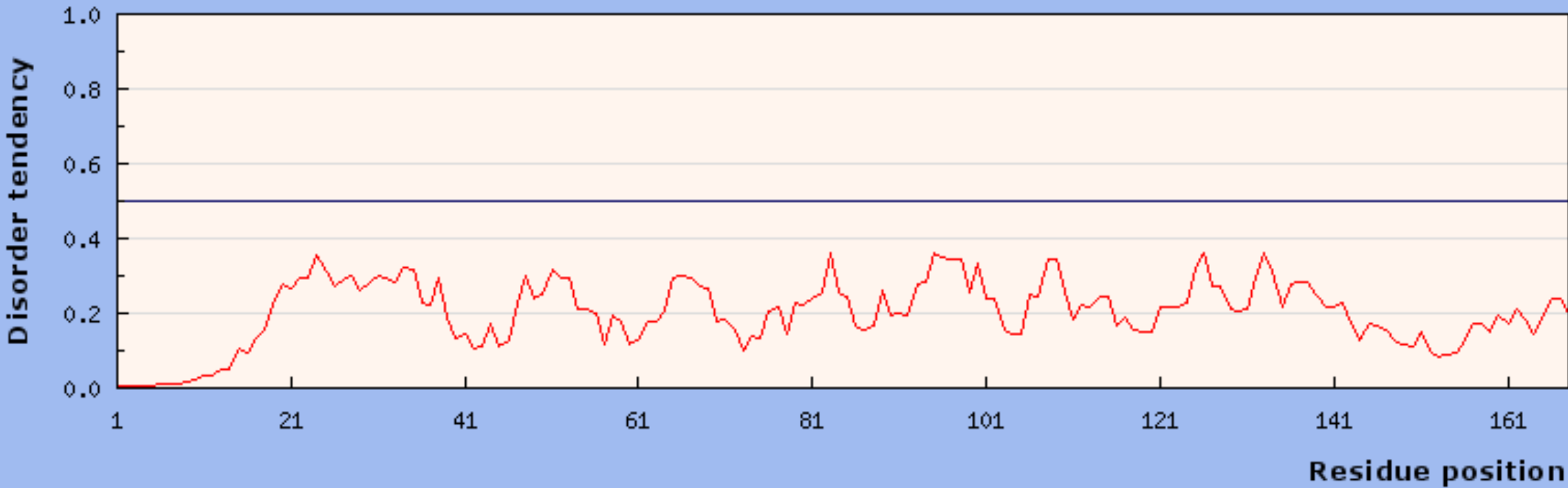
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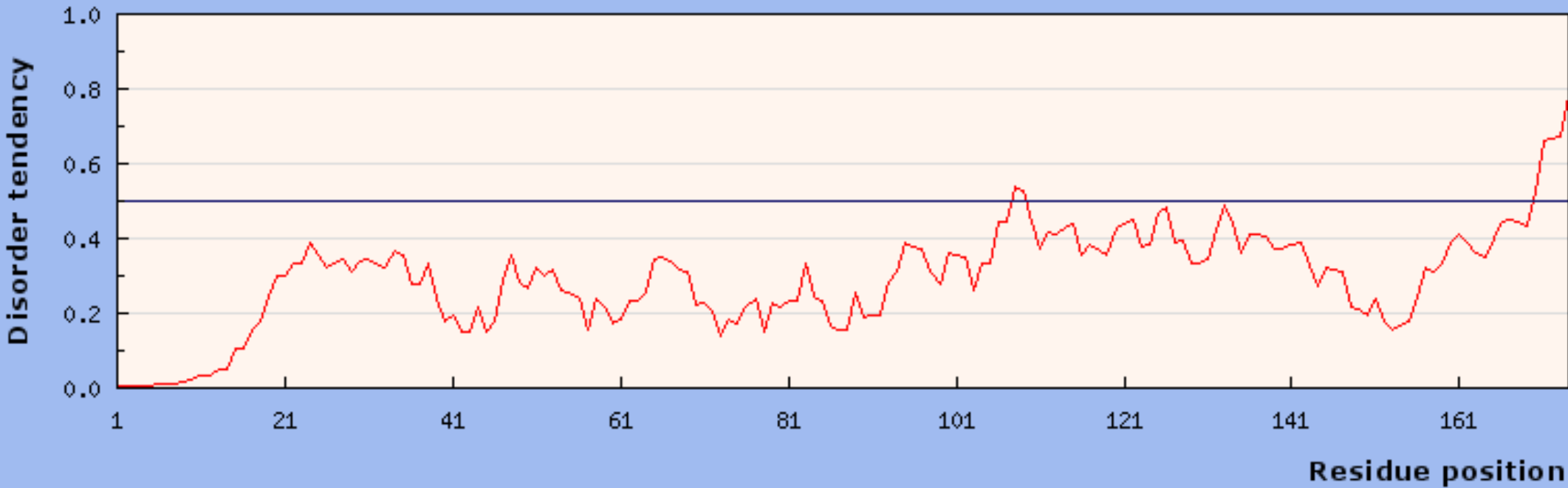
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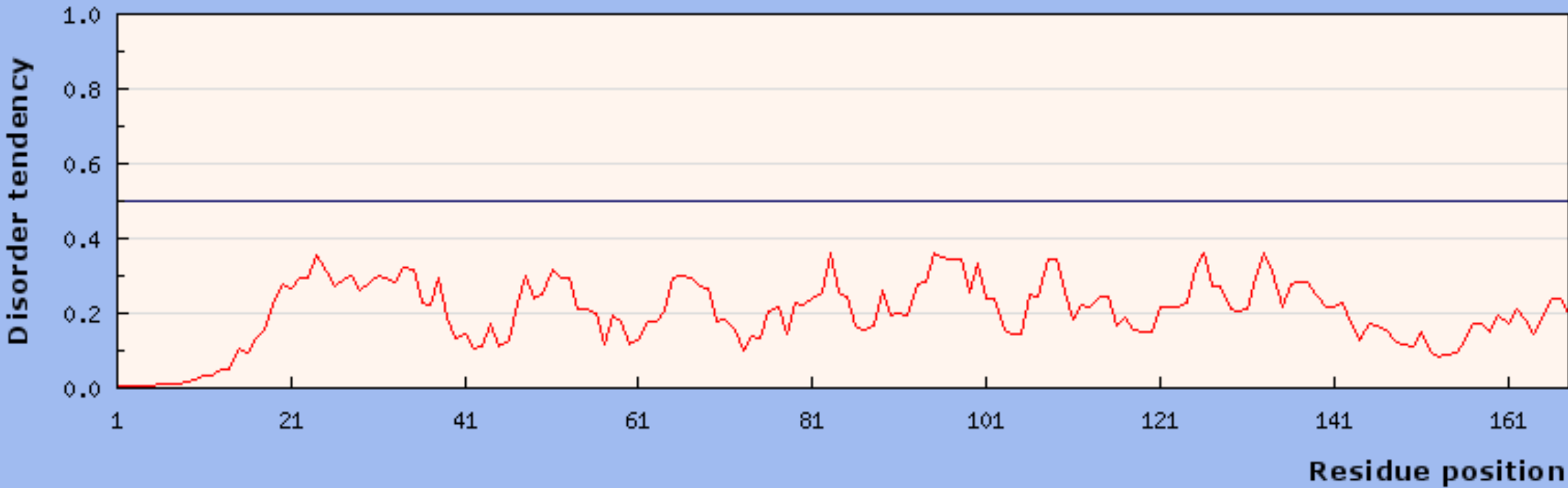
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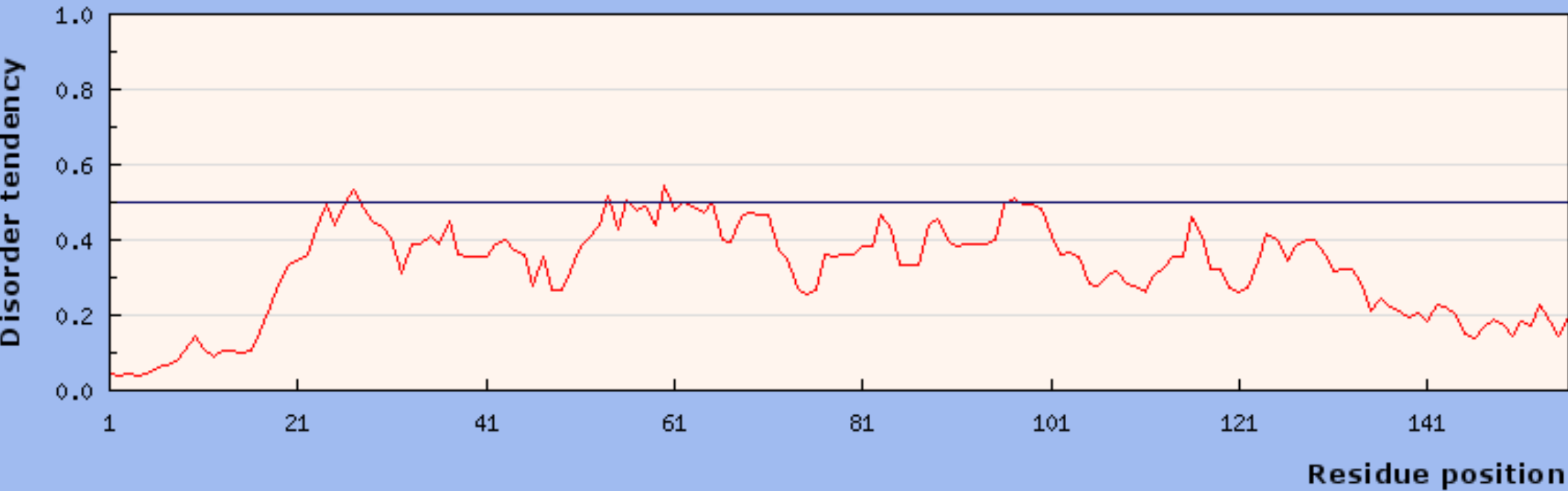
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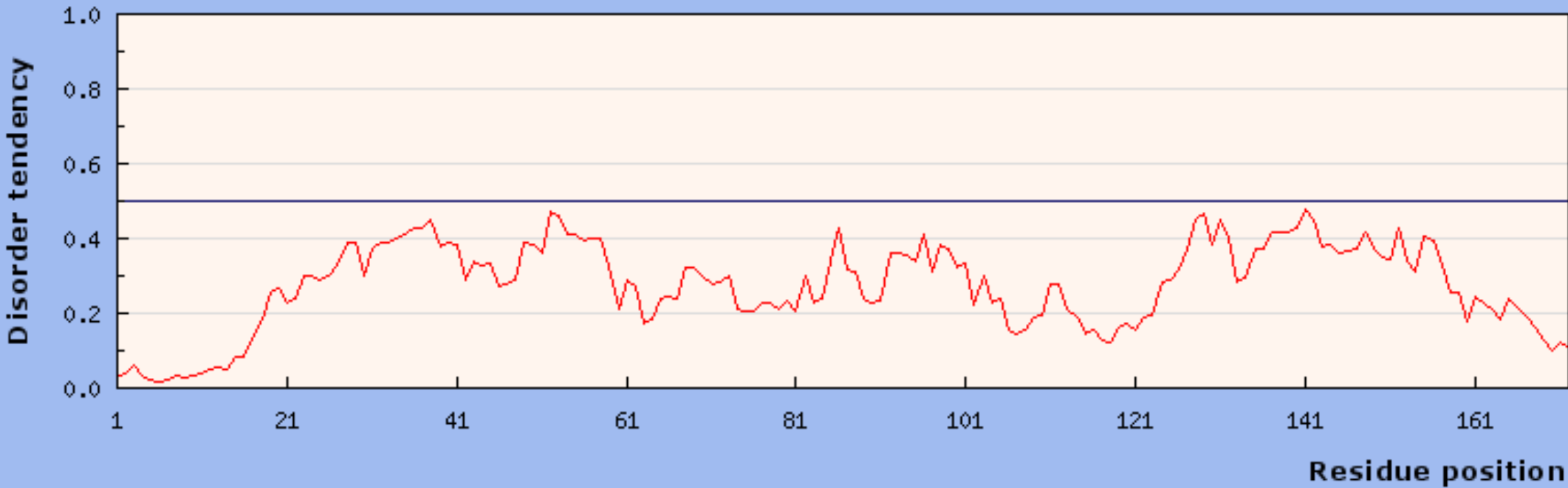
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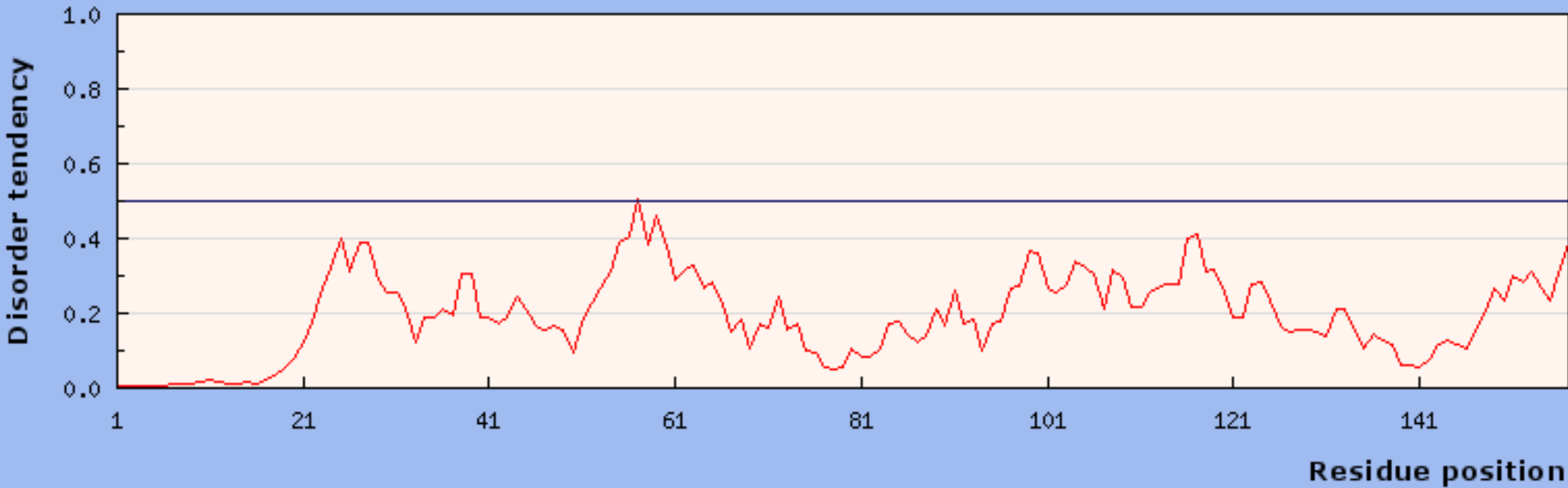
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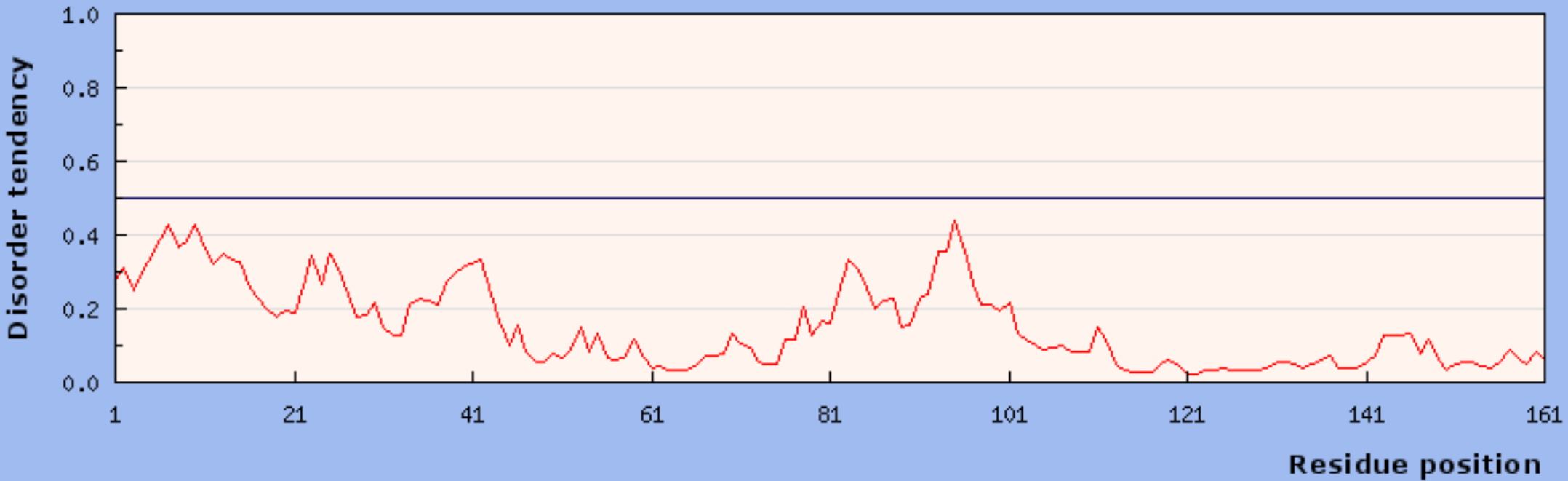
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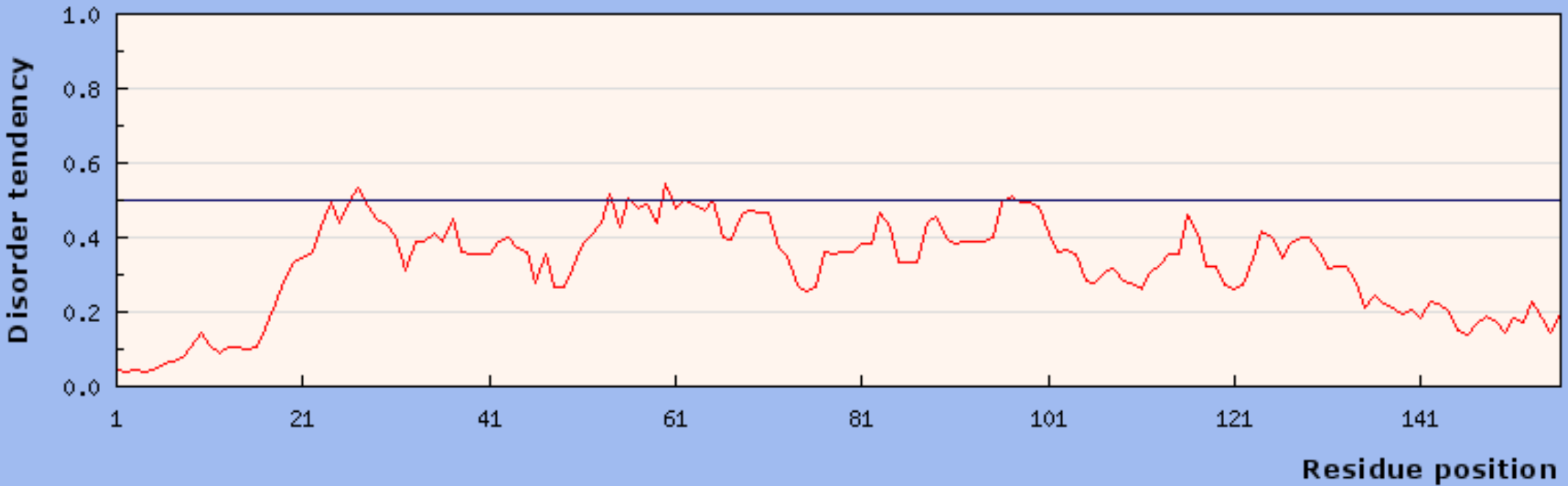
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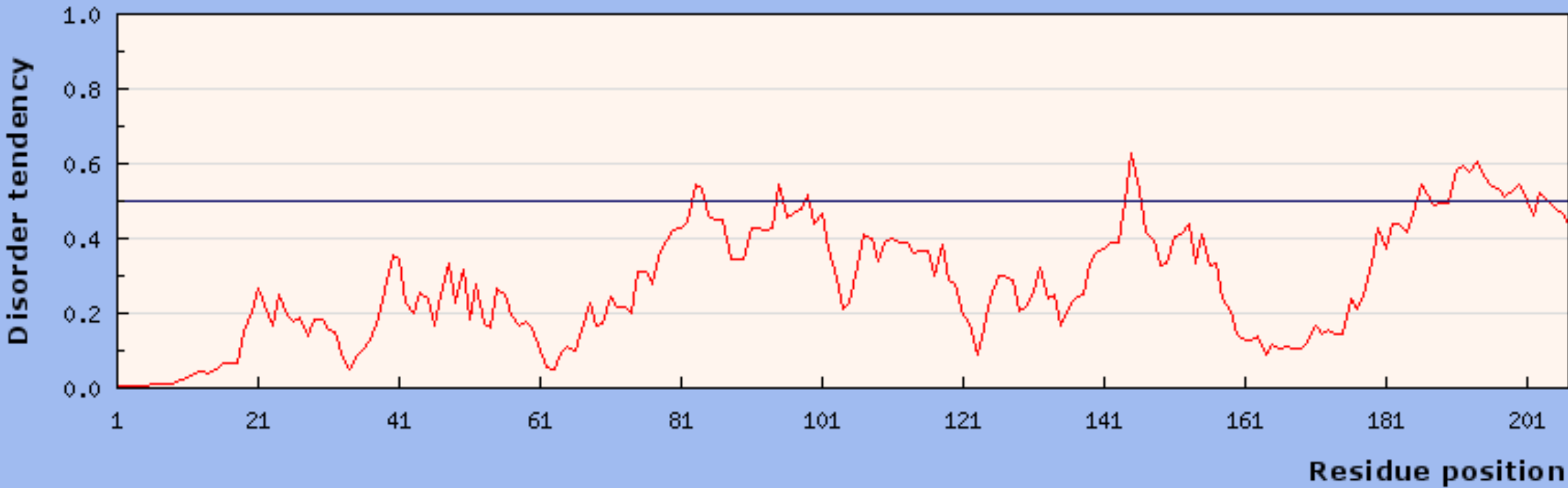
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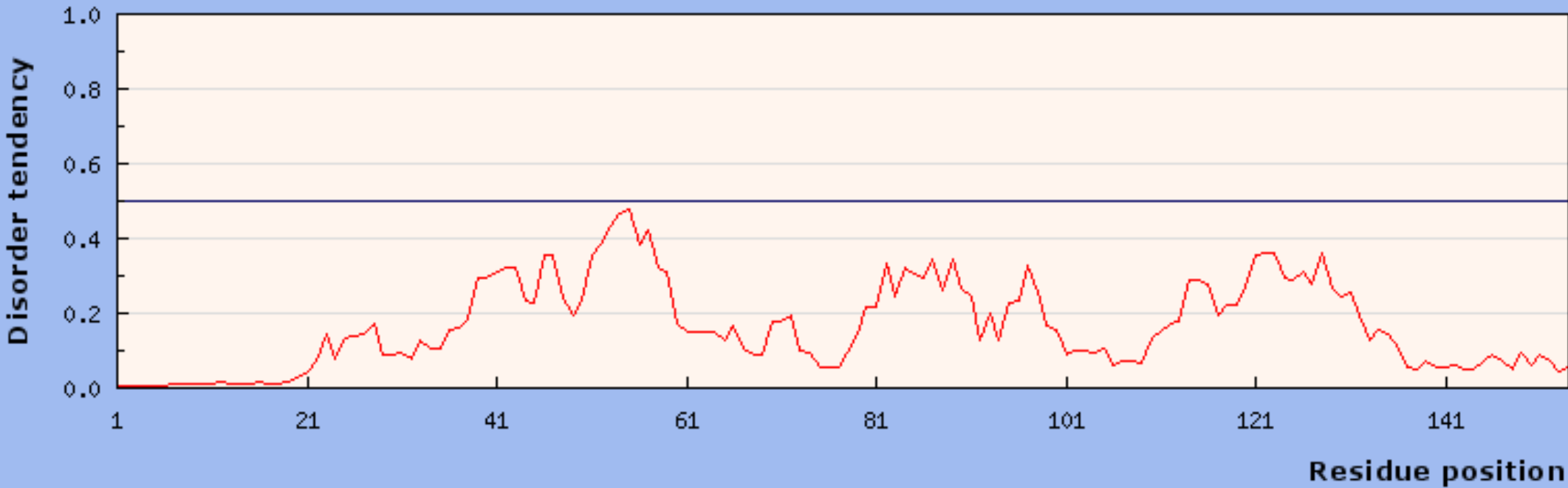
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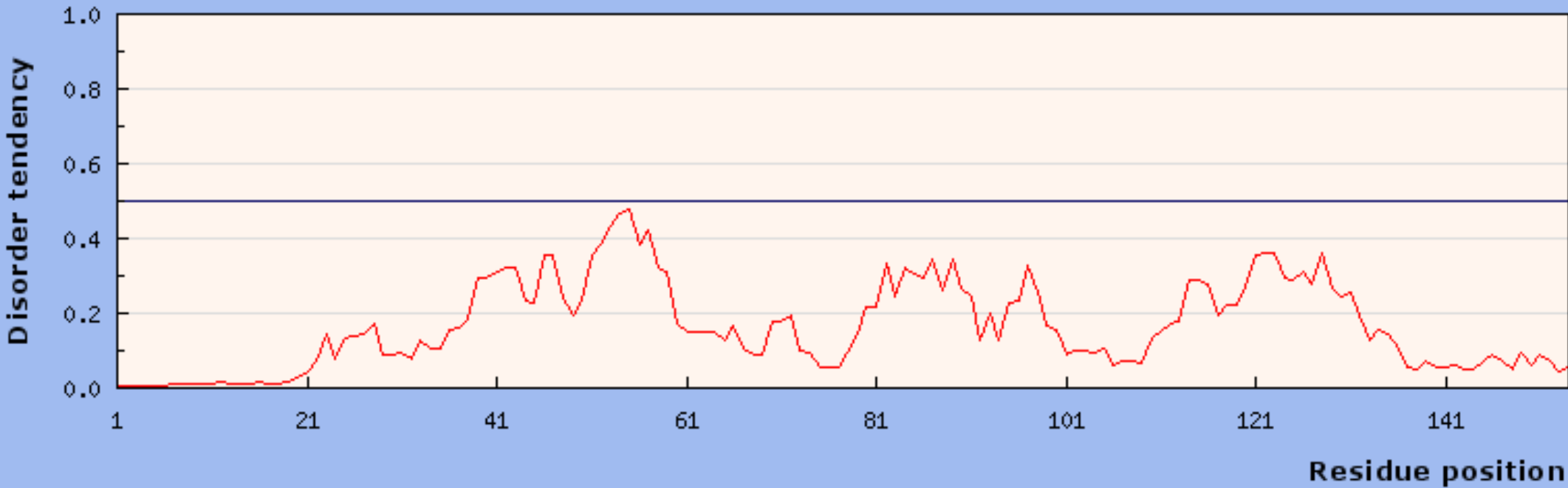
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