

# Structure Search Report

General Summary	AlphaFold Predictions	AlphaFold Links
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## Input Statistics

Results for input ID / file:

test\_file2.txt

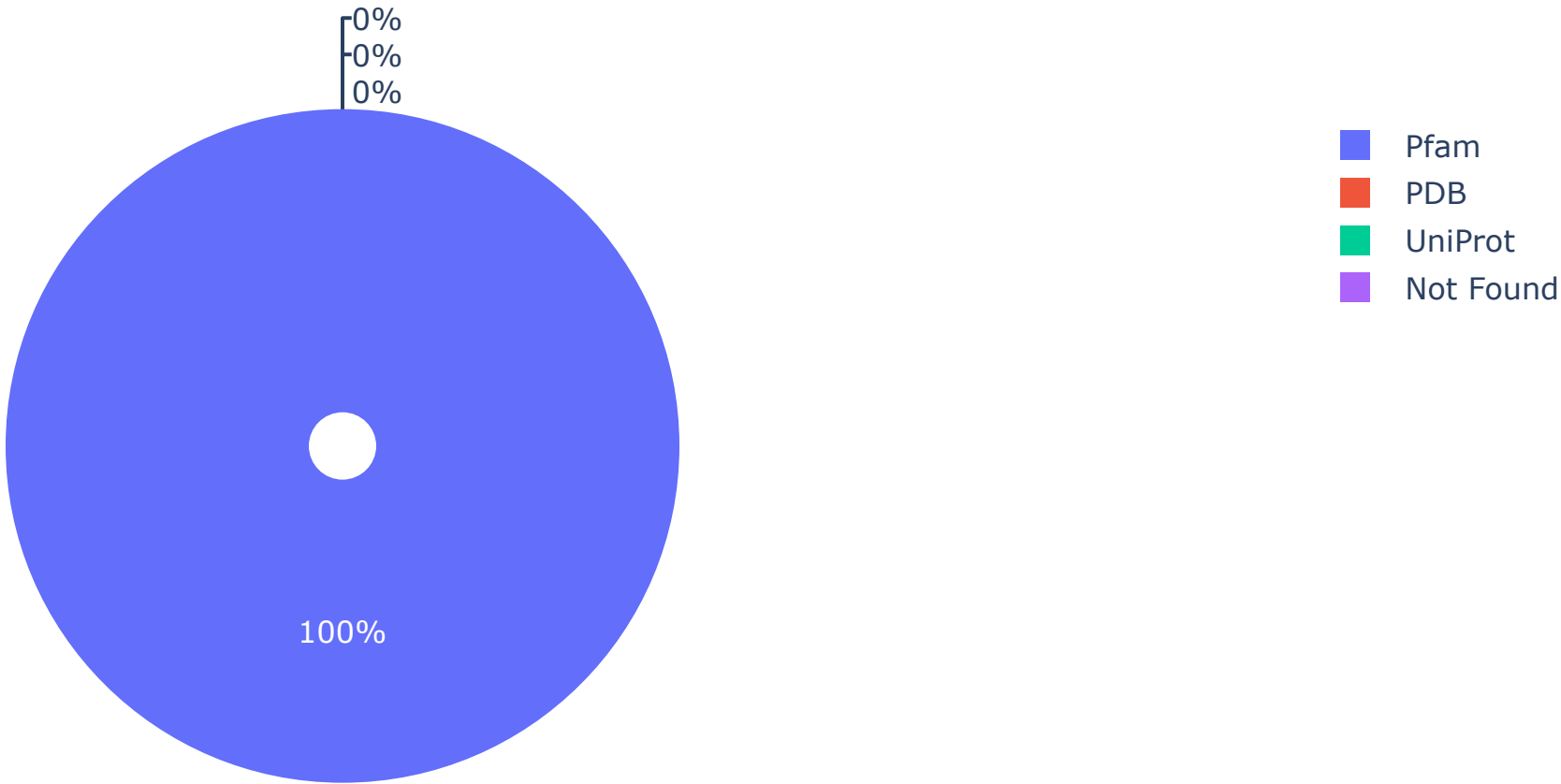
Total number of input ID's  
(provided directly or as files' content):

1

Identifiers recognized  
as Pfam / UniProt / PDB entries:

1 / 1

Percent of input ID's found in Pfam / UniProt / PDB databases:



## Uniprot Summary

Number of structures found

2241

Percentage of reviewed structures

0.71%

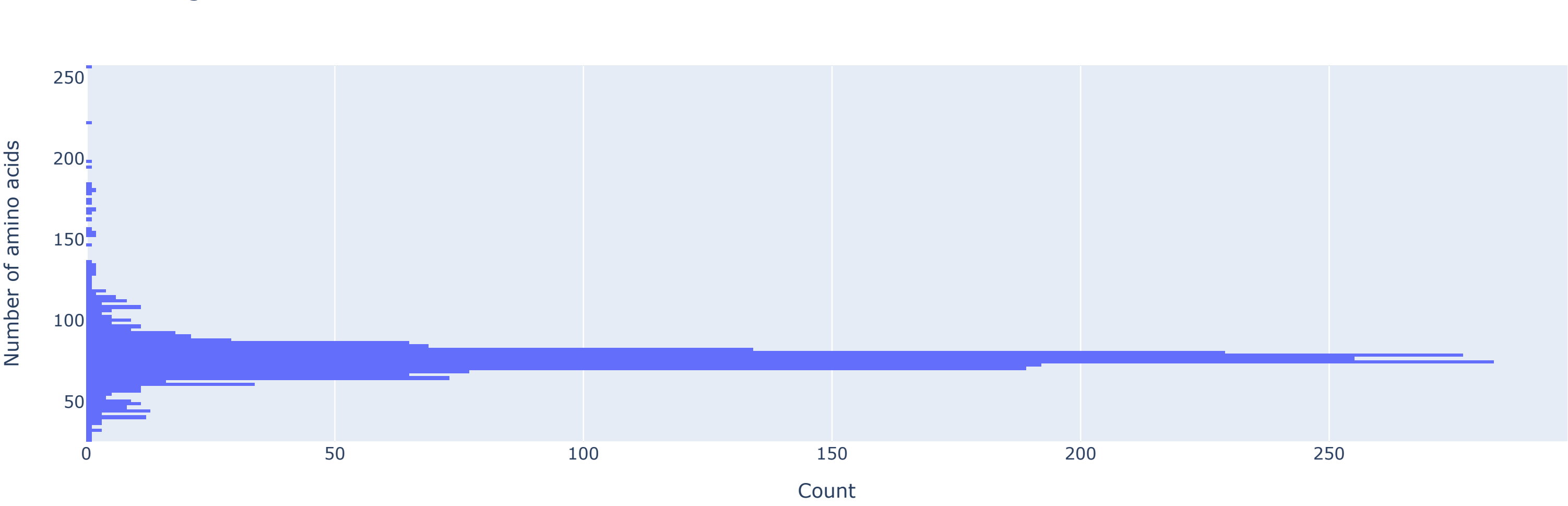
Average protein length:

77

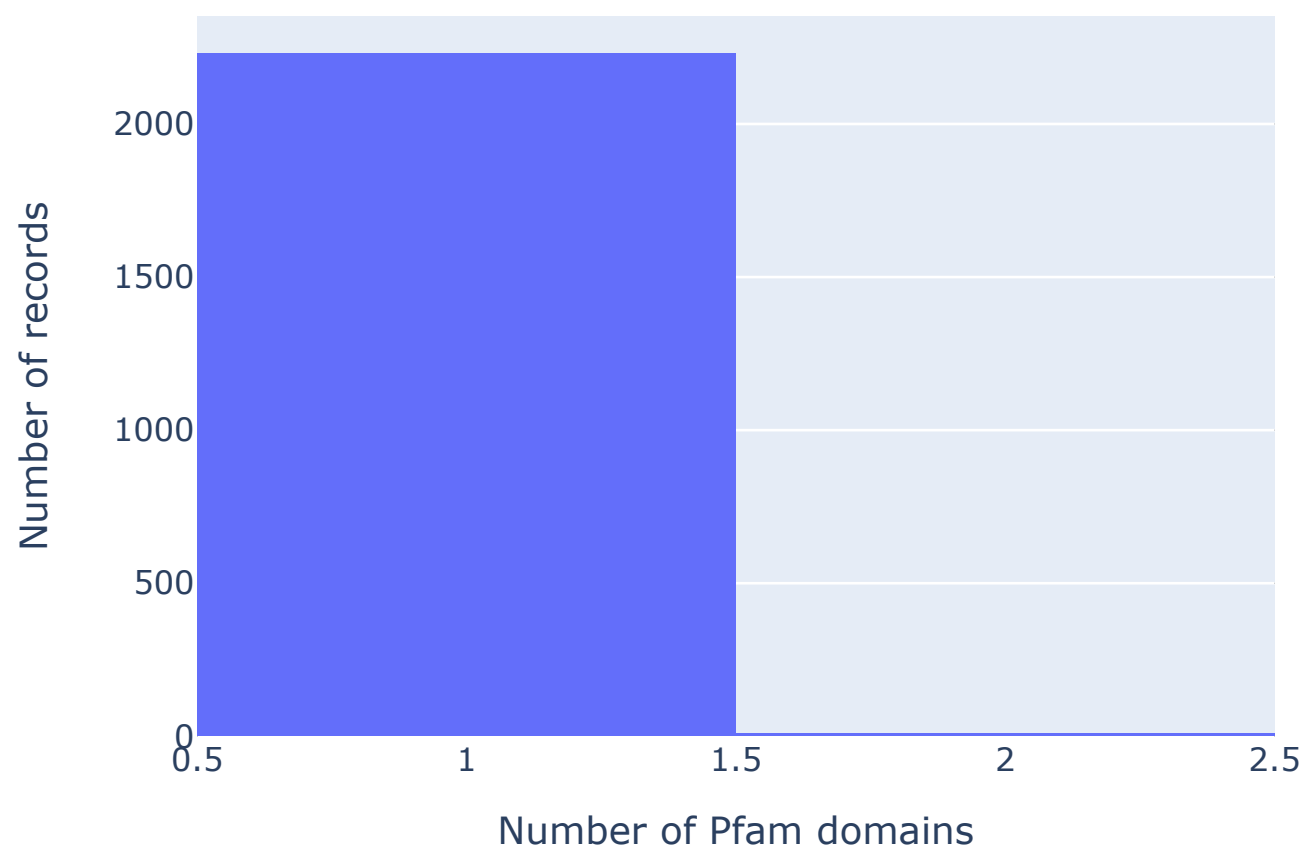
Entries with known 3D structures  
No entries with known 3D structures

## Protein lengths

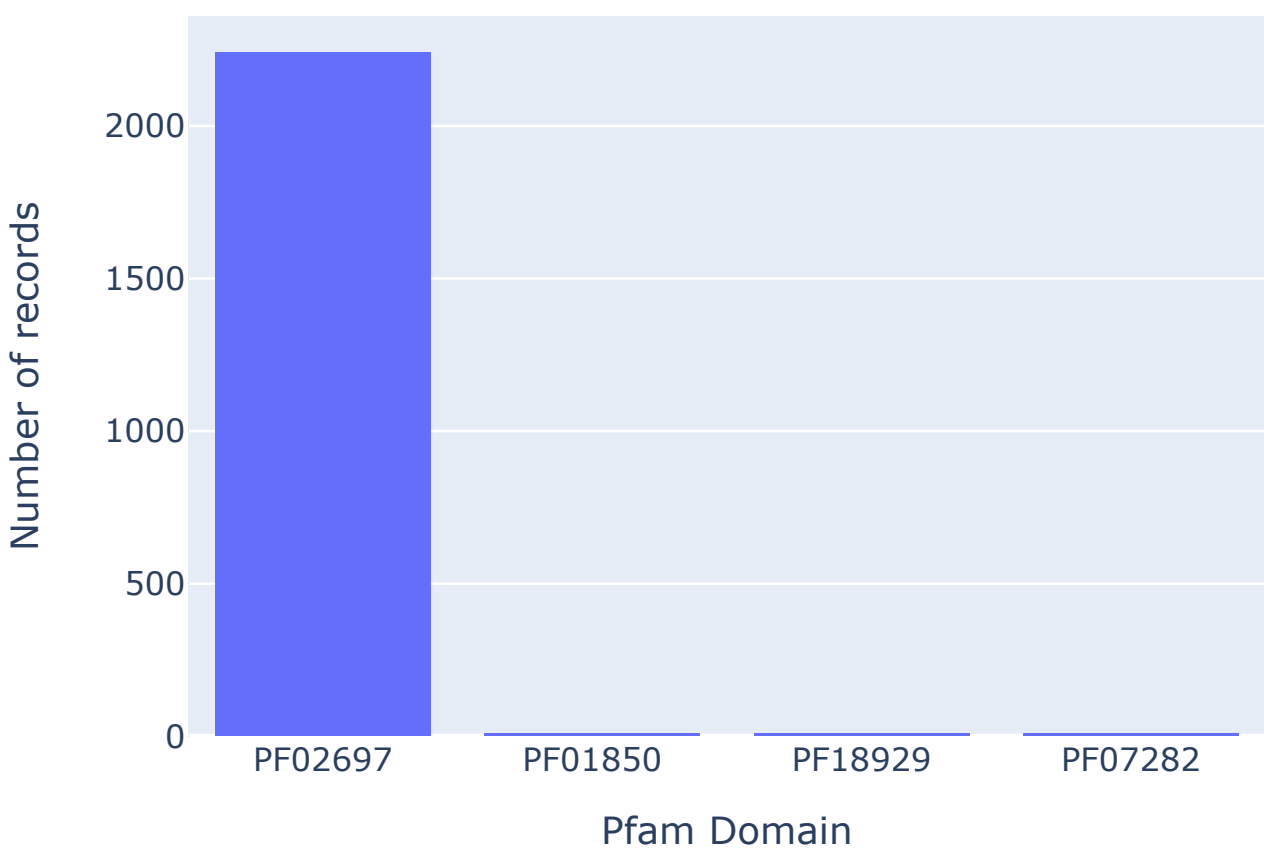
Protein length distribution



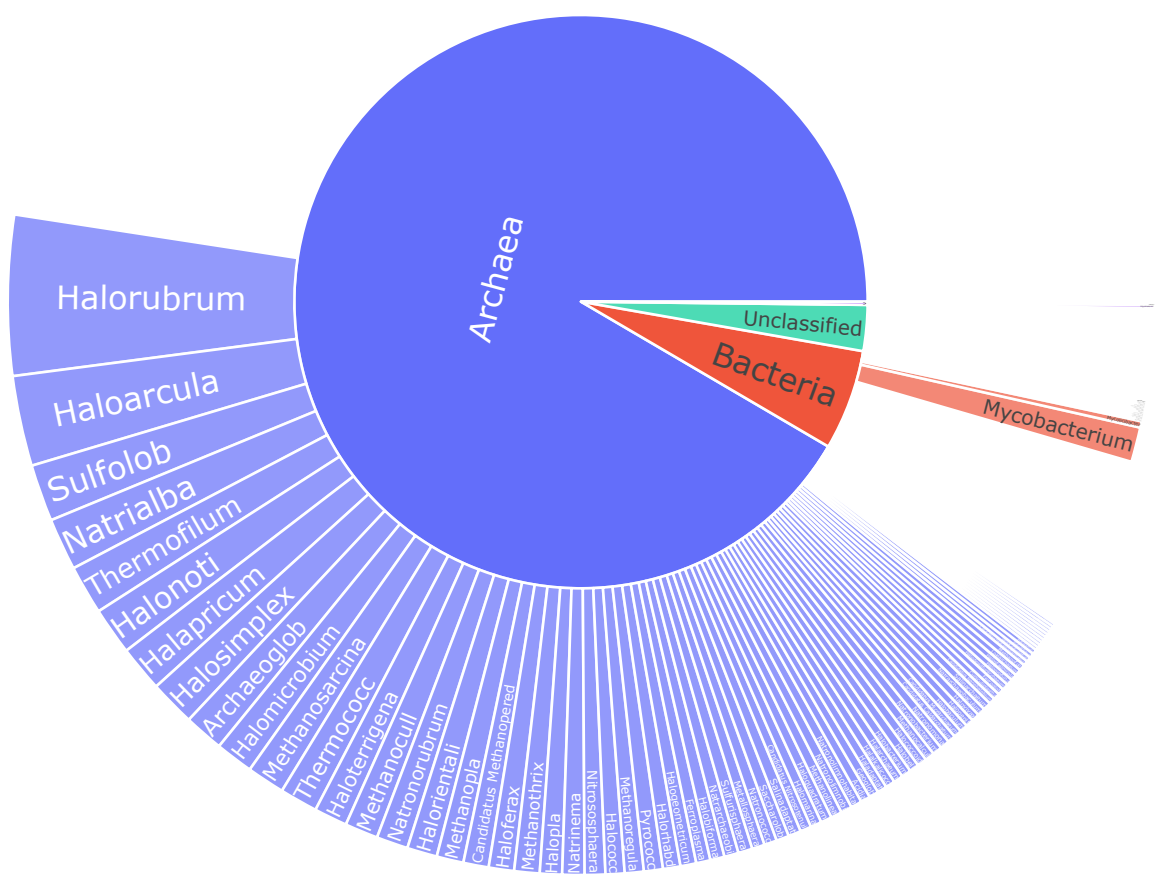
## Number of Pfam domains



## Most frequent Pfam domains



## Lineage of the protein structures



## AlphaFold short summary

AlphaFold predictions found for:

16 / 2241

UniProt structures

Structure with highest mean pLDDT:  
[UniProt Id : pLDDT]

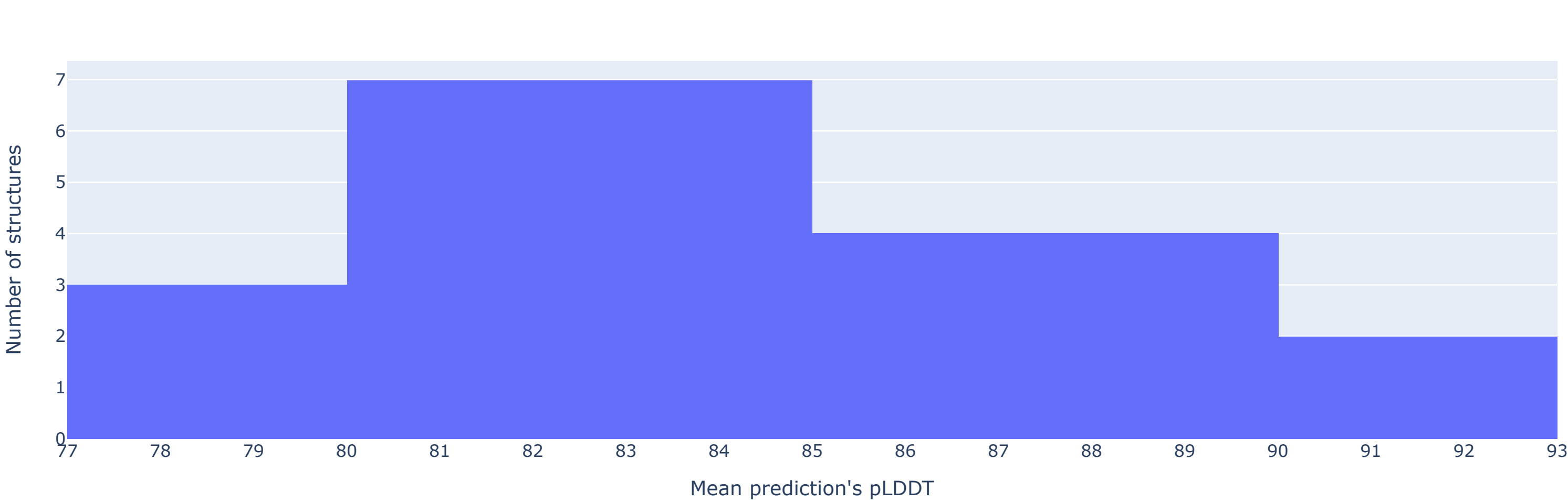
Q96Z89: 91.43

Mean pLDDT score for found predictions:

83.73

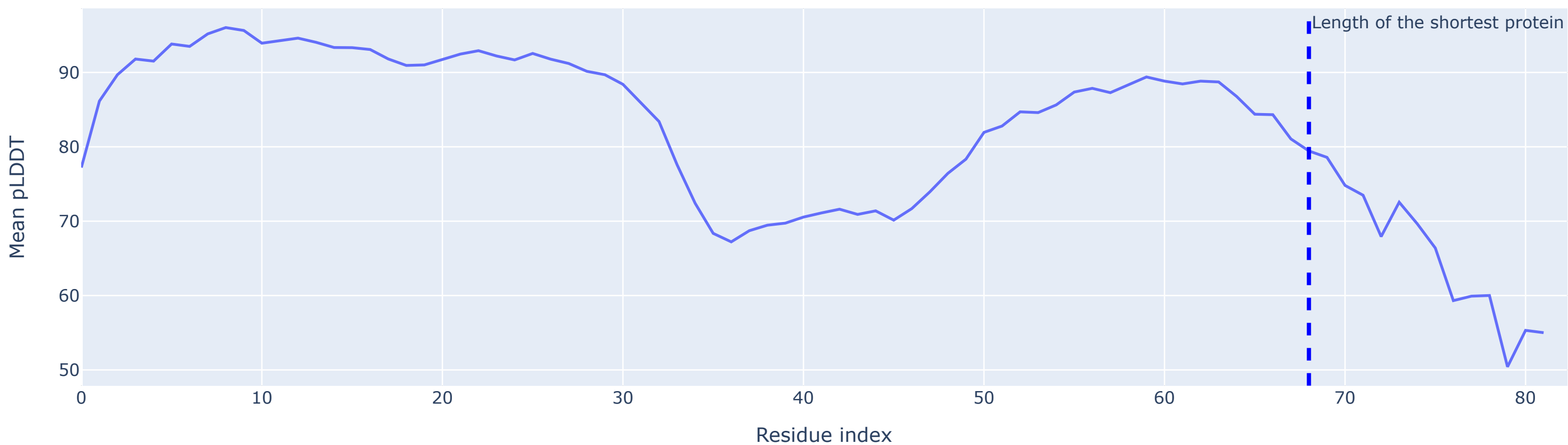
## General pLDDT info

Histogram of mean pLDDT in AlphaFold predictions



## Mean per-residue pLDDT

Mean per-residue pLDDT in AlphaFold predictions



## Per-residue pLDDT in prediction with maximal mean pLDDT (Q96Z89: 91.43)

Prediction's per-residue pLDDT

