

ConSurf Job Information

Go to [Results of Job 1678103534](#) (until they are deleted from the server).

The information below is obtained from the header of PDB file
AF_eaa2NAT_rank1_with_seqres_consurf_firstglance.pdb

This PDB file can be [saved to your computer](#).

Job Parameters

Job 1678103534 by ConSurf version 3.0 on 2023-03-06.

- PDB ID: **AF_EAA2NAT_RANK1_WITH_SEQRES**
- Chain processed: **A**
- Chains in the deposited model identical in sequence to chain processed: **A**
- Multiple sequence alignment source: **Generated by ConSurf**
- Multiple sequence alignment method: **MAFFT**
- Phylogenetic tree source: **Generated by ConSurf**

- Homologous sequences obtained from: **UNIREF90**
- PSI Blast E value cutoff: **0.0001**
- PSI Blast Iterations: **1**
- Maximum homologous sequences to use: **150**
- Conservation score method: **Bayes**
- Amino acid substitution model: **CpREV**

For an explanation of the Job Parameters and Results, please see the on-line documentation for the [ConSurf Server](#).

Job Results

- SEQRES Length: **574** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **413**
- Unique homologous sequences found: **1766**
- Sequences used in the MSA: **150**

Number of amino acids at each conservation grade, 1-9:
Black: excluding amino acids with insufficient data.
Yellow: including amino acids with insufficient data, shown only if different.

1.	10	Variable
2.	9	
3.	25	
4.	35	
5.	47	
6.	53	
7.	67	
8.	80	
9.	87	Conserved

Sum	413	413
+	0	(Amino acids with insufficient data)
=	413	(0% with insufficient data)

Close