ConSurf Job Information

Go to Results of Job 1692022806 (until they are deleted from the server).

The information below is obtained from the header of PDB file
AF_VAChTnat_rank1_with_seqres_consurf_firstglance.pdb
This PDB file can be saved to your computer.

Job Parameters

Job 1692022806 by ConSurf version 3.0 on 2023-08-14.

- PDB ID: **AF_VACHTNAT_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: **WAG**

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

Job Results

- SEQRES Length: **532** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **398**

- Unique homologous sequences found: **945**
- 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.    4 Variable
2.    3
3.   22
4.   39
5.   48
6.   35
7.   48
8.   75
9.  124 Conserved

Sum 398     398
 +    0 (Amino acids with insufficient data)
 =  398 (0% with insufficient data)
```

Close