ConSurf Job Information

Go to Results of Job 1692022772 (until they are deleted from the server).

The information below is obtained from the header of PDB file
AF_VMAT1nat_rank1_with_seqres_consurf_firstglance.pdb
This PDB file can be saved to your computer.

Job Parameters

Job 1692022772 by ConSurf version 3.0 on 2023-08-14.

- PDB ID: **AF_VMAT1NAT_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: **525** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **401**

- Unique homologous sequences found: **1198**
- 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.    7 Variable
2.    5
3.   22
4.   36
5.   57
6.   38
7.   67
8.   87
9.   82 Conserved

Sum 401     401
 +    0 (Amino acids with insufficient data)
 =  401 (0% with insufficient data)
```

Close