

ConSurf Job Information

Go to [Results of Job 1692021508](#) (until they are deleted from the server).

The information below is obtained from the header of PDB file
AF_SERTnat_rank1_with_seqres_consurf_firstglance.pdb

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

Job Parameters

Job 1692021508 by ConSurf version 3.0 on 2023-08-14.

- PDB ID: **AF_SERTNAT_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: **LG**

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

Job Results

- SEQRES Length: **630** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **518**
- Unique homologous sequences found: **6341**
- 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. **16** Variable
2. **11**
3. **38**
4. **70**
5. **67**
6. **60**
7. **94**
8. **68**
9. **94** Conserved

Sum **518** **518**
 + **0** (Amino acids with insufficient data)
 = **518** (0% with insufficient data)

Close