# ConSurf Job Information

Go to Results of Job 1692021478 (until they are deleted from the server).

The information below is obtained from the header of PDB file
**AF_DATnat_rank1_with_seqres_consurf_firstglance.pdb**
This PDB file can be saved to your computer.

## Job Parameters

Job 1692021478 by ConSurf version 3.0 on 2023-08-14.

- PDB ID: **AF_DATNAT_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: **620** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **518**

- Unique homologous sequences found: **6580**
- 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.   22 Variable
2.   11
3.   34
4.   67
5.   72
6.   62
7.   83
8.   79
9.   88 Conserved

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

Close