

ConSurf Job Information

Go to [Results of Job 1678461320](#) (until they are deleted from the server).

The information below is obtained from the header of PDB file
AF_ylat2NAT_rank1_with_seqres_consurf_firstglance.pdb

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

Job Parameters

Job 1678461320 by ConSurf version 3.0 on 2023-03-10.

- PDB ID: **AF_YLAT2NAT_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: **515** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **438**
- Unique homologous sequences found: **3659**
- 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. **13** Variable
2. **5**
3. **32**
4. **46**
5. **68**
6. **64**
7. **77**
8. **74**
9. **59** Conserved

Sum **438** **438**
 + **0** (Amino acids with insufficient data)
 = **438** (0% with insufficient data)

Close