

## ConSurf Job Information

Go to [Results of Job 1692022288](#) (until they are deleted from the server).

The information below is obtained from the header of PDB file  
**AF\_VPATnat\_rank1\_with\_seqres\_consurf\_firstglance.pdb**

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

### Job Parameters

Job 1692022288 by ConSurf version 3.0 on 2023-08-14.

- PDB ID: **AF\_VPATNAT\_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: **456** amino acids in experimental protein.
- Amino acids with coordinates (ATOM records): **405**
- Unique homologous sequences found: **715**
- 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.	15	Variable
2.	7	
3.	32	
4.	48	
5.	65	
6.	49	
7.	61	
8.	68	
9.	60	Conserved

Sum	405	405
+	0	(Amino acids with insufficient data)
=	405	(0% with insufficient data)

Close