

ConSurf Job Information

Go to [Results of Job 1678461301](#) (until they are deleted from the server).

The information below is obtained from the header of PDB file
AF_vglut3NAT_rank1_with_seqres_consurf_firstglance.pdb

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

Job Parameters

Job 1678461301 by ConSurf version 3.0 on 2023-03-10.

- | | |
|--|--|
| <ul style="list-style-type: none"> • PDB ID: AF_VGLUT3NAT_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 | <ul style="list-style-type: none"> • 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 |
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For an explanation of the Job Parameters and Results, please see the on-line documentation for the [ConSurf Server](#).

Job Results

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|--|--|-----------|----|----------|----|---|--|----|----|--|----|----|--|----|----|--|----|----|--|----|----|--|----|----|--|----|----|-----------|
| <ul style="list-style-type: none"> • SEQRES Length: 589 amino acids in experimental protein. • Amino acids with coordinates (ATOM records): 287 • Unique homologous sequences found: 1876 • Sequences used in the MSA: 150 | <p>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.</p> <table> <tr><td>1.</td><td>12</td><td>Variable</td></tr> <tr><td>2.</td><td>7</td><td></td></tr> <tr><td>3.</td><td>23</td><td></td></tr> <tr><td>4.</td><td>31</td><td></td></tr> <tr><td>5.</td><td>39</td><td></td></tr> <tr><td>6.</td><td>25</td><td></td></tr> <tr><td>7.</td><td>62</td><td></td></tr> <tr><td>8.</td><td>51</td><td></td></tr> <tr><td>9.</td><td>37</td><td>Conserved</td></tr> </table> <p>Sum 287 287
 + 0 (Amino acids with insufficient data)
 = 287 (0% with insufficient data)</p> | 1. | 12 | Variable | 2. | 7 | | 3. | 23 | | 4. | 31 | | 5. | 39 | | 6. | 25 | | 7. | 62 | | 8. | 51 | | 9. | 37 | Conserved |
| 1. | 12 | Variable | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 2. | 7 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 3. | 23 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 4. | 31 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 5. | 39 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 6. | 25 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 7. | 62 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 8. | 51 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 9. | 37 | Conserved | | | | | | | | | | | | | | | | | | | | | | | | | | |

Close