

## ConSurf Job Information

Go to [Results of Job 1678459912](#) (until they are deleted from the server).

The information below is obtained from the header of PDB file  
**AF\_vglut2NAT\_rank1\_with\_seqres\_consurf\_firstglance.pdb**

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

### Job Parameters

Job 1678459912 by ConSurf version 3.0 on 2023-03-10.

- |  |  |
|--|--|
| <ul style="list-style-type: none"> <li>• PDB ID: <b>AF_VGLUT2NAT_RANK1_WITH_SEQRES</b></li> <li>• Chain processed: <b>A</b></li> <li>• Chains in the deposited model identical in sequence to chain processed: <b>A</b></li> <li>• Multiple sequence alignment source: <b>Generated by ConSurf</b></li> <li>• Multiple sequence alignment method: <b>MAFFT</b></li> <li>• Phylogenetic tree source: <b>Generated by ConSurf</b></li> </ul> | <ul style="list-style-type: none"> <li>• Homologous sequences obtained from: <b>UNIREF90</b></li> <li>• PSI Blast E value cutoff: <b>0.0001</b></li> <li>• PSI Blast Iterations: <b>1</b></li> <li>• Maximum homologous sequences to use: <b>150</b></li> <li>• Conservation score method: <b>Bayes</b></li> <li>• Amino acid substitution model: <b>LG</b></li> </ul> |
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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

- |  |   |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
|--|---|--------------------------------------|---|----------|----|---|--|----|----|--|----|----|--|----|----|--|----|----|--|----|----|--|----|----|--|----|----|-----------|-----|-----|-----|---|---|--------------------------------------|---|-----|-----------------------------|
| <ul style="list-style-type: none"> <li>• SEQRES Length: <b>582</b> amino acids in experimental protein.</li> <li>• Amino acids with coordinates (ATOM records): <b>294</b></li> <li>• Unique homologous sequences found: <b>2124</b></li> <li>• Sequences used in the MSA: <b>150</b></li> </ul> | <p>Number of amino acids at each conservation grade, 1-9:<br/> <b>Black: excluding amino acids with insufficient data.</b><br/> <b>Yellow: including amino acids with insufficient data, shown only if different.</b></p> <table> <tr><td>1.</td><td>8</td><td>Variable</td></tr> <tr><td>2.</td><td>7</td><td></td></tr> <tr><td>3.</td><td>22</td><td></td></tr> <tr><td>4.</td><td>40</td><td></td></tr> <tr><td>5.</td><td>32</td><td></td></tr> <tr><td>6.</td><td>36</td><td></td></tr> <tr><td>7.</td><td>60</td><td></td></tr> <tr><td>8.</td><td>48</td><td></td></tr> <tr><td>9.</td><td>41</td><td>Conserved</td></tr> </table><br><table> <tr><td>Sum</td><td>294</td><td>294</td></tr> <tr><td>+</td><td>0</td><td>(Amino acids with insufficient data)</td></tr> <tr><td>=</td><td>294</td><td>(0% with insufficient data)</td></tr> </table> | 1.                                   | 8 | Variable | 2. | 7 |  | 3. | 22 |  | 4. | 40 |  | 5. | 32 |  | 6. | 36 |  | 7. | 60 |  | 8. | 48 |  | 9. | 41 | Conserved | Sum | 294 | 294 | + | 0 | (Amino acids with insufficient data) | = | 294 | (0% with insufficient data) |
| 1.   | 8   | Variable                             |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 2.   | 7   |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 3.   | 22  |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 4.   | 40  |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 5.   | 32  |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 6.   | 36  |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 7.   | 60  |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 8.   | 48  |                                      |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| 9.   | 41  | Conserved                            |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| Sum  | 294   | 294                                  |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| +  | 0   | (Amino acids with insufficient data) |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |
| =  | 294   | (0% with insufficient data)          |   |          |    |   |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |  |    |    |           |     |     |     |   |   |                                      |   |     |                             |

Close