**Supplementary File 6:** Structural features analyzed in the massive nitrogenase structure prediction, with their respective programs.

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| --- | --- | --- |
| Variable | Program | Explanation |
| Total area | FreeSASA  (Mitternacht, 2016) | Exposed protein surface, in Å2 |
| Buried area | FreeSASA (Mitternacht 2016) | The sum of the individual chains surfaces minus the protein surface. |
| Polar area | FreeSASA (Mitternacht 2016) |  |
| Polar buried area | FreeSASA (Mitternacht 2016) |  |
| Apolar area | FreeSASA (Mitternacht 2016) |  |
| Apolar buried area | FreeSASA (Mitternacht 2016) |  |
| Intermolecular contacts | Prodigy (Vangone and Bonvin, 2015) | Number of contacts between residues of different chains. |
| Charged-charged contacts | Prodigy (Vangone and Bonvin 2015) | Number of interactions between charged residues of different chains. |
| Charged-polar contacts | Prodigy (Vangone and Bonvin 2015) | Number of interactions between charged residues and polar residues of different chains. |
| Charged-apolar contacts | Prodigy (Vangone and Bonvin 2015) | Number of interactions between charged residues and apolar residues of different chains. |
| Apolar-polar contacts | Prodigy (Vangone and Bonvin 2015) | Number of interactions between apolar residues and polar residues of different chains. |
| Apolar Non-Interacting-Surface | Prodigy (Vangone and Bonvin 2015) | See (Kastritis et al., 2014) |
| Charged Non-Interacting-Surface | Prodigy (Vangone and Bonvin 2015) | See (Kastritis et al. 2014) |
| Binding affinity | Prodigy (Vangone and Bonvin 2015) | Free energy of binding of the complex, in kcal/mol. The lower, the more stable the complex. |
| Gaussian Normal Mode eigenvalues (first five) | Prody (Bakan et al., 2011; Zhang et al., 2021) | Lowest eigenvalues associated with the Gaussian Normal Mode analysis. These values are associated with the frequency of normal mode oscillations (Bauer et al., 2019) |
| Radius of gyration | Prody (Bakan et al. 2011; Zhang et al. 2021) | See (Lobanov et al., 2008) |
| Residue-Residue average shortest path | RING (Clementel et al., 2022) /NetworkX (Hagberg et al., 2008) | Mean length of the shortest path joining two random nodes in a connected network. |
| Residue average clustering | RING (Clementel et al. 2022) /NetworkX (Hagberg et al. 2008) | Number of edges connecting the node and its neighbors between them divided by the number of edges of a complete subgraph involving all its neighbors. |
| Residue network density | RING (Clementel et al. 2022) /NetworkX (Hagberg et al. 2008) | Number of edges divided the number of edges that would be expected if the graph was complete. |
| Residue average degree | RING (Clementel et al. 2022) /NetworkX (Hagberg et al. 2008) | Mean number of neighbors of each residue. |

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