Supplementary Material

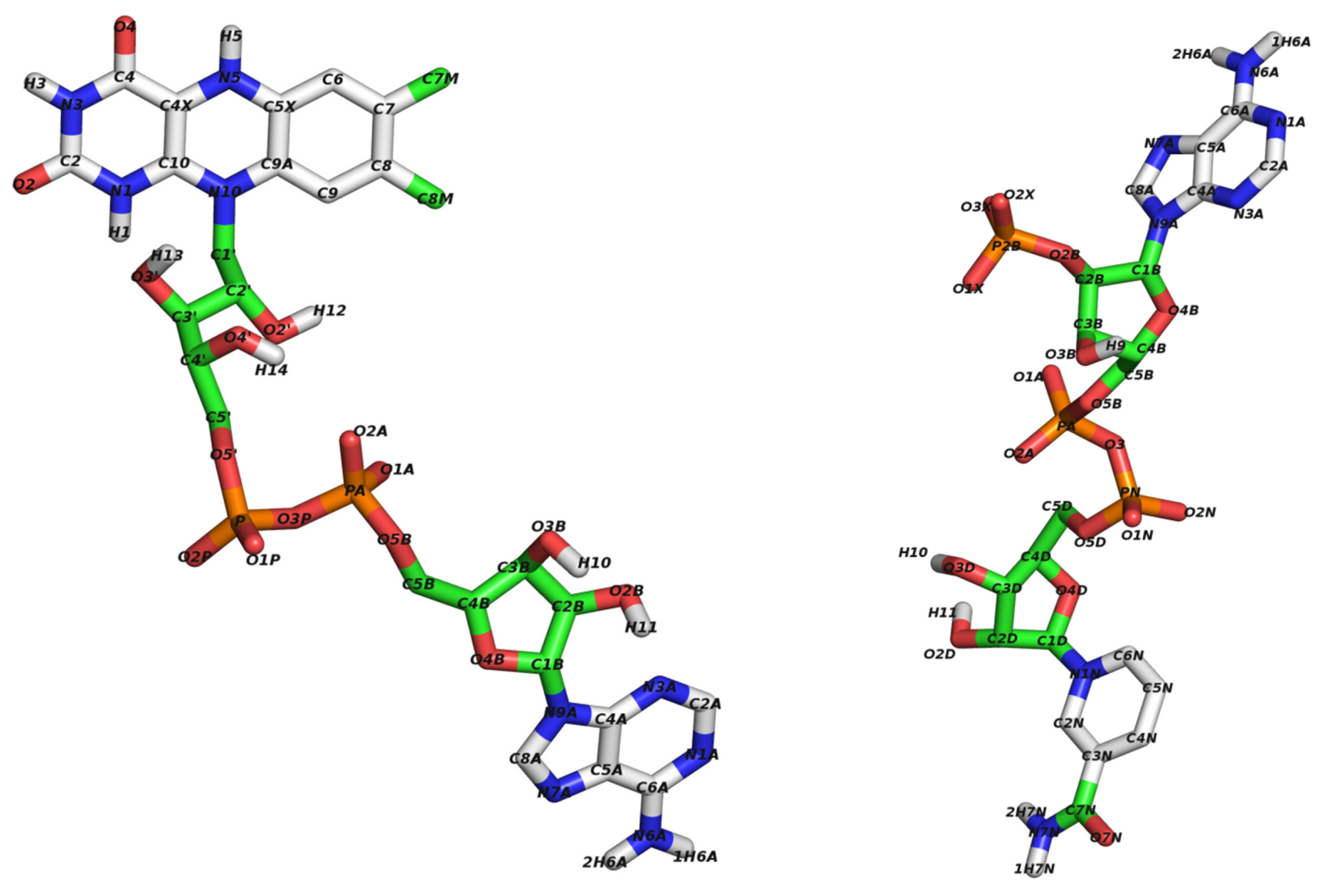
**Sup. Table 1:** Average and range pairwise sequence identity percentage of the different groups obtained from the circular cladogram presentation of the phylogenetic analysis.

**Sup. Fig. 1:** Atom labeling for the FAD (left) and NADPH (right) cofactors. Visualization done with PyMol software.

**Sup. Table 2:** Amino acid positions of the multiple sequence alignment that are conserved in more than 70% of the sequences.

**Sup. Table 1:** Average and range pairwise sequence identity percentage of the different groups obtained from the circular cladogram presentation of the phylogenetic analysis.

|  |  |  |
| --- | --- | --- |
| **Groups** | **Average sequence identity** | **Sequence identity range** |
| *Red* | 49.5 | 36 – 89 |
| *Blue* | 52.6 | 43 – 87 |
| *Green* | 53.9 | 43 – 88 |
| *Red-Blue* | 26.4 | 20 – 34 |
| *Red-Green* | 44.1 | 34 – 60 |
| *Blue-Green* | 27.4 | 20 – 34 |



**Sup. Fig. 1:** Atom labeling for the FAD (left) and NADPH (right) cofactors. Visualization done with PyMol software.