**Consolidated List of Test Scripts – Saved under the 5. Tests folder**

1. **test\_sequence\_matching.py**
   * Tests the functionality of reading sequences from input files.
   * Verifies correct sequence alignment using pairwise2.
   * Confirms the best match selection based on alignment scores.
2. **test\_probability\_calculator.py**
   * Tests the probability calculation based on alignment scores.
   * Verifies the p-value calculation for statistical significance.
   * Tests edge cases, such as extremely high or low alignment scores.
3. **test\_phylogeny\_builder.py**
   * Tests the construction of the phylogenetic tree.
   * Validates the tree structure using a set of known sequences (identical, divergent, etc.).
   * Confirms that the tree reflects evolutionary relationships correctly.
4. **test\_input\_validation.py**
   * Tests input file validation for missing or incorrectly formatted files.
   * Verifies that sequences in the FASTA files are correctly loaded into the program.
5. **test\_alignment\_logic.py**
   * Verifies the correct alignment of sequences using the pairwise2 function.
   * Tests with a variety of sequence types (similar, dissimilar, very short, very long).
6. **test\_output\_generation.py**
   * Verifies that the results are correctly written to classification\_results.txt.
   * Ensures that the output contains the correct sequence IDs and alignment scores.
7. **test\_edge\_cases.py**
   * Tests edge cases for the entire system:
     + Empty sequences or files.
     + Identical sequences.
     + Sequences with no matching database sequences.