Input: Structure information of query and reference proteins.
Output: Matched SSEs list among query and reference proteins.
Let Q and R as Query and Reference proteins, respectively.
Let TS_Q and TS_R as Topology String of Query and Reference proteins, respectively.
Let P as an array of 24 permuted topology strings.

1. $TS_Q \leftarrow$ MakeTopologyString (Q)
2. P = MakePermutedSequences(TS_Q)
3. $TS_R \leftarrow$ MakeTopologyString (R)
4. PS = H (TS_R, TS_R)   // *Perfect Score*
5. **for** i =1 **to** 24 **do**
6. $D[i]$ = |H(TS_Q, TS_R) – PS|
7. **end for**
8. i = Min (D)
9. **for** n-gram = n **down to** m **do**
10.   **for each** $W_i \in TS_R$ **do**
11.   **if** not matched (W_i) **then**
12.   **Begin**
13. j = Search (W_i, TS_Q)
14.   **if** j > 0 **then** MarkSSEsMatched (W_i, W_j)
15.   **end if**
16.   **end for**
17. **end for**