Table 1: HP energy model [23].

	H	P
H	−1	0
P	0	0

model. Later, Patton [43] used relative encodings to represent conformations and a penalty method to enforce the self-avoiding walk constraint. GAs have been used by Hoque et al. [22] for cubic and 3D HCP lattices. They used DFS-generated pathways [44] in GA crossover for protein structure prediction. They also introduced a twin-removal operator [45] to remove duplicates from the population to prevent the search from stalling. Ullah et al. in [12, 46] combined local search with constraint programming. They used a 20 × 20 energy model [25] on FCC lattice and found promising results. In another hybrid approach [47], tabu metaheuristic was combined with genetic algorithms in two-dimensional HP model to observe crossover and mutation rates over time.

However, for the simplified model (HP energy model and 3D FCC lattice) that is used in this paper, a new genetic algorithm GA$^+$ [8] and a tabu-based local search algorithm Spiral Search [9] currently produce the state-of-the-art results.

3.2. Empirical 20 × 20 Matrix Energy Based Approaches. A constraint programming technique was used in [48] by Dal Palù et al. to predict tertiary structures of real proteins using secondary structure information. They also used constraint programming with different heuristics in [49] and a constraint solver named COLA [50] that is highly optimized for protein structure prediction. In another work [51], a fragment assembly method was utilised with empirical energy potentials to optimise protein structures. Among other successful approaches, a population-based local search [52] and a population-based genetic algorithm [13] were used with empirical energy functions.

In a hybrid approach, Ullah and Steinöfel [12] applied a constraint programming-based large neighbourhood search technique on top of the output of COLA solver. The hybrid approach produced the state-of-the-art results for several small sized (less than 75 amino acids) benchmark proteins.

In another work, Ullah et al. [46] proposed a two stage optimisation approach combining constraint programming and local search. The first stage of the approach produced compact optimal structures by using the CPSP tools based on the HP model. In the second stage, those compact structures were used as the input of a simulated annealing-based local search that is guided by the BM energy model.

In a recent work [10], Shatabda et al. presented a mixed heuristic local search algorithm for PSP and produced the state-of-the-art results using BM energy model on 3D FCC lattice. The mixed heuristic local search in each iteration randomly selects a heuristic from a given number of heuristics designed by the authors. The selected heuristics are then used in evaluating the generated neighbouring solutions of the current solution. Although the heuristics themselves are weaker than the BM energy, their collective use in the random mixing fashion produces results better than the BM energy itself.

3.3. Parallel Approaches. Vargas and Lopes [53] proposed an Artificial Bee Colony algorithm based on two parallel approaches (master slave and a hybrid hierarchical) for protein structure prediction using the 3D HP model with sidechains. They showed that the parallel methods achieved a good level of efficiency while compared with the sequential version. A comparative study of parallel metaheuristics was conducted by Trantar et al. [54] using a genetic algorithm, a simulated annealing algorithm, and a random search method in grid environments for protein structure prediction. In another work [55], they applied a parallel hybrid genetic algorithm in order to efficiently deal with the PSP problem using the computational grid. They experimentally showed the effectiveness of a computational grid-based approach. All-atom force field-based protein structure prediction using parallel particle swarm optimization approach was proposed by Kandov in [56]. He showed that asynchronous parallelisation speeds up the simulation better than the synchronous one and reduces the effective time for predictions significantly. Among others, Calvo et al. in [57, 58] applied a parallel multiobjective evolutionary approach and found linear speedups in structure prediction for benchmark proteins and Robles et al. in [59] applied parallel approach in local search to predict secondary structure of a protein from its amino acid sequence.

4. Our Approach

The driving force of our parallel search framework is SS-Tabu [9] that has two versions: (i) the existing algorithm, designed for HP model (as shown in Algorithm 1 and described in Section 4.1) and (ii) the customised spiral search algorithm, designed for 20 × 20 BM energy model (as shown in Algorithm 5 and described in Section 4.2). We feed the two versions of spiral search algorithms in different threads in different combinations. The variations are described in the experimental results section.

4.1. SS-Tabu: Spiral Search. SS-Tabu is a hydrophobic core directed local search [9] that works in a spiral fashion. This algorithm (the *pseudocode* in Algorithm 1) is the basis of the proposed parallel local search framework. SS-Tabu is composed of H and P move selections, random-walk [60], and relay-restart [9]. However, this algorithm is further customised for detailed 20 × 20 energy model as described in Section 4.2. Both versions of SS-Tabu are used in parallel threads with different combinations within the parallel framework. The features of existing SS-Tabu are described in Algorithm 1.

4.1.1. Applying Diagonal Move. In a tabu-guided local search (see Algorithm 1), we use the diagonal move operator (shown in Figure 2) to build H-core. A diagonal move displaces ith amino acid from its position to another position on the lattice without changing the position of its succeeding $(i + 1)$th and