Figure S1
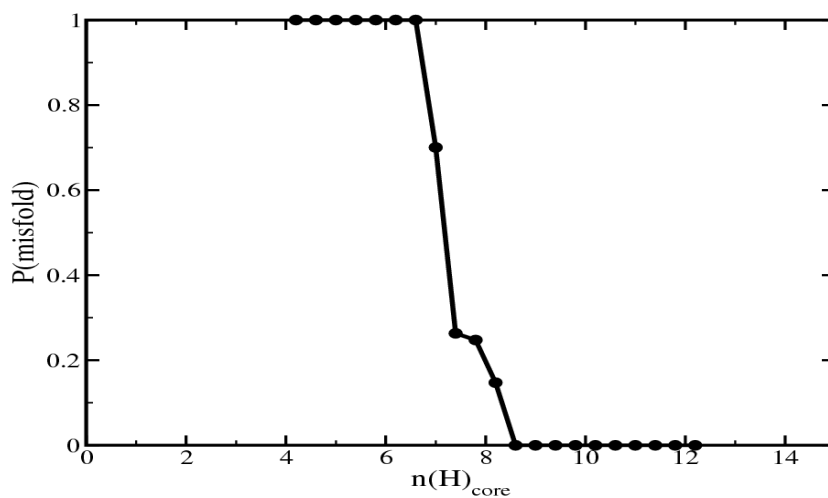

Figure S1. Probability of misfolding (P(misfold)) of the mutated sequences is plotted against nH_{core} for protein 2PM1.

Figure S2
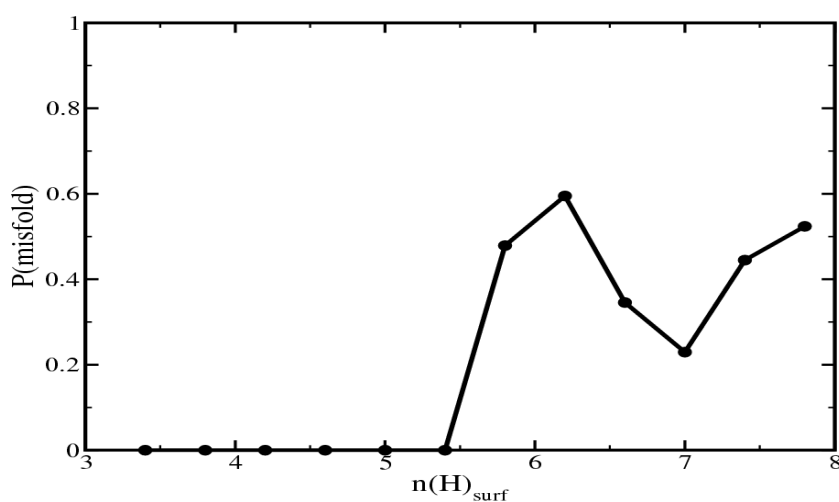

Figure S2. Probability of misfolding (P(misfold)) of the mutated sequences is plotted against nH_{surf} for protein 2PM1.

1

Figure S3

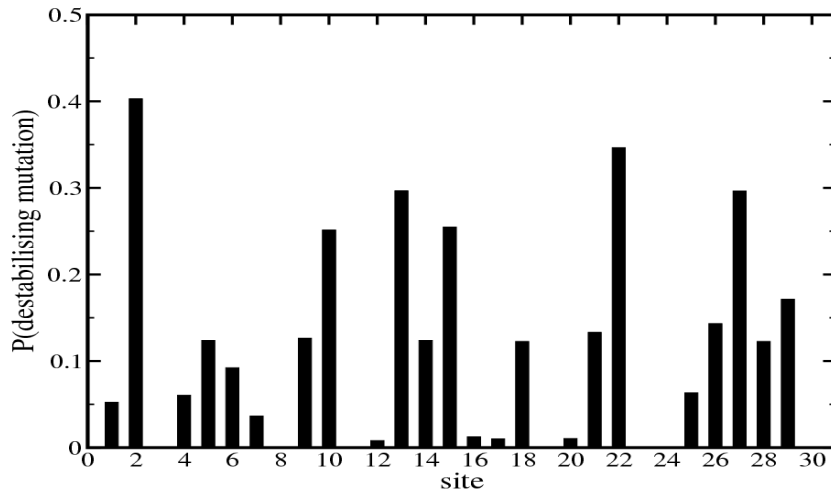**Figure S3. Probability of destabilizing mutations (P(dmut)) is plotted against the corresponding mutated site for protein 2PM1.**

The core sites are 2, 4, 5, 8, 9, 13, 14, 15, 18, 19, 26, 27, 28, 29, 30

The surface sites are 1, 3, 6, 7, 10, 11, 12, 16, 17, 20, 21, 22, 23, 24, 25

sites 2(core), 13(core), 22(surface), 27(core) have the most destabilizing effect upon mutation.

8 out of 15 surface sites (3, 11, 12, 16, 17, 20, 23, 24) have minimal destabilizing effect upon mutaion.

2 out of 15 core sites (8, 19) have minimal destabilizing effect upon mutation.
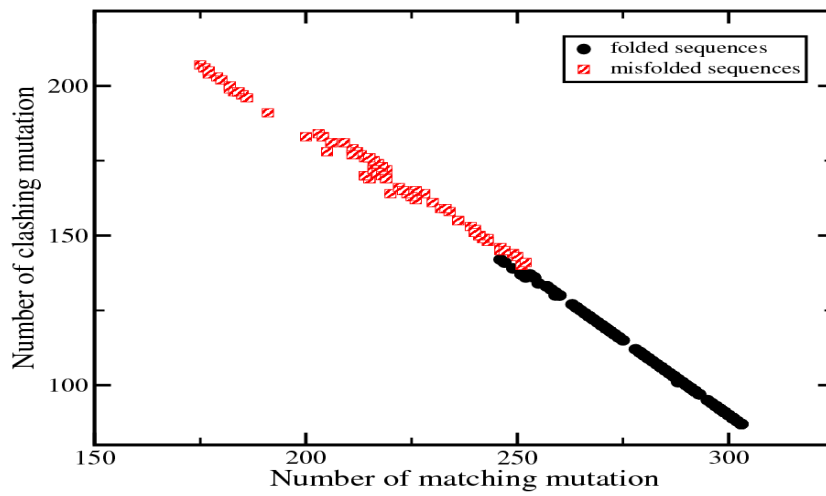
Figure S4

Figure S4. Number of clashing mutation is plotted against the number of matching mutation for folded and misfolded sequences.