**Table S2.** RMS deviation of C-α in the 4 models of mutants, as compared to the WT structure.

|  |  |  |
| --- | --- | --- |
| pVHL missense mutation | Root Mean Square (RMS) | Number of C-α atoms aligned |
| F136L | 0.458 | 132 to 132 atoms |
| F119L | 0.258 | 141 to 141 atoms |
| N78S | 0.233 | 136 to 136 atoms |
| Y98H | 0.218 | 136 to 136 atoms |