**Table S2 Presumed hydrophobic substrate interacting amino acid residues.**

|  |  |  |  |
| --- | --- | --- | --- |
| Residue | Identity(1) [%] | Conservative  Exchange | Distance [Å](2) |
| F11 | 69 | + | 3.2 |
| P54 | 100 |  | 3.3 |
| V56 | 57 | + | 3.3 |
| F144 | 84 | or Y | 3.3 |
| F147 | 0 | 100 % | 3.9 |
| A471 | 89 | - | 5.2 |
| I473 | 0 | 100 %(3) | 3.6 |
| V476 | 100 |  | 3.9 |

(1)Identity refers to 200 accessions grouping into eleven subgroups including *Bacteria* and *Archaea*. Multiple alignements and phylogenetic trees were obtained using the PipeAlign server at http://bips.u-strasbg.fr/PipeAlign/. (2)The distance between residues and the docked carotene substrate was determined in PyMol. (3)With the exception of *Archaea*.