

Annex 1

Multiple alignment of *Pg* DODA and its homologues with *Sphingomonas* PCA 4,5-dioxygenase LigAB shows the conservation of the LigB domain (pfam02900). Based on the LigAB crystal structure 1B4U, we indicated on the first line in bold characters the position of the amino acids responsible for the orientation of the aromatic substrate (A, D, E) and the those responsible for the orientation of the iron cofactor (B, C, F or G). Highlighted in blue characters, we show a comparison of *Sphingomonas* LigAB secondary structure with those predicted for *Portulaca* DODA and for its *Physcomitrella* homologue realized with PROF tool (1) and a selection with an accuracy > 82% in PROF predictions in (2). Alpha-helices are highlighted in red and beta-sheets in green. For Genbank accession numbers see Annex 2.





