

## 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 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.

## Positions

Secondary structure Sphingomonas LigAB

Sphingomonas LigAB

Portulaca DODA

Secondary structure Portulaca 1

Secondary structure Portulaca 2

Beta vulgaris DODA

Mesembryanthemum 2

Mesembryanthemum 1

Iresine

Mammillaria

Phytolacca

Arabidopsis

Glycine 1

Medicago

Lotus

Lycopersicon 1

Zea

Oryza

Triticum

Pseudomonas putida

Physcomitrella

Secondary structure Physcomitrella 1

Secondary structure Physcomitrella 2

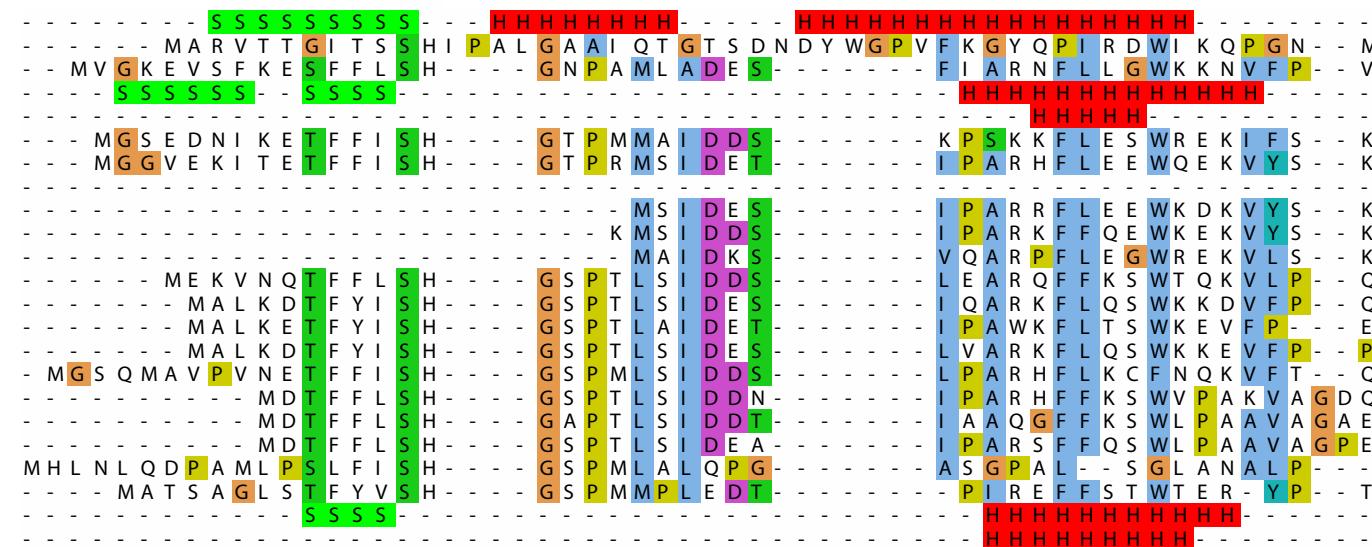
10

20

30

40

50

**AB**

## Positions

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Sphingomonas LigAB

Portulaca DODA

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Zea

Oryza

Triticum

Pseudomonas putida

Physcomitrella

Secondary structure Physcomitrella 1

Secondary structure Physcomitrella 2

60

70

80

90

100

110

**C**