



STRUCTURAL  
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**Supporting information for article:**

**Structural studies of a cold-adapted dimeric  $\beta$ -D-galactosidase from *Paracoccus* sp. strain 32d**

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**Figure S1** Structure-based sequence alignment of *Par* $\beta$ DG monomer with typical GH2  $\beta$ DGs: *Arthrobacter* sp. C2-2  $\beta$ DG (ArtBDG)(PDB ID: 1YQ2) and *E. coli lacZ* (EcoBDG) (PDB ID: 4DUV); with similar in fold 5-domain  $\beta$ DGs: *B. vulgatus* (3GM8) and *S. pneumoniae* (4CUC); with smaller 3-domain GH2: human  $\beta$ -glucuronidase (3HN3) and 4-domain *B. fragilis*  $\beta$ DG (3CMG). The sequences of the fragments with the highest structural homology are colored red and with the smallest are green, and the most structurally different fragments are violet or colorless (TCS index). The Domains are separated by vertical black lines.