

Table S3. Tertiary structure comparison of the N-terminal domain of cyclomaltodextrinase from *Flavobacterium* sp. No. 92 with individual representatives of real SBD CBM families.^a

CBM family	Source ^b	PDB code (UniProt) ^c	C α	RMSD (Å)
CBM20	GH15 GAMY, <i>Aspergillus niger</i>	1AC0	45	1.99
CBM21	GH15 GAMY, <i>Rhizopus oryzae</i>	2V8M	53	2.05
CBM25	GH13_19 M6H, <i>Bacillus halodurans</i>	2C3W	44	2.04
CBM26	GH13_19 M6H, <i>Bacillus halodurans</i>	2C3H	38	1.51
CBM34	GH13_21 AAMY, <i>Thermoactinomyces vulgaris</i> (TVA-I)	1UH4	48	1.74
CBM41	GH13_14 PUL, <i>Thermotoga maritima</i>	2J73	35	1.97
CBM45 (model)	AGWD, <i>Solanum tuberosum</i>	Template: 2C3W (Q9AWA5)	38	2.09
CBM48	AMPK β 1-subunit, <i>Rattus norvegicus</i>	1Z0M	40	1.81
CBM53 (model)	GT5 SS3, <i>Arabidopsis thaliana</i>	Template: 2C3W (F4IAG2)	41	2.04
CBM58	GH13_36 AAMY, <i>Bacteroides thetaiotaomicron</i> (SusG)	3K8M	39	1.89
CBM68	GH13_14 PUL <i>Anoxybacillus</i> sp.	3WDJ	39	1.94
CBM69	GH13_37 AAMY uncultured bacterium	5X5S	33	2.03
CBM82 (model)	GH13_41 AAMY <i>Eubacterium rectale</i>	Template: 2C3H (D6DYL9)	30	2.05
CBM83 (model)	GH13_41 AAMY <i>Eubacterium rectale</i>	Template: 2J73 (D6DYL9)	38	1.94
N-domain ^d	GH13_5 AAMY, <i>Halothermothrix orenii</i> (AmyB)	3BC9	62	1.77

^a Results of superposition of the *Flavobacterium* sp. No. 92 cyclomaltodextrinase N-terminal domain ([24]; PDB code: 1H3G) with its SBD CBM counterparts are shown as the number of corresponding C α atoms and the RMSD value (the last two columns). For those with no three-dimensional structure available until now (CBM45, CBM53, CBM82 and CBM83), a homology model has been created based on a template.

^b The individual enzymes are abbreviated as follows: GAMY, glucoamylase; M6H, maltohexaose-producing amylase; AAMY, α -amylase; PUL, pullulanase; AGWD, α -glucan, water dikinase; AMPK, AMP-activated protein kinase; SS3, starch synthase 3.

^c UniProt means the accession No. from the UniProt database for the sequence of the enzyme possessing the particular CBM for which the three-dimensional structure has not been solved until now.

^d Although the domain N from the GH13_5 α -amylase AmyB from *H. orenii* [43] has not been assigned any SBD CBM family as yet [14], it is shown for comparison here since it exhibits a significant structural similarity with the N-terminal domain of the studied cyclomaltodextrinase.