Figure S1. Sequence alignment of the newly proposed subfamily GH13_46 represented by the cyclomaltodextrinase from *Flavobacterium* sp. No. 92. The alignment of all 108 selected members (Table S1) covers their complete sequences, i.e. the canonical family GH13 domains A (catalytic TIM-barrel), B (inserted roughly between CSR-I and CSR-II) and C (succeeding the CSR-VII) as well as the domain N (preceding the catalytic TIM-barrel). All seven family GH13 CSRs are boxed by black frames, the N-terminal domain is indicated by the red horizontal lane above the alignment. The residues of the catalytic triad are located in CSR-II (aspartic acid), CSR-III (glutamic acid) and CSR-IV (aspartic acid). Identical and similar positions are signified by asterisks and dots/semicolons under the alignment blocks. The colour code for the selected residues: W, yellow; F, Y – blue; V, L, I – green; D, E – red; R, K – cyan; H – brown; C – magenta; G, P – black. The labels of protein sources consist of the UniProt accession number and the name of the organism, the four experimentally characterized enzymes being marked by an asterisk. The four individual groups distinguished from each other by different colours correspond to representatives shown in Figure 2; the sequence order in the alignment (starting from the top) reflects their order in the tree in the anticlockwise manner (starting from the first sequence in the red cluster).


N-terminal module
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-CSR-I
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A0A5C7BVB6_Empedobacter_haloabium
*CMD_Q8KKG0_Flavobacterium_sp_No_92
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*CMD_A0A3GLBI3_Massilia_timonae
A0A318IT25_Undibacterium_pigrum
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A0A315D4L5_Limnohabitans_sp_Bal53
A0A1I6J9V2_Mitsuaria_sp_PDC51
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A0A397R1F9_Pelomonas_sp_BT06
A0A2N8KS59_Paucibacter_aquatile
A0AF6R6N0L4_Kinneretia_asaccharophila
A0A143HP13_Microbulbifer_thermotolerans
F7NX40_Rheinheimera_sp_A13L
A0A5C8LY70_Pararheinheimera_tangshanensis
J1QM75_Alishewanella_aestuarii
A0A2E6EH58_Alteromonadaceae_bacterium
A0A5B7ZRZ5_Thermomonas_sp_SY21
A0A4Q6FW84_Xanthomonadaceae_bacterium
A0A0Q7PH17_Lysobacter_sp_Root494
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A0A353X3L2_Cytophagales_bacterium
A0A098SAM2_Phaeodactylibacter_xiamenensis
A1ZWA8_Microscilla_marina
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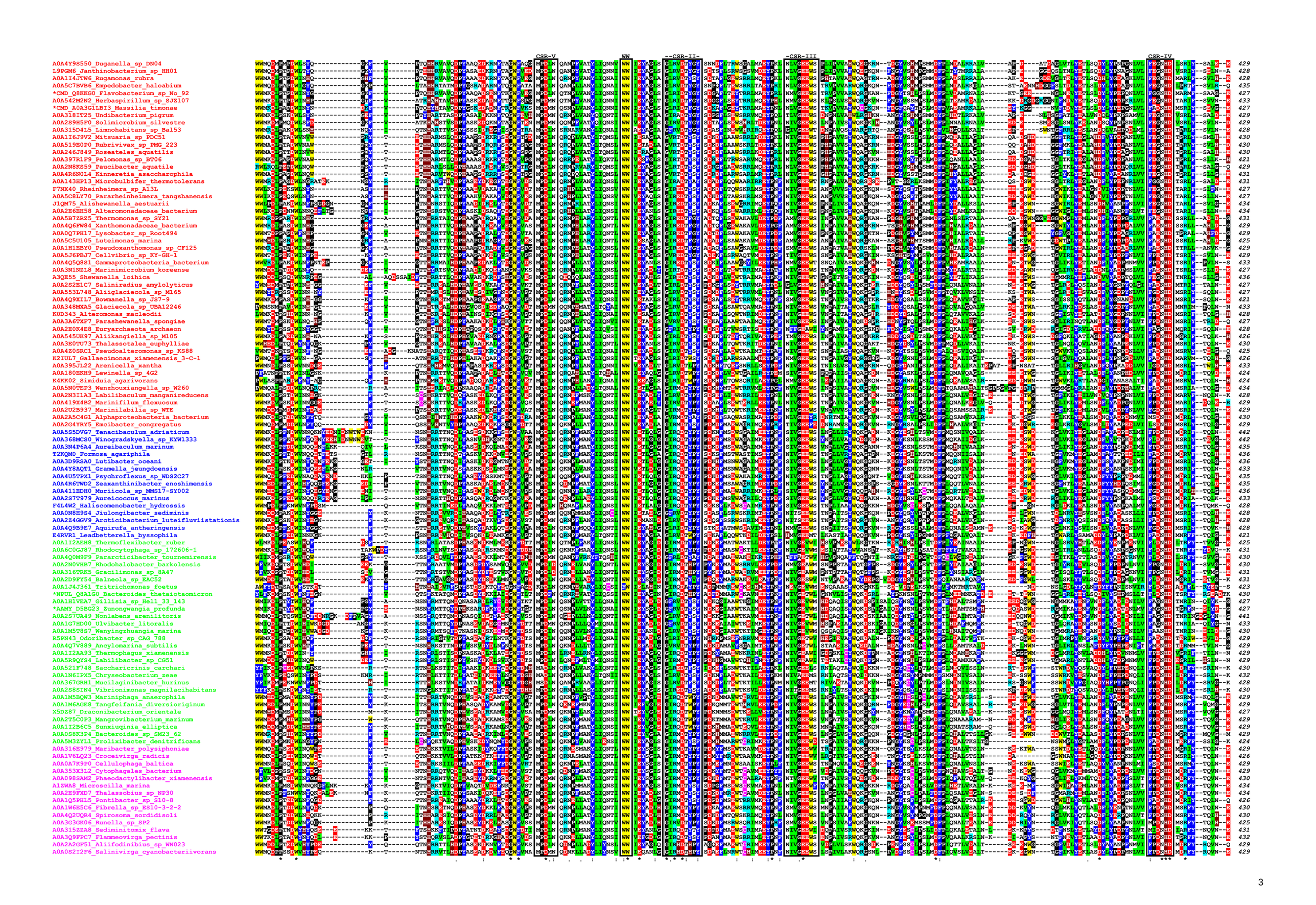
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A0A098SAM2_Phaeodactylibacter_xiamenensis
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A0A2N8KS59_Paucibacter_aquatile
A0A4R6N0L4_Kinneretia_asaccharophila
A0A143HP13_Microbulbifer_thermotolerans
F7NX40_Rheinheimera_sp_A13L
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J1QM75_Alishewanella_aestuarii
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A0A5B7ZRZ5_Thermomonas_sp_SY21
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