



Figure S1. Schematic representation of the genome-encoded carotenoid biosynthesis pathway in strain Ch08.

Table S1. Carotenoid biosynthesis genes in strain Ch08 in comparison with reference amino acid Sequences.

Reference amino acid sequence	Closest hit in strain Ch08	Identity, %	Function
DXR (EC:2.2.1.7, P77488)	WP_406698708.1	40.1	MEP pathway
DXP (EC:1.1.1.267, P45568)	WP_406696055.1	44.1	
IspD (EC:2.7.7.60, P69834)	WP_406699555.1	33.3	
IspE (EC:2.7.1.148, P62615)	WP_406700145.1	34.7	
IspF (EC:4.6.1.12, P62617)	WP_406699962.1	46.8	
IspG (EC:1.17.7.1, 1.17.7.3, P62620)	WP_406696392.1	46.5	
IspH (EC:1.17.7.4, P62623)	WP_406695357.1	53.7	
FDS (WP_064029043.1)	WP_406701139.1	48.1	C15, C30 synthesis
HpnC (WP_010035789.1)	WP_406699927.1	57.9	
HpnD (WP_010034650.1)	WP_406699928.1	42.3	
HpnE (WP_010034634.1)	WP_406699929.1	47.8	
CrtN (WP_010037865.1)	WP_406701214.1	63.9	C30 carotenoids
CrtP (WP_010037863.1)	WP_406694412.1	63.4	
AldH (AGA25803.1)	WP_406693525.1	32.0	
CrtQ (A0A0M6XTT3)	WP_406694410.1	47.1	
CrtO (MLCJFOMH_05351)	WP_406694411.1	100.0	