```
                                   **
Ca LCY   1 ---------118  WPNNYGVWVDEFEAMDLLDCLDATWSGAAVYIDDKTTKDLNRPY 161
CaCCS    1 ---------118  WPNNYGVWVDEFEKLGLEDCLDHKWPVSCVHISDHKTKYLDRPY 161
Sy LCY   1 -----------39 WENTYGIWGPELDSLGLEHLFGHRWSNCVSYFGEAPVQHQYN-Y  81
Eh LCY   1 -----------44 WSFHEDDLTPG-QHAWLAPLVAHAWPGYEVQFPDLRRRLARG-Y  85

Ca LCY 162 GRVNRKQLKSKMMQKCILNGVKFHQAKVIKVIHEESKSMLICNDGITIQA 211
CaCCS  162 GRVSRKKLKLKLLNSCVENRVKFYKAKVLKVKHEEFESSIVCDDGRKISG 211
Sy LCY  82 GLFDRAQLQQHWLRQCEQGGLQWQLGKAAAIAHDSHHSCVTTAAGQELQA 131
Eh LCY  86 YSITSERFAEALHQALGEN--IWLNCSVSEVLPNS----VRLANGEALLA 129

                                                          *
Ca LCY 212 TVVLDATGFSRSLVQYDKPYNPGYQVAYGILAEVEEHPFDVNKMVFMDWR 261
CaCCS  212 SLIVDASGYASDFIEYDKPRNHGYQVAHGILAEVDNHPFDLDKMMLMDWR 261
Sy LCY 132 RLVVDTTGHQAAFIQRPHSDAIAYQAAYGIIGQFSQPPIEPHQFVLMDYR 181
Eh LCY 130 GAVIDGRGVTASSAMQT-----GYQLFLGQQWRLTQ-PHGLTVPILMD-- 171

                                                **
Ca LCY 262 DSHLKNNVELKERNSRIPTFLYAMPFSSNRIFLEETSLVARPGLGMDDIQ 311
CaCCS  262 DSHLGNEPYLRVKNTKEPTFLYAMPFDRNLVFLEETSLVSRPMLSYMEVK 311
Sy LCY 182 SDHLSPE--ERQ---LPPTFLYAMDLGNDVYFVEETSLAACPAIPYDRLK 226
Eh LCY 172 ATVAQ-Q--QGYR------FVYTLPLSADTLLIEDTRYANVPQR-DDNAL 211

                                        *
Ca LCY 312 ERMVARLSH-LGIKVKSIEEDEH-CV-IPMGGPLPVLPQRVVGI---GGT 355
CaCCS  312 RRMVARLRH-LGIKVRSVLEEEK-CV-ITMGGPLPRIPQNVMAI---GGT 355
Sy LCY 227 QRLYQRLAT-RGVTVQVIQHEEY-CL-FPMNLPLPDLTQSVVGF---GGA 270
Eh LCY 212 RQTVTDYAHSKGWQLAQLEREETGCLPITLAGDIQALWADAPGVPRSGMR 261

           *
Ca LCY 356 AGMVHPSTGY 365-------- 498
CaCCS  356 SGIVHPSSGY 365-------- 498
Sy LCY 271 ASMVHPASGY 280-------- 411
Eh LCY 262 AGLFHPTTGY 271-------- 386
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Supplemental Figure S2. Multiple alignment of deduced amino acid sequence of selected lycopene beta-cyclases (LCYs) and capsanthin-capsorubin synthase (CCS) *Capsicum annuum* (Ca). Ca LCY (Accession CAA60119), Ca CCS (Accession CAA53759), *Synechocystis* Sy LCY (Accession CAA52677) and *Erwinia herbicola* Eh LCY (Accession QO1331) were used. The positions of the first and last amino acids in each sequence are shown. Identical residues are shown on a black background and residues selected for point mutations are indicated by an asterisk.