

Additional file 4. Protein characterisation of the carotenoid cleavage dioxygenases from *A. thaliana* and the *V. vinifera* orthologues present in the grapevine genome

CCD	Accession ¹	Length (aa)	Subcellular localisation ²	Transit peptide ³	pI ⁴	MW ⁵	Conserved histidines (aa position) ⁶
AtCCD1	At3g63520	538	Cytosol	-	6.05	60908.11	H ₂₂₁ —H ₃₃₅ —H ₄₈₆ —H ₅₂₂
VvCCD1.1	VV13G12460	542	Cytosol	-	6.14	61364.44	H ₂₂₂ —H ₃₃₆ —H ₄₉₀ —H ₅₂₆
VvCCD1.2	VV13G12530	542	Cytosol	-	5.97	61150.21	H ₂₂₂ —H ₃₃₆ —H ₄₉₀ —H ₅₂₆
AtCCD4	At4g19170	595	Chloroplast; membrane bound	1-30	6.42	65601.73	H ₂₈₆ —H ₄₀₃ —H ₅₄₆ —H ₅₈₂
VvCCD4a	VV02G12270	573	Chloroplast; membrane bound	1-32	6.49	63381.46	H ₂₆₉ —H ₃₈₃ —H ₅₂₄ —H ₅₆₀
VvCCD4b	VV02G12290	589	Chloroplast; membrane bound	1-6	6.63	65607.28	H ₂₈₁ —H ₃₉₆ —H ₅₄₀ —H ₅₇₆
VvCCD4c	VV16G01030	586	Chloroplast; membrane bound	1-8	5.78	65088.35	H ₂₈₆ —H ₄₀₁ —H ₅₃₆ —H ₅₇₂
AtCCD7	At2g44990	629	Chloroplast; membrane bound	1-25	6.30	70850.30	-
VvCCD7	VV15G01930	626	Chloroplast; membrane bound	1-29	7.68	70328.58	-
AtCCD8	At4g32810	570	Chloroplast	1-29	6.65	63956.91	-
VvCCD8	VV04G03390	563	Chloroplast	1-27	7.27	62343.90	-

¹ Accession number for the CCD protein sequences in TAIR (At-) (<http://www.arabidopsis.org/>) and PLAZA version 1 (At- and Vv-)

(http://bioinformatics.psb.ugent.be/plaza_v1/)

² Softberry Protcomp (<http://linux1.softberry.com/berry.phtml>) prediction of the subcellular localisation of the predicted CCD protein sequence

³ Length (in amino acids) of predicted transit peptide from Softberry Protcomp prediction

⁴ Theoretical isoelectric point (pI) of the predicted CCD protein sequence (http://web.expasy.org/compute_pi/)

⁵ Theoretical molecular weight (MW) of the predicted CCD protein sequence (http://web.expasy.org/compute_pi/)

⁶ Position of the conserved histidines in the predicted CCD protein sequence (from the multiple protein alignments in Supplementary figure X)