

CPT1_At2g23410	1	MLSL-----LSSDSSL
CPT2_At2g23400	1	MLSL-----LST---LV
CPT6_At5g58780	1	MLSI-----LSS---LL
CPT7_At5g58770	1	MLSL-----RVPTPTSDFRFRYQAGDLERRWRLS
CPT8_At5g58782	1	MNFMIHANHLLVFLTLSTM-----LSMLWFL
CPT9_At5g58784	1	MLSL-----FSVVFTRL
CPT3_At2g17570	1	MAEL-----PGQIRHIGGRMSQLLEQIYGFS---
CPT4_At5g60510	1	MNNT-----REEV---GEFTQIFNALMSLM---
CPT5_At5g60500	1	MN-T-----LEEVE---DESTHIFNALMSLM---
LEW1_At1g11755	1	MDSNQSMRLLSAWIGQIGDLGLNLLWRFIHIVVSLWYIVSGIFEAE-----

CPT1_At2g23410	13	SLLFLFLIPCLFITSYIGFPVF--LLKLIGLIKIKAAARD---NEKRDEGTYVVDREDA-----LQRELMR
CPT2_At2g23400	10	ALPFLFLIPCLFITSYICFPVF--LTKLLGLIKFKAARDDDDNEKRDEATCVVREEE-----LQRELMR
CPT6_At5g58780	10	SLLFLFIISCFITSHFWFPLS--LPKILGFIKITSSRDYDNEQRDEGTYVVGVEE-----LQRELMR
CPT7_At5g58770	30	RDSFLSFSP-----KFEENRGFRFGVKSSKSDVSFTAAEEEEETLPEELHAELMPK
CPT8_At5g58782	28	SLLSLLLLPCL----RPCFPKAGSLK-----NKKKIDKGTYYVVGEEET--PKELQRELMR
CPT9_At5g58784	13	AL---FLIPGLFISRRLNVPLS--LTNILRFIKI IASKYD-DEEERNEKRGTMGKEQK-RG---RNIMPK
CPT3_At2g17570	27	-----RRSLFRVISMGPITP
CPT4_At5g60510	23	-----RKFIKVLRVGPITP
CPT5_At5g60500	22	-----RKFLFRVLCVGPITP
LEW1_At1g11755	48	----->

CPT1_At2g23410	73	HVAFILDGNRRWA----KRALG--TTSQGHEAGAKRLIDIAELCFELGVHTVSAFAFSTENWGRDKIEI
CPT2_At2g23400	73	HVSFILDGNRRWA----KRDGL--TTAQGHEAGTKRIIEIAEVCFELGIHTVSAFAFSTENWGRDKFEV
CPT6_At5g58780	73	HVAVIMDGNRRWA----KRALG--LTSQGHEAGAKRLIEFSELCKLGIHTVSAFAFSTENWGRHKIEV
CPT7_At5g58770	80	HVAIIMDGNRWA----KNRGL--QPWDGHRAGVEALKEIVELCGKWGIQVLTVFASFSTDNWIRPRIEI
CPT8_At5g58782	78	HVAVIMDGNRRWA----KQTGL--LTSQGYEAGAKRLLEFADLCKLGINTVSAFAFSTENWGRHKIEV
CPT9_At5g58784	73	HVAVILDGNRRWA----EKRGL--GTSEGHEAGARRLMENAKDCFAMGTNTISLFAFSTENWERPEDEV
CPT3_At2g17570	42	HIAFIMDGNRRYA----KKCGL--LDGSGHKAGFSALMSMLQCYELGIKYVTIYAFSIDNFRRKPEEV
CPT4_At5g60510	38	NISFIMDGNRRFA----KKRNLEGLD-AGHRAGFISVKYILQYCKEIGVPYVTLTAFGMDNFKRGPEEV
CPT5_At5g60500	37	NISFIMDGNRRFA----KKHNLIGLD-AGHRAGFISVKYILQYCKEIGVPYVTLTAFGMDNFKRGPEEV
LEW1_At1g11755	48	SYAITLGLNKKYGSIDLEKLRCLAVVVDIEAAQDVANVVELLQWLTTIGVKQVGLF----DSQGLLKKSK

I

II

III

CPT1_At2g23410	136	DNLM-----SLIQHYRNS-----N---IKFFHRESEVRVSVIGNKTKIPESLLKEIH-EIEEATKGYKNK
CPT2_At2g23400	136	KCLM-----SLFNHYL-KS-----N---IQYFQRKEVRVSVIGNKTKIPESLLKEIH-EIEEATKATR--
CPT6_At5g58780	136	KCLM-----SLIQHYL-KS-----K---IQYFQREETRVSVIGNLTKIPESLLRTVQ-EIEEATRSYKKK
CPT7_At5g58770	143	DFLF-----SLFERSL-KT-----E---FQNLAKNNVRISIIGDSSKLPKSLLRVIN-EVEEVTKNNTRL
CPT8_At5g58782	141	KCLM-----YLFQRYLKS-----IQFFQSKAIRVSVIGNLAKIPESLLRTVH-ELEEATKSYYKK
CPT9_At5g58784	136	KCLM-----ALFEKYL-AS-----D---MPYLRSDKIKISVIGNRTKLPELGLIE-EVEEATKSIEGK
CPT3_At2g17570	105	ESVM-----DLMLEKIKSL---LEK---ESIVHQYGIRVYFIGNLALLNDQVRAAE-KVMKATAKNSRV
CPT4_At5g60510	102	KCVM-----DLMLEKVELT---IDQ---AVSGNMNGVRIIFAGDLNSLNERFRAATK-KLMELTEENRDL
CPT5_At5g60500	101	KCVM-----DLMLEKVELA---IDQ---AVSGNMNGVRIIFAGDLNSLNEHFRAATK-KLMELTEENRDL
LEW1_At1g11755	114	DLILETVPGSMLLEEIEKDVADPGKRIALEFISSSDNKEAVMKAANILLQRYLKSSHPEDDKG-----

<.....

CPT1_At2g23410	192	HLIMAVDYSKGFDMHACK-SLVKKSEK-----GLIREEDVDEALIERELL
CPT2_At2g23400	189	-----ISISSW-HLVKKSEK-----GLIREEDVDEALIERELL
CPT6_At5g58780	191	HLILAIDYSGRLDILRACK-SIVKKSEK-----GLIREEDVDEALIERELL
CPT7_At5g58770	198	QLIVAVGYSGKYDVLQACR-GIARRVKD-----GEIEVEEIDERLIEEELE
CPT8_At5g58782	196	HLILAIDYSGRFDILGAC-KNIVKKSEQ-----GLIREEDVDETLEFERELQ
CPT9_At5g58784	191	NLIIAIDYSGRYDILQACK-SLANKVKD-----GLIQVEDINEKAMEKELL
CPT3_At2g17570	163	VLLICIAYNSTDEIVQAVKSKCINKSDNIEASNYKHEDSDSDIEGTMENQEKKIQLVDIEENMQ----
CPT4_At5g60510	160	IVVVCVAYSTSVEIVHAVRSCVRKSKT-----GDGSS-----ALELSDIEECMY-----
CPT5_At5g60500	159	IVVVCVAYSTSLEIVHAVRKSCVRKCTN-----GDDLIV-----LLELSDVEECMY-----
LEW1_At1g11755	177	-----EDFFTESHLDNALR

IV

CPT1_At2g23410	237	TNCSDFPSPDLMIRTSGEQRISNFFLWQLAYSELFFSPVFWPDFDKDKLLEALASYQRRER ^{RFG} CRV---
CPT2_At2g23400	221	TNCSDFPSPDLMIRTSGEQRISNFFLWQLAYTELFYSPVLWPDFDKDKLLEALASYQGRER ^{RFG} CRV---
CPT6_At5g58780	236	TNCTEFPSPDLLIRTSGEQRISNFFLWQLAYTELFYSPVLWPDFDKDKLLEALVSYQRRER ^{RFG} CRV---
CPT7_At5g58770	243	TNCTEFPSPDLLIRTSGEQRLVSNFFLWQLAYTELFFAQELWPDFGRSGFIEALMSFQQRQR ^{RFG} GRKS--
CPT8_At5g58782	241	TRCTEFPSPDLLIRTSGEQRISNFFLWQLAYTEFFSPVLWPDFDKQKFIEALVSYQRRDR ^{RFG} SRL---
CPT9_At5g58784	236	TKCFEFPNPDLLIRTSGEQRISNFFLWQSAYTELYFPTVLWPDFGEAEYLEALTWYQQRQR ^{RFG} RRV---
CPT3_At2g17570	228	--MSVAPNPDILIRSSGETRLSNFFLWQTGNTQLCSPAALWPEIGLRHLLWAILNFQRNHSYLEKRRKQL
CPT4_At5g60510	205	--TSVVPVVDLVVRTGGGDRLSNFMWTQTSRALLHRTEALWPELGLWHLVWAILKFQRMQDYLTQKKKKLH
CPT5_At5g60500	204	--TSIVPVVDLVIRTGGGDRLSNFMWTQTSRSLHRTEALWPELGLWHLVWAILKFQRMQDYLTQKKKKLD
LEW1_At1g11755	191	VVGENVHPDLLLLVYGPISRHLGFPWRLRYTEIVHMGTL-KYMRYSLLKAIHKFTGVHQ ^{NYGT} -----

V

RXG
NXG

Figure S1. Multiple sequence alignment for *Arabidopsis* cis-PTs listed in Table 1. Highly conserved regions are highlighted in gray. They are not present in CPT binding protein LEW1. Motifs essential for binding of substrate are highlighted in black. RXG (eventually NXG) motif highlighted in green is critical for catalysis [65] and is missing in heteromeric CPT enzymes.