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-102 CTCTAGATCTGTTGAAATTGAAGCAAGGATCGATCAGAATTCAGAAAGTAGTGCAACAA
    GCTCGAGCTCGACTCCTAAGATCTCCCGTAGTATACTACGAAAGAACCACATAGAATTTG
1   ATGAATGGCGCTTCAACATCTAGTACCATCCGAGCAGCCTTCTCCCACTGTGTACAACAA
    M N G A S T S S T I R A A F S H C V Q Q
61  GTACGAAGCTATGATTACCAACATTACCTTTGCCTCCTCCAGCTGTCCCCTAACATGCGG
    V R S Y D Y H H Y L C L L Q L S P N M R
121 AAAGCTGCATTTGCTCTGCGTGCTTTCAATGTAGAACTGCCAGAGCCATGGATGTTGCT
    K A A F A L R A F N V E T A R A M D V A
181 TCTGATCCAAGAATTGGTCTTATGCGCCTCCTTTGGTGGCAAGAAGCCATAGACAAAATC
    S D P R I G L M R L L W W Q E A I D K I
241 TTCGCCCACAAGAAAATCGAACATCCCACTGCTCAAGCTCTCTCTTCGATAATCTCTGAA
    F A H K K I E H P T A Q A L S S I I S E
301 CACAAAATCAGCAAAAGTTGGCTAAAGAGGTCTGTTGAAGCTCGGATTATCGATGCAAGA
    H K I S K S W L K R S V E A R I I D A R
361 AGGGAGGAAAATGAAATCCCACAGTCGATCGAAGAATTGGAAAAATATGCCGAATCCACT
    R E E N E I P Q S I E E L E K Y A E S T
421 GTTTCACCATATTATATATGACACTTCAAGCTGGAGGAATAAGGTCCACGGCAGCGGAT
    V S T I L Y M T L Q A G G I R S T A A D
481 CATGCAGCTTCACACATTGGGAAGGCAAGCGGTCTCCTTTTGCTCCTTAGATCATTACCT
    H A A S H I G K A S G L L L L L R S L P
541 TACCACCATAGTCGTAATTCCCAACTTCGCTATATACCATTTGAAGTGGCATCCAAGCAC
    Y H H S R N S Q L R Y I P F E V A S K H
601 GGATTGTTAAGTCACGAGGGAGGTCAAAATCAAGTTCAGCTGGGTTACCGTGAGGGTTTA
    G L L S H E G G Q N Q V Q L G Y R E G L
661 CCAAATGCAGTATTTGAGATAGCTTCCGTTGCTAGTGTTCAATTCAGAAAGGCTCGTGAG
    P N A V F E I A S V A S V H L Q K A R E
721 TTGGCAAAGACTGTGCCTGCGGAGGCTCTTCCCGTGTGCTTCCAGCTGTGCCTGCACAG
    L A K T V P A E A L P V L L P A V P A Q
781 GTTATATTGGACTCTCTACGAAGAGTGCATTTTGACGTGTTTGATCCAAGGTTGATGAGA
    V I L D S L R R V H F D V F D P R L M R
841 GGGATTCTGGGTATTTACCCTTATGGTTTCAATTAAAGCTGAAGTGAATGCATGGAAA
    G I L G I S P L W F Q L K L K W N A W K
901 AGTACATATTGA +1
    S T Y *

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**Figure S1A.** The nucleotide sequence and deduced amino acid sequences of CmPSY. An asterisk (\*) represents a stop codon.



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      ATTCCTCCTCCTCCTCTTTCTCTCTCTAGCTTTCTCTCTCTAACTTACACTCGTTA
1  ATG GCGTCTCCTCTTCTCCTCTCTAATTCTACCTTCTCCTTCTCTCACCACCGCTCTCAC 60
   M  A S P L L L S N S T F S F S H H R S H
61 AATGGCAGCAGCAGACCCATCACTTCAAACCGTAGCTTAACCCTCTCTTCTTTAAACCCA 120
   N G S S R P I T S N R S L T L S S L N P
121 ATAAAAATCCCTAATTTTGATTCAAAATTGAAGAGAAACCCTAAAACTCTTTCAGTTTG 180
   I K I P N F D S K L K R N P K T S F S L
181 CTGCAATTACACCGGAGGAAGTAATTGTAGGAGCATCGCTTGGAGAAAGGAAACGGAA 240
   L Q L H R R K V I V G A S L G E R E T E
241 GAGAAGAATTCTTCTTCGGTTGTAGCTGATGATGAGATTCAAGTTGGTGAGGATTCAGCT 300
   E K N S S S V V A D D E I Q V G E D S A
301 TTCTTTGATTTGGGTGAGCAGAAGATTATTTCTTGGGTTTATTTTACGGGAATTCTGGGA 360
   F F D L G E Q K I I S W V Y F T G I L G
361 GTTGTTTTGTTCGCACTCGATGTAATTTGGATTGATTCGTCGACTGGGGTTGGACTCGGG 420
   V V L F A L D V I W I D S S T G V G L G
421 AAGGCGTTTGTGATTCTGTTTCAGGGATTTTCAGAAAGTCATGAGATTGTAATGCTGATC 480
   K A F V D S V S G I S E S H E I V M L I
481 CTTATTTTCATTTTCGCTGCTGTCCACAGTGGCCTGGCTAGTTTCCGGGACATCGGAGAG 540
   L I F I F A A V H S G L A S F R D I G E
541 AAGTTAATTGGAGAACGAGCTTACCGTGTTCTATTTGCAGGGATCTCTCTTCTTTGGCA 600
   K L I G E R A Y R V L F A G I S L P L A
601 GTTAGTACTGTTGTGTACTTCATTAACCACCGATACGATGGAATGCAATTGTGGCAGCTC 660
   V S T V V Y F I N H R Y D G M Q L W Q L
661 CAGAGTGTTCCTGGGCTTCATCACTACTGTGGATTGCGAATTCATCTCCTTCTTTTC 720
   Q S V P G L H Q L L W I A N F I S F F F
721 TTATATCCTTCGAC 734
   L Y P S

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**Figure S1C.** The nucleotide sequence and deduced amino acid sequences of CmZ-ISO. An asterisk (\*) represents a stop codon.



GCATGTTATTTGATC

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1  ATGCGCTTCTTTTCTTCAACTTCTTTTCTTGCTACTTCATCAGCTTCCATACTAGTAAGC
   M A S F S S T S F L A T S S A S I L V S
61  CAAAGCAGCTTCTGCAAAGAGATTAGGGGACGGGGTATTAATGGCTCTTCTTTGTTTAT
   Q S S F C K E I R G R G I N G S S F V Y
121 CGTTGCCGTGGGCATAAGACTCCATTGAAAACCTCGGAGCTTCGAAATTAAATCTTCTTC
   R C R G H K T P L K T R S F E I K S S S
181 TTGGATACAAATGTCTCTGACATGAGGATTAACGCACCGAAAGGCTTATTTCCACCGGAA
   L D T N V S D M R I N A P K G L F P P E
241 CCTGAGTGTTATAGAGGACCAAAATTGAAAGTGGCAATCATCGGAGCCGGGCTCGCGGGC
   P E C Y R G P K L K V A I I G A G L A G
301 ATGTCAACTGCAGTGGAACTTTTGGATCAAGGCCACGAGGTTGATATATACGACTCAAGA
   M S T A V E L L D Q G H E V D I Y D S R
361 ACCTTAGTTGGCGGGAAAGTGGGTTCTTTGTGCGATAAACATAGTGGAAATCATATTGAA
   T L V G G K V G S F V D K H S G N H I E
421 ATGGGGCTACATGTTTCTTTGGCTGCTACAATAACCTTTTCCGCTTGATGAGAAAGGTG
   M G L H V F F G C Y N N L F R L M R K V
481 GGCGCAGACGAAAATTTACTGGTGAAGAACATACTCATACTTTTATCAATGAAGGGGGC
   G A D E N L L V K E H T H T F I N E G G
541 CGAGTCGGGTGAAGTTGATTTTCGATTTTCCAATTGGAGCACCATTACATGGAGTTAATGCA
   R V G E V D F R F P I G A P L H G V N A
601 TTTTGAATACAAAACAGCTCAAGGCTTATGATAAAGCTAGGAATGCATTAGCTCTATCC
   F L N T K Q L K A Y D K A R N A L A L S
661 CGCAGCCCAATCGTTCCGGGCACTTGTGTATCCAGATGGTGCAATGAGGGATATTCGAAAC
   R S P I V R A L V D P D G A M R D I R N
721 TTAGATAATATAAGCTTCTCCGATTGGATCTTGTCAAAGGTGGCAGCGCATGTGTATC
   L D N I S F S D W I L S K G G T R M C I
781 GACCGATTGTGGGATCCTGTTTCGTACGCTCTTGGATTTATTAACAGTGACAATATGAGT
   D R L W D P V S Y A L G F I N S D N M S
841 GCTCGTTGCATGCTCACAATTCTCACTTTGATTGCCACTAAGACAGAGGCTTCTCTATTG
   A R C M L T I L T L I A T K T E A S L L
901 CACATGCTTAAAGGCTCTCTGATGTTTACTTAACTGGTCCTATCAAAAAGTATATTACA
   H M L K G S P D V Y L T G P I K K Y I T
961 GACAAAGGTGGAAGGTTCCATCTCAGGTGGGGTTGCAGAGAAATACTTTACGATAAATCT
   D K G G R F H L R W G C R E I L Y D K S
1021 GTTAATGGAGACACGTATGTTTCAGGAATTAAGTGTCTAAGGCGACAAATAGGAAAATA
   V N G D T Y V S G I K V S K A T N R K I
1081 GTGAAAGCTGACGTTTATGTGGCAGCATGTGATGTACCAGGAATCAAAAGACTCATTCCA
   V K A D V Y V A A C D V P G I K R L I P
1141 CCAGACTGGAGGGAATTGGAGTTTTTCGACAACATCTATAAACTAGTTGGAGTACCAATT
   P D W R E L E F F D N I Y K L V G V P I
1201 GTGATGTACAGTTGAGATACAATGGCTGGGTTACAGAATTACAAGACCTAGAAAAGTCG
   V T V Q L R Y N G W V T E L Q D L E K S
1261 AGGCAGTTGAGTGGAGCTGCAGGTTTGGATAACCTCCTTTATAGTCCAGATGCAGATTTT
   R Q L S G A A G L D N L L Y S P D A D F
1321 TCGTGCTTCGCCGACCTTGCACTCACATCTCCAGAAGATTACTACATTGAGGGTCAAGGT
   S C F A D L A L T S P E D Y Y I E G Q G
1381 TCATTGCTCCAATGTTTGCTTACACAGGGAGCCCTTACATGCCATTACCAAAAGATAAA
   S L L Q C L L T P G S P Y M P L P K D K
1441 ATCGTAGAAAAAGTTGCGAATCAGGTTTCAGCTTTATTCCCATCTTCTCAAGGCTTGGAA
   I V E K V A N Q V S A L F P S S Q G L E
1501 GTTATTTGGTCTAATGTTTTTAAACTTGGGCAATCGTTATATCGCGAAGGTCCTGGAAAT
   V I W S N V L K L G Q S L Y R E G P G N
1561 GATCCTTTTCAGACCTGATCAAAAGACCTGTGAAAAATTTCTTCCTTGCTGGCTCCTAC
   D P F R P D Q K T P V K N F F L A G S Y
1621 ACTAAACAGGATTACATTGATAGCATGGAAGGAGCAACTCTATCAGGAAGACAAGCATCA
   T K Q D Y I D S M E G A T L S G R Q A S
1681 GCCTATGTTTGTGAAAGCGGGGAAGAATTGGCAGCTCTTAGGAAGATGCTTTCTGCCATT
   A Y V C E S G E E L A A L R K M L S A I
1741 GAAGCCCAAGAAGTCACAAAATCTGAAAACATTATTGACGAGCTAAGTGTGTCTGATGT
   E A Q E V T K S E N I I D E L S V V *
   ATAGCTATCATTTGTTGAGTTCCACTAATTCACTCATCTCAGGCTGCCCGAAAGC +183

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**Figure S1D.** The nucleotide sequence and deduced amino acid sequences of CmZDS. An asterisk (\*) represents a stop codon.



-41 TCCCCAACCTCATCATCAAATCATGTACAACAACATCCACTCTCACAACCACCACCATCC  
 1 **ATG**GCCGAATTAGGGTTCCGCTCTCCATCTCTTACTTACAGTCTCCCTTCTCTATCTCAT  
**M** A E L G F R S P S L T Y S L P S L S H  
 61 CCTTTCAAACACTACCATTCAATACTCTCAATCTTTGTTGTTTTTGGAAACCCATTGAG  
 P F K T L P F N T L N L C C F W K P I E  
 121 GGTTTTGAGCTGAGGAAAAGTGGGAAATTGGGATTTCTTTTGAATAAGAGGAGAATTGGG  
 G F E L R K S G K L G F L L N K R R I G  
 181 AGTTTGACGAAATCAGTGTTGAGTGTGGAGAAAGAAGTGAGTAGAAGTGGTAGTGAAAGT  
 S L T K S V L S V E K E V S R S G S E S  
 241 GGAGAGAGAGATAATTTTGATGCGATTGTTATTGGTTCCTGGAATTGGTGGATTGGTTGCT  
 G E R D N F D A I V I G S G I G G L V A  
 301 GGGACGCGAGTTGGCAGTGAAAGGAGCTAGGGTTTTGGTGTAGAGAAGTATGTGATTCCCT  
 G T Q L A V K G A R V L V L E K Y V I P  
 361 GGTGGAAGTTCTGGGTTTTACCAGAAGGATGGGTATACGTTTGATGTTGGATCATCTGTG  
 G G S S G F Y Q K D G Y T F D V G S S V  
 421 ATGTTTGGGTGCGGCGATAAGGGCAATCTGAATTTGATTACTCGAGCATTAGCTGCAGTT  
 M F G C G D K G N L N L I T R A L A A V  
 481 GGGTGTAAAGTTGGATATGTTACCGGACCCGTCAACTGTGCATTACCATCTACATGACAAT  
 G C K L D M L P D P S T V H Y H L P D N  
 541 CTATCTGTTTCGAGTACACAGAGAGTATAGTGACTTCGTCATGGAACCTCATCAATAGATTT  
 L S V R V H R E Y S D F V M E L I N R F  
 601 CCTCATGAAAAGGAAGGAATCCATAAATTTTACGGTGAATGTTGGAAGATATTTAATGCC  
 P H E K E G I H K F Y G E C W K I F N A  
 661 TTGAACTCGCTGGAATTGAAGTCACTCGAGGAGCCACTTTACCTTTTTGGACAATTCCTT  
 L N S L E L K S L E E P L Y L F G Q F F  
 721 CGAAAACCGCTTGAATGCTTAACGCTTGCTTATAATTTGCCTCAAAATGCTGGAGCCATT  
 R K P L E C L T L A Y N L P Q N A G A I  
 781 GCTCGGAAGTTTCATACGAGATCCCCAGTTGTTATCTTTTATAGATGCCGAGTGTTCATT  
 A R K F I R D P Q L L S F I D A E C F I  
 841 GTAAGCACCACTAATGCTTTGCGGACACCGATGATCAATGCGAGCATGGTTGTGTGAG  
 V S T T N A L R T P M I N A S M V M C E  
 901 AGGCATTTTGGTGGGAATCAACTACCCCGTTGGTGGTGTGGGAGAATTGCAAAATCCTTA  
 R H F G G I N Y P V G G V G R I A K S L  
 961 GCAAAAGGCCTGCTTGATAAGGGCAGTAACATAATTTATAAGGCAAATGTGACTAGCATT  
 A K G L L D K G S N I I Y K A N V T S I  
 1021 ATACTTAAGGATGAAAAGCTGTAGGAGTTAAGCTTTTCAGACGGAAGAGAGTTCTTTTCA  
 I L K D G K A V G V K L S D G R E F F S  
 1081 AAAACCATAATATCAAATGCAACTAGATGGGATACCTTTGGAAAGCTTTTAAAAGGAAAA  
 K T I I S N A T R W D T F G K L L K G K  
 1141 GAACTTCCGAAGGAAGAGGAAAACTTTTCAGAACTTTATGTCAAGTCCCCATCCTTTCTT  
 E L P K E E E N F Q K L Y V K S P S F L  
 1201 TCCATCCACATGGCGGTTGAAGCAAAAGTTTTGCCTCCAGACACAGATTGCCATCATTTTC  
 S I H M A V E A K V L P P D T D C H H F  
 1261 ATTCTTGAGAATGACTGGACCAAATTAGAGGAGCCATATGGAAGCATCTTTTGTAGCATT  
 I L E N D W T K L E E P Y G S I F L S I  
 1321 CCAACTGTTCTTGATTCTCTCTTGGCTCCAGAAGGACGTCACATCCTTCACATATTCACG  
 P T V L D S S L A P E G R H I L H I F T  
 1381 ACATCTTCCATTGAGGATTGGAAGGGCCTCCCTCAGAAAGATTATGATGCGAAAAAGGAG  
 T S S I E D W K G L P Q K D Y D A K K E  
 1441 CACGTGGCAGATGAAATCATCAGTCGACTGGAAAAGAACTTTTTCCAGGGCTTAAATCG  
 H V A D E I I S R L E K K L F P G L K S  
 1501 TCCATTGTTTTCAAAGAGGTAGGGACGCCCAAGACACATAGACGTTTTCTTGCTCGAGAT  
 S I V F K E V G T P K T H R R F L A R D  
 1561 AGTGGTACATATGGACCCATGCCACGTGGTACCCCAAAAGGCTTATTAGGGATGCCGTTTC  
 S G T Y G P M P R G T P K G L L G M P F  
 1621 AATACAACAGCTATAGATGGGCTCTACTGTGTCGGAGATAGCTGCTTTCCAGGACAAGGT  
 N T T A I D G L Y C V G D S C F P G Q G  
 1681 GTTATAGCTGTAGCCTTTTCAGGGATAATGTGTGCTCATCGAGTGGCCGCTGATATCGGG  
 V I A V A F S G I M C A H R V A A D I G  
 1741 CTTGAGGAAAGATCCCCAATATTAGATGGTGCCTTACTTAGACTTCTTGGCTGGTTAAGG  
 L E E R S P I L D G A L L R L L G W L R  
 1801 ACAATTGCAT**GA**AGATCATAGGCTTCATTTATTGAGTGGATGGATGAAACTTGACCTATT  
 T I A \*  
 GTATGAATGGGGTTCTGCTATACTTCTGCTTTGGAGATCTTGAAGGAACCCATC +321

**Figure S1E.** The nucleotide sequence and deduced amino acid sequences of CmCrtISO. An asterisk (\*) represents a stop codon.

-242 AGACTTTCTTGCAAAACCCACATCTTAGTCTTCTGAGATTTTATCTGAGATTTTTTA  
 1 **ATG**GGTACTCTACTCAGAACCCATAATAAGCTTGAGTTGCTTCACCCACTACATGGGTTT  
 M G T L L R T H N K L E L L H P L H G F  
 61 GCAGAAAAACACAACCTTTTAACTCTTCCAAGCTTCAAAACCATGAATATAGGTTTAGA  
 A E K H N L L T S S K L Q N H E Y R F R  
 121 ACAGCGAAGAAAAAGTCATCGAAATTGGTGTGTTAATGGTCTGTTAAGGCCAGTAGTAGT  
 T A K K S H R N W C V N G S V K A S S S  
 181 GCTCTTCTGGACCTTGTTCAGAAAACCAAGAAGGAGAATCTTGAATTTGAGCTTCCCATG  
 A L L D L V P E T K K E N L E F E L P M  
 241 TATGACCCATCAAAGGGTCTTACTGTGGACCTCGCAGTTGTTGGAGGCGGTCCGGCCGGC  
 Y D P S K G L T V D L A V V G G G P A G  
 301 CTTGCTGTGGCTCAACAGGTCTCTGAAGCTGGCCTCTCAGTTTGTTCGATAGACCTTTT  
 L A V A Q Q V S E A G L S V C S I D P F  
 361 CCCAAATTGATCTGGCCTAACCAATTACGGTGTGTGGGTTGATGAATTTGAAGCCATGGAT  
 P K L I W P N N Y G V W V D E F E A M D  
 421 CTTCTTGATTGCCTTGACACCACCTGGTCCGGTGCCGTTGTGTTTCGTCGATGATAAATCA  
 L L D C L D T T W S G A V V F V D D K S  
 481 AAAAAAGTATCTCGACAGACCTTATGGAAGGGTTAATCGCAAACAGTTGAAATCTAAGATG  
 K K Y L D R P Y G R V N R K Q L K S K M  
 541 ATGAAAAAATGCATAGAAAAATGGTGTCAAGTTTCATCAAGCTAAGGTCATTAAGGTTATT  
 M K K C I E N G V K F H Q A K V I K V I  
 601 CATGAGGAATCTAAGTCCCTTTTAACTCTGCAATGATGGTGTAAACGATTCAAGCAACTTTG  
 H E E S K S L L I C N D G V T I Q A T L  
 661 GTTCTTGATGCCACAGGGTTTTCAAGGTGCCTGGTTCAGTATGATAAACCTTATAACCCT  
 V L D A T G F S R C L V Q Y D K P Y N P  
 721 GGGTACCAAGTTGCTTATGGTATTTTAGCAGAAAGTAGAAGAACATCCATTTGAAGTAGAT  
 G Y Q V A Y G I L A E V E E H P F E V D  
 781 AAGATGCTTTTCATGGATTGGAGAGATTCTCATCTTAATCTGAACCATGAACAGAAAGAA  
 K M L F M D W R D S H L N L N H E Q K E  
 841 AAGAATTCCAAAATTCCCACTTTTCTTTATGCAATGCCGTTTTTCATCAAATAGAATTTTT  
 K N S K I P T F L Y A M P F S S N R I F  
 901 CTAGAAGAAACATCTCTGGTTGCTCGACCGGGAGTTTCCATGGAAGATATTCAGGAAAGG  
 L E E T S L V A R P G V S M E D I Q E R  
 961 ATGGCTCTTAGATTGAAGCACTTGGGTATAAAGGTTAAAAGCATTGAAGAGGATGAACGG  
 M A L R L K H L G I K V K S I E E D E R  
 1021 TGTGTTATTCCAATGGGTGGGCCACTTCCTGTAAATCCCTCAAAGGGTTGTTGGAATAGGT  
 C V I P M G G P L P V I P Q R V V G I G  
 1081 GGCCTGCGGCATGGTTTCATCTTCGACAGGATACATGGTAGCGAGAACTCTTGCGGCA  
 G T A G M V H P S T G Y M V A R T L A A  
 1141 GCCCCAATAGTTGCAAAGTCGATAGTTCAAGTATCTTGGATCTGAACAAGGATTTTCTGGT  
 A P I V A K S I V Q Y L G S E Q G F S G  
 1201 AATGAATTATCTGCAGGAATTTGGAATAATTTGTGGCCTATAGAGAGAAGGAGGCAACGG  
 N E L S A G I W K N L W P I E R R R Q R  
 1261 GAGTTCTTCTGTTTTGGTATGGATATTCTGCTTAACTTGATTACAAAGGAACAAGGAGC  
 E F F C F G M D I L L K L D L Q G T R S  
 1321 TTCTTTGATGCATTTTTTGACCTTGAACCTCATTATTGGCATGGATTCTTGTCCTCTCGA  
 F F D A F F D L E P H Y W H G F L S S R  
 1381 TTGTTTTTTCCGGAACCTTATATATTTTCGGGCTTTCTCTGTTCTCACATGCCTCTAATGCT  
 L F F P E L I Y F G L S L F S H A S N A  
 1441 TCAAGGATTGAGATTATGGCCAAGGGCACTGTTCCCTTAGGTAAGATGATCAACAACCTTA  
 S R I E I M A K G T V P L G K M I N N L  
 1501 ATACGGGATGGAGAA**TAG**GATTGAAGGAATTTAAGTCTGTTGAATGTAAGATGAAATGAA  
 I R D G E \*  
 GCATCTACATCTAAATCTTACTTTTTGTTTGCTGTCAAATGTCAATGTAACCACT **+41**

**Figure S1F.** The nucleotide sequence and deduced amino acid sequences of CmLCYB. An asterisk (\*) represents a stop codon.



-75 CCGTCTGACACTAACACTTTCTCTGCCTAGCTTTTTAAAGCAGAGAGTAATGTGTCGGTC  
 TCTTGCTTCTTAAAAGCAGAGTAATGTAACAGAGGAGCTTCATTAACATTACTAGTAACA  
 1 **ATG**GAGTACTGTATTGGAGCTCGTAGTAACATTACAGCAATGGCGATTTCTCCTTCTTGC  
**M** E Y C I G A R S N I T A M A I S P S C  
 61 CCTGTTTTGAGGTCAAGAACAAGGAGACTTCTCAGTACAACAAGTATCTCTTCTTCTTCT  
 P V L R S R T R R L L S T T S I S S S S  
 121 TCTTCTCACCTAATTCATGGATATTCCTTTTCTTCTCTCAATGTGAAGGCTTGTCTATGCC  
 S S H L I H G Y S F S S L N V K A C H A  
 181 GATTCTACAACCCAAAGTTGTAGTGTCTGTTAAAGAAGGTGGGTTTGTGTGATGAAGAA  
 D S T T Q S C S V S V K E G G F V D E E  
 241 GATTATATCAAAGCTGGAGGTTCTGAGATTCTGTTTGTCAAATGCAACAGACAAAGCCA  
 D Y I K A G G S E I L F V Q M Q Q T K P  
 301 ATGGAAGAGCTAACCAAGATTTCGGACAAGTTGCCACCGATATCCATTGGAGACTCTATA  
 M E E L T K I S D K L P P I S I G D S I  
 361 CTAGATCTGGTAATAATTGGTTGTGGCCCGCGGTCTTCCCTGGCTGCAGAAGCAGCT  
 L D L V I I G C G P A G L S L A A E A A  
 421 AAATTAGGCTTGCAAGTTGGGCTAATTGGACCTGATCTACCTTTTACAAATAATTATGGC  
 K L G L Q V G L I G P D L P F T N N Y G  
 481 GTGTGGGCGGATGAATTTAAAGATCTTGGGCTAGAAAGGTGATTGAGCATGTTTGGAAA  
 V W A D E F K D L G L E R C I E H V W K  
 541 GATACAATTGTATATCTTGATAGTGATGAACCGATTATGATTGGCCGTGCTTATGGAAGA  
 D T I V Y L D S D E P I M I G R A Y G R  
 601 GTTAGTCGACAGTTGCTATATGAAGAGCTGTTGAAAAGGTGTGTAGAGTCGGGTGTTTCG  
 V S R Q L L Y E E L L K R C V E S G V S  
 661 TACCTTAACTCTAAAGTGGAAAGGATAATTGAAGCTACAGAGGGACATAGTCTGTAGCG  
 Y L N S K V E R I I E A T E G H S L V A  
 721 TGTGAAAGCGGGATTGTTATCCCTTGACAGGCTTGCTACTGTGGCATCTGGAGCAGCTTCA  
 C E S G I V I P C R L A T V A S G A A S  
 781 GGGAACTATTAAAGTATGAAGTAGGAGGTCTCGAGTTTCTGTACAGACAGCTTATGGT  
 G K L L K Y E V G G P R V S V Q T A Y G  
 841 TTGGAGGTTGAGGTGGAAAAGTGTCCATATGATCCCAGCCTAATGGTTTTTCATGGATTAT  
 L E V E V E N C P Y D P S L M V F M D Y  
 901 AGAGACTACATTAAACCAAAAGTCCAATGCTTGGAAAGAATAACCTTCATTTCTGTAT  
 R D Y I K P K V Q C L E E E Y P S F L Y  
 961 GCCATGCCCATGTACCAACAAGAGTTTTCTTTGAGGAACTTGTCTGGCTTCCAGAAAT  
 A M P M S P T R V F F E E T C L A S R N  
 1021 GCCATTCCTTTTGATCTATTGAAGAAGAACTGATGTCAAGATTGAAGACGATGGGAGTT  
 A I P F D L L K K K L M S R L K T M G V  
 1081 CGAATTACAAAAGTTTATGAAGAGGAGTGGTCTTATATTCCTGTTGGTGGTTCCTTACCA  
 R I T K V Y E E E W S Y I P V G G S L P  
 1141 AACACCGAGCAAAAGAACCTTGCAATTTGGTGTGTCAGCCAGCATGGTGCATCCAGCCACC  
 N T E Q K N L A F G A A A S M V H P A T  
 1201 GGTATTTCAGTTGTTAGATCTTTGTCTGAAGCTCCAAGATATGCTTCTGTAATTGCAAAG  
 G Y S V V R S L S E A P R Y A S V I A K  
 1261 ATTTTGAAGCAATCTCATGAAAGGAGCACCAAGAATATCTCAGTACAAGCATGGAACACT  
 I L K Q S H E R S T K N I S V Q A W N T  
 1321 CTCTGGCCACAAGAGAGAAAACGACAAAGAGCATTCTTCTCTTTGGATTAGAGCTGATT  
 L W P Q E R K R Q R A F F L F G L E L I  
 1381 TTGCAACTCGATATTGAAGGCATAAGAACATTCTTCCAACTTTTTTCAGCTTGCCAAAT  
 L Q L D I E G I R T F F Q T F F S L P N  
 1441 TGGATGTGGAAGGGCTTCTCGGATCTTCTACTGTCTCATCCACTGATCTTCTACTATTTGCC  
 W M W K G F L G S S L S S T D L L L F A  
 1501 CTCTATATGTTTATATTAGCACCAACAGTTTGCGAATGGGCCTTGTCTAGACATCTACTA  
 L Y M F I L A P N S L R M G L V R H L L  
 1561 TCTGATCCTACTGGAGCAACTATGGTAAAAGCATATCTCACT**TAG**TAGCTCAAGCCCTTA  
 S D P T G A T M V K A Y L T \*  
 ATATATTTCATAAGCCTGTTTCTTTATTTAGACTATAATCTCACACACCCACTGTACTGA  
 ACGTCTCCAAAGTCCGTCTGTGTGTATATAAACTTCTTTATGGGGGGGGATC +298

**Figure S1G.** The nucleotide sequence and deduced amino acid sequences of CmLCYE. An asterisk (\*) represents a stop codon.



-72 ATTCCTTTTATACTCCTCCAGATTTCTATCTCCCTCTCTAAGACTCTAACCACTCTCTCTCTCTC  
 TCTGTGAGTACTGACCTTTCAAAGTTCAACAACTGAATAAGCTCCAATCTCAAACGTCA  
 1 **ATG**GCGGCCGGATTCTCTGTGCGCCATAAGCGCCAGAACGTTCCGGTTTGGTCAGAATCCT  
**M** A A G F S V A I S A R T F R F G Q N P  
 61 TTCATAGGTTCAAAACCCAATTCTCTCATAAACCCATCTTCATTTCTCTCTCCATCAATT  
 F I G S K P N S L I N P S S F L S P S I  
 121 CGCCGACCTAATAAATTCTTCACGGCGAAGAAGAAGAGCACCTTTACTGTCTATTTTGT  
 R R P N K F F T A K K K S T F T V Y F V  
 181 TTGGAAGAACAACAAACAGGGGATTAGTAGATTTATTGAAGAAGAAGAAGATAAAGCAGAA  
 L E E Q K Q G I S R F I E E E E D K A E  
 241 GCTGATGTTAGTTCATCATCAGAGGAATTGAATAGGGTCTCAGTACGAGTTGCAGAGAAA  
 A D V S S S S E E L N R V S V R V A E K  
 301 TTAGCCAGAAAGAAATCAGAACGACACACTTATCTTGTGCGCAGCAATTATGTCTACTCTT  
 L A R K K S E R H T Y L V A A I M S T L  
 361 GGAATAACTTCTATGGCTGTTGCTGCTGTTTATTACAGATTTTCATGGCAAATGGAGGGT  
 G I T S M A V A A V Y Y R F S W Q M E G  
 421 GGAGAGGTTCTGTTTCTGAGATGTTTGGTACATTTGCTCTAGCTGTTGGTGCTGCTGTT  
 G E V P V S E M F G T F A L A V G A A V  
 481 GGGATGGAATTTTGGGCAAGATGGGCTCACAAAGCACTCTGGCAGCCTTCTTTATGGCAC  
 G M E F W A R W A H K A L W H A S L W H  
 541 ATGCACGAGTCTCATCATCAACCAAGAGAAGGTCCTTTTGAATAAATGATGTTTTCGCC  
 M H E S H H Q P R E G P F E L N D V F A  
 601 ATTATCAACGCTGTTCCAGCTATAGCTCTTCTCAATTATGGTTTCTTTACAAAGGCCTC  
 I I N A V P A I A L L N Y G F F H K G L  
 661 TTTCTGGTCTCTGTTTTGGTGCTGGACTTGAATTACTGTATTTGGTATGGCCTACATG  
 F P G L C F G A G L G I T V F G M A Y M  
 721 TTTGTTTCATGATGGTCTTGTTCACCGTAGATTTCCAGTGGGACCCATTGCTAATGTTCT  
 F V H D G L V H R R F P V G P I A N V P  
 781 TATTTTCGGAAGTTGCTGCTGCACACAAAATTCATCACATGGACAAATTTGAGGGAGTT  
 Y F R K V A A A H K I H H M D K F E G V  
 841 CCATATGGGTTGTTTTTAGGACCTATGGAATTAGAAGAGGTAGGAGGTAATGAAGAATTA  
 P Y G L F L G P M E L E E V G G N E E L  
 901 GAGAAGGAAATTAGCCGTAGGATCAAGCAATCCAACGATTGAGAT**TGA**AGTTTCGCGGTGG  
 E K E I S R R I K Q S N D S R \*  
 GGTCCATTTTAATGTTTATGGTGTGTGATTAACGGTTTTTGGTTACAATGTAAAAA +6

**Figure S1H.** The nucleotide sequence and deduced amino acid sequences of CmCHXB. An asterisk (\*) represents a stop codon.

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-31 AAATGAGAAGCAATGTGAACAGAATTGTTTAATCTTTTCATTTCTGTCTCACAATCCGCC
1  ATGACATCTTCTTCATCTTGTACTTCGCTAACCCCTCTCTCTCTCTCTCTCTCTAAC
M T S S S S C T S L T L S S L S S L S N
61 CCTAACCACCAAATCCTCCAAAACAAACCCATCTTCTTCTTCCCAAGAAACCCATCTCAA
P N H Q I L Q N K P I F F F P R N P S Q
121 ATTCTCTCCATTAAATCCTCCATTAAAAAAGAGTCTTCTTATTCTAGCAGTAATGGGTCA
I L S I K S S I K K E S S Y S S S N G S
181 TGGGTTAGTCCAGATTGGCTCACTTCTTTAACCAAATCACTCACCATCAGTACCAGTCAA
W V S P D W L T S L T K S L T I S T S Q
241 GATGATTACGGGATACCCATTGCCAGTGCTAAGCTTGATGATGTGTCTGATCTCTTGGGT
D D S G I P I A S A K L D D V S D L L G
301 GGTGCTCTTTTCTTCCATTGTTCAAATGGATGAATGAATATGGACCCATTTATCGTCTT
G A L F L P L F K W M N E Y G P I Y R L
361 GCAGCTGGACCCCGTAATTTTGTGGTTGTTAGTGACCCTGCCATTGCCAAGCATGTTCTG
A A G P R N F V V V S D P A I A K H V L
421 AGGAACTATGGGAAGTATGGTAAGGGACTTGTAGCTGAAGTCTCTGAGTTCTTATTCGGC
R N Y G K Y G K G L V A E V S E F L F G
481 TCTGGGTTTCGCCATTGCTGAAGGCCCTCTTTGGACGGCGAGGCGGAGAGCTGTGGTTCCA
S G F A I A E G P L W T A R R R A V V P
541 TCTCTTCACAAGAAGTACTTGTCCATAATGGTTGATAGGGTATTTTCCAAGTGTGCCCAG
S L H K K Y L S I M V D R V F S K C A Q
601 AGGTTAGTGGAGCAGCTTAAACAGATGCAGACAATGGTTCTCCCGTGAATATGGAGGCG
R L V E Q L K T D A D N G S P V N M E A
661 AAGTTTTCTCAATTAACCTTTAGATGTTATAGGTTTGTCTGGTGTTTAACTACAATTTGAT
K F S Q L T L D V I G L S V F N Y N F D
721 GCACTTACTGCGGATAGTCCTGTTATCGATGCTGTCTACACTGCATTGAAAGAGGCAGAG
A L T A D S P V I D A V Y T A L K E A E
781 GCTCGTTTCGACGGATCTTTTACCCTATTGGAAGATTGACGCATTATGCAAAATAATTCCA
A R S T D L L P Y W K I D A L C K I I P
841 AGACAAATAAAAGCTCAAAATGCAGTTAATGTTATTAGAAC
R Q I K A Q N A V N V I R

```

**Figure S1I.** The nucleotide sequence and deduced amino acid sequences of CmCHXE. An asterisk (\*) represents a stop codon.

-189 CTCTTCTTCTTCATTCATCAGCTCATCACAACAAGAAGAACTGAAGAAGCTTGAAGTATTA  
 1 **ATG**GCTTTAACAGCTTTATACAGTTCACTCAACCCCTCATCAACAATATTCTCAAAAACC  
 M A L T A L Y S S L N P S S T I F S K T  
 61 CACCTTCCAATACCAACAGCCAAAGACTTCTCTGAAGAAATTTTGCCTTCTCTTCATTAC  
 H L P I P T A K D F S E E I L P S L H Y  
 121 AACTATTTATTTAGAAGTAAACCCCTTTGATCAGAAAAAGAGAAAACAGTGAAAATTTCA  
 N Y L F R S K P F D Q K K R K P V K I S  
 181 GCAGTAGTAGCTCCAGAAGCTGTTACTTCCACTCAAAATGGAATTAATGGTGGTGGGTTG  
 A V V A P E A V T S T Q N G I N G G G L  
 241 TCGAAGAACTGCGGATCCTAATTGCTGGTGGTGGGATTGGTGGGTTGGTTTTTGCCTTG  
 S K K L R I L I A G G G I G G L V F A L  
 301 GCTGCTAAGAGAAAAGGGTTTGATGTGTTGGTATTTGAGAGGGATGTTAGTGCTATAAGA  
 A A K R K G F D V L V F E R D V S A I R  
 361 GGAGAGGGCCAAATATAGGGGGCCAAATTCAGATACAAAGTAATGCCTTGGCTGCATTAGAA  
 G E G Q Y R G P I Q I Q S N A L A A L E  
 421 GCTATTGATATGGAGTGGCTGAGGAAGTTTGAAGCTGGCTGTATTACTGGTGATAGG  
 A I D M E V A E E V L K A G C I T G D R  
 481 ATTAATGGATTGGTTGATGGGATCTCAGGTGCTTGGTATATCAAGTTTGATACATTACACA  
 I N G L V D G I S G A W Y I K F D T F T  
 541 CCTGCGGTGGAACGGGGGCTCCCTGTCACAAGGGTTATTAGCCGAATGACTTTGCAAGAA  
 P A V E R G L P V T R V I S R M T L Q E  
 601 ATTTTTGCCAAGGCAGTTGGGCAGGATTCATTATTAATGACAGTAATGTTGTTGATTTT  
 I F A K A V G Q D S I I N D S N V V D F  
 661 GAAGATGATGGAACAAGGTTACTGTAGTACTTGAGAACGGACAGCGATATGAAGGTGAT  
 E D D G N K V T V V L E N G Q R Y E G D  
 721 CTTTATAGTTGGAGCTGATGGTATCTGGTCAAAGGTACGGAAGAATTTATTTGGGCCCAAG  
 L L V G A D G I W S K V R K N L F G P K  
 781 GATGCGCAGTACTCTGGTTACACTTGTATATACTGGAATCTGCGATTTTGTTCCTCCAGAT  
 D A Q Y S G Y T C Y T G I C D F V P P D  
 841 ATTGAAAGTGTGGGTACCGAGTATTTTGGGTGACAAGCAATCTTTGTGTCTTCAGAT  
 I E S V G Y R V F L G H K Q Y F V S S D  
 901 GTGGGTGCTGGAAAGATGCAGTGGTATGCATTCCATAACGAACAGCTGGTGGCACTGAT  
 V G A G K M Q W Y A F H N E P A G G T D  
 961 GCTCCAAATGGTAAAAAGGAACGATTACTTCAGATATTTGGTTCCCTGGTGTGATAATGTG  
 A P N G K K E R L L Q I F G S W C D N V  
 1021 GTTGACTTGTAAATGCCACGGATGAGGATGCAATTCTTCGACGTGACATATATGATCGA  
 V D L L N A T D E D A I L R R D I Y D R  
 1081 GTGCCTATTTTACCTGGGGAAAGGGTCGTGTAACCTTGCTGGGTGATTCCGTTTCATGCT  
 V P I F T W G K G R V T L L G D S V H A  
 1141 ATGCAGCCAAATATGGGTCAAGGTGGATGCATGGCTATTGAGGATAGCTATCAACTTGCT  
 M Q P N M G Q G G C M A I E D S Y Q L A  
 1201 GTAGAGCTCGAGAAATCTTGAACGAAAGTGTAGAATCTGGAATCTCTATTGATGTCACA  
 V E L E K S W N E S V E S G I S I D V T  
 1261 TCTGCTCTAAAGCGTTATGAGAAAGAAAGACGATTGCGTGTGTCAGTCATCTATGGAATG  
 S A L K R Y E K E R R L R V A V I Y G M  
 1321 GCAAGGATGGCCGCAATAATGGCGTCCACTTATAAACCATATTTGGGTGTAGGGCTTGCT  
 A R M A A I M A S T Y K P Y L G V G L G  
 1381 CCACTGTCGTTTATTACAAAATTTTCGGATACCACATCCAGGAAGAGTTGGCGGGAGATTT  
 P L S F I T K F R I P H P G R V G G R F  
 1441 TTCATTGACATAGGCATGCCCTTAATGCTAAGTTGGGTCTTAGTGGTAACAGTTCAAAG  
 F I D I G M P L M L S W V L G G N S S K  
 1501 CTTGAAGGGAGGTGATGCTGTGCGACTCTCGGACAAGGCAAACGATCAATTAAGAAGA  
 L E G R S V C C R L S D K A N D Q L R R  
 1561 TGGTTCGAAGATGATGATGCACTGGAGCGTGCCCTTAATGGAGAGTGGTTTCTTTTCC  
 W F E D D D A L E R A L N G E W F L F P  
 1621 TCTGAAAATAATAGTGGTTCCCAAGAACCTATTCAATTTGAGTAGAGATGAAAACAAGCCG  
 S E N N S G S Q E P I H L S R D E N K P  
 1681 TGCCTTATTGGGAATGTTTACACGCTGACGTTGCAGGAACGTCGATAGCCATACCTTCA  
 C L I G N V S H A D V A G T S I A I P S  
 1741 CCTCAGATTTCCAAAATGCACGCTCGTATAAGCTATAAAGATGGCGCCTTCTATCTCACC  
 P Q I S K M H A R I S Y K D G A F Y L T  
 1801 GATTTGCAGAGTGAACACGGCACTTGGATCACCGATATCGAGGGAAGCGTTACCGTGTG  
 D L Q S E H G T W I T D I E G R R Y R V  
 1861 CCTCCCAATCTCCCTCTAGATTCCGTCCATCTGACGTAATTGAGTTTGGTTCTGAGGCC  
 P P N L P S R F R P S D V I E F G S E A  
 1921 ACCTTTAAAGTGAAGGTGCTGGCGGTTCTTCAAATATTCCAGACAAGAAACAACTCCA  
 T F K V K V L A V P S N I P D K K Q T P  
 1981 GTCCTCAGTGCCACA**TGA**CGATTGGAAGTTTCTGCTTTTGTATCACCTTATACTGTACA  
 V L S A T \*  
 GCAAGCATTCACTGCCAGAGCAAAATAGCGTGCCACTGTTTTCTGTACGGGATA +135

**Figure S1J.** The nucleotide sequence and deduced amino acid sequences of CmZEP. An asterisk (\*) represents a stop codon.



-63 TCGTCTCCTCTGCAAGTACTTTTGGCTGCTGTCATGCAAAATATTGTCTACTTCATTTCTT  
 CAATATCTTCTCTCTTCAATTGTCCTCACCAGGTAAATTTGGCCTTCAAACCATTGTAAT  
 1 **ATGG**CATCTGCCGCATATTCAACCTGCTTATCCTATGACAAGAATGTTGTTACATGTATT  
**M** A S A A Y S T C L S Y D K N V V T C I  
 61 GAGTTGCTAAAGCAAAGCAATGAAAGGTTTCTTCTGAAGGTCAAACCTGGAAGCATCAAGGT  
 E L L K Q S N E R F L R R S N W K H Q G  
 121 TTAATTAAGATGAAATTGTGGTCCAATACCATAGATTCAAAGATAACCCAGTGGACTAGA  
 L I K M K L W S N T I D S K I T Q W T R  
 181 TCTTACAAAAATTATTTCCAGTTGAAGTCTAGAGGTTCTCATGTCTATATTAGGTGGGAAA  
 S Y K N Y F Q L K S R G S H V I L G G K  
 241 GACCATAGTGCTTCAGCACGTAGTGGCAATACGGAAGGCCGCTGTCCTGAGGTAGTGGAA  
 D H S A S A R S G N T E G R C P E V V E  
 301 GCTGATTTTCCCGATCCGATGCTGTTGGGTGTTATGCAGCAGTGGAGGCAAATGCAGGTC  
 A D F P D P M L L G V M Q Q W R Q M Q V  
 361 ATGGCAGTAGCTGGTGTACTTACATGCATATTCTTGGTTGTGCCATCTGCTGATGCTGTA  
 M A V A G V L T C I F L V V P S A D A V  
 421 GATGCACTGAAGACATGTGCTTGTGTTTATTGAAAGAGTGCAGGGTGAATTGGCCAAGTGT  
 D A L K T C A C L L K E C R V E L A K C  
 481 ATCGCAAACCCATCTTGTGCAGCCAATGTTGCATGTTTACAGACCTGCAACAACCGGCCC  
 I A N P S C A A N V A C L Q T C N N R P  
 541 GATGAGACCGAATGCCAGATTAAATGTGGTGATCTGTTTGAGAATAAAGTCGTAGATGAG  
 D E T E C Q I K C G D L F E N K V V D E  
 601 TTCAATGAATGTGCTGTTTTCACGCAAGAAATGCGTTCCACAAAAGTCAGATGTTGGTGAA  
 F N E C A V S R K K C V P Q K S D V G E  
 661 TTTCCAATACCAGATCCTGCGGCACTCGTCAAAAATTTCAATGTTGGGGATTTTAGTGGA  
 F P I P D P A A L V K N F N V G D F S G  
 721 AAGTGGTATATTTCTAGTGGCTTAAATCCCACCTTTTCGATGCTTTTGATTGCCAATTGCAC  
 K W Y I S S G L N P T F D A F D C Q L H  
 781 GAGTTCCATATGGAGGGCAACAACTCGTAGGCAATTTATCATGGCGTATACGGACTCCT  
 E F H M E G N K L V G N L S W R I R T P  
 841 GATAGTGGTTTTTTCACTCGAACAGCTACGCAGAAGTTTGTGCAGGATCCATTGCAGCCT  
 D S G F F T R T A T Q K F V Q D P L Q P  
 901 GGAATTCTTTACAATCATGACAACGAGTTTCTTCACTACCAAGATGATTGGTACGTCTTG  
 G I L Y N H D N E F L H Y Q D D W Y V L  
 961 TCATCCAAGATAGAAAACAATCCGGATGATTACGTGTTTGTATACTATCGTGGTAAGAAT  
 S S K I E N N P D D Y V F V Y Y R G K N  
 1021 GATGCATGGGATGGATATGGCGGTGCTTTTGTGTACACGAGAAGCGCAGTTTTACCTGAT  
 D A W D G Y G G A F V Y T R S A V L P D  
 1081 AGCATAGTACCCGAAC TAGAAAGAGCAGCAAAAAGTGTAGGACGGGATTTCAACACGTTT  
 S I V P E L E R A A K S V G R D F N T F  
 1141 ATCAGAACAGATAATACTTGTGGGCCTGAACCTCCTTTAGTTGAAAGACTTGAGAAGACC  
 I R T D N T C G P E P P L V E R L E K T  
 1201 GTGGAAGAAGGAGAGAGGACGATCATACGAGAGGTAGAGGAAATAGAAGGAGAGATAGAA  
 V E E G E R T I I R E V E E I E G E I E  
 1261 AGTGAGGTTGAGAAAGTGGAGAAGACTGAAATGAATCTGCTCCAAAGGTTGTTTGATGGA  
 S E V E K V E K T E M N L L Q R L F D G  
 1321 TTTAAGGAGCTCCAGCAAGATGAAGAAAACCTTCTAAAAGGTCTTAGCCAGGAAGAGATG  
 F K E L Q Q D E E N L L K G L S Q E E M  
 1381 GAGATTTTAAATGATCTTAAGATGGAAGCAAAAGAGGTAGAAAACCTTTTGGGCAGGCA  
 E I L N D L K M E A K E V E K L F G Q A  
 1441 ATACCACTGAGGAAGCTAAGGT**TAGA**ATGCAGTTGGATGAATTTTAAGCCTTGTTACAAGT  
 I P L R K L R \*  
 ATCTTATAAGCAACATGCTTAATGAGTTCCACTCTAAATGAATTTGAGTGCTTAGAAACC  
 CCAAAGTGTTATTGCAAAGTTACATTGCTTTTAGGAAAGAAGTGGGGCTCTGGAA +136

**Figure S1K.** The nucleotide sequence and deduced amino acid sequences of CmVDE. An asterisk (\*) represents a stop codon.

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-44 1  GATTCTTTTTTGTTTCATACCCCTGAAAATATTTCTTAGTTCTCATTGGAACATCAATAGA
      D S F L F I P L K I F L S S H L N I N R
61  ACTTGGCTAGTTTTCTCAAATTTACAGCTTCTCCCATCTCAGGTTTCTCATGTCGACT
      T W L V F S K F H S F S H L R F L M S T
121 CTTCTCAGGTCTCCTATGCTTTCCACTCTTACAGTCCCAACCCTCAAACCTGCTCCATCA
      L L R S P M L S T L T V P T L K T A P S
181 TTCTTCCCAATCACTTCCACCAATTCAAGAAAACATAAGCAACCCAGAATTCAAATCAGT
      F F P I T S T N S R K L K Q P R I Q I S
241 TCTAAATTTAACAGCTTCCTAGATCTGAAGCCTGAATCAAAACCCGAGTTTTTAACCTTT
      S K F N S F L D L K P E S K P E F L T F
301 GATTTACCGTTCCACGACAAGTCTGATCGTGTAAAGTATGATGTGATCATCATTGGTGCA
      D L P F H D K S D R V K Y D V I I I G A
361 GGACCAGCTGGTCTTCGTTTAGCTGAAAG
      G P A G L R L A E

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**Figure S1L.** The nucleotide sequence and deduced amino acid sequences of CmCCS. An asterisk (\*) represents a stop codon.

```

-1 1  ATG GATTCCCTCTCTTCTTCTTCTTCTTCCACAAAATTTTCATCCACATAAACTCATTCTCTCT
      M D S L S S S F F T K F H P H K L I L S
61  CCTCCTTCTCCCACTAAAAATCCTCTCTTCTACATATCTGCTGTAAATGTAGAAGATAGA
      P P S P T K N P L F Y I S A V N V E D R
121 CTGACCATCAATGATCCAAAACCAACACCTTTCATCTCCATTATCTCAAAACCTACTAAC
      L T I N D P K P T P S S P L S Q N P T N
181 CGAACACCAATTACATCATCATCAGTAGCAACAAAAGCTAAAAACGTTGGAAAAGATCCA
      R T P I T S S S V A T K A K N V G K D P
241 AAGAAATCAACAATAACTAGAAGAAGATCAATAACAACAACAGATCTTCCATCAGTTCCA
      K K S T I T R R R S I T T T D L P S V P
301 ACTAGCATTTTCAACGCATTTGATAGCATCATAAATAACTTCATTGACCCGGCAATCCGT
      T S I F N A F D S I I N N F I D P A I R
361 CCTTCTGTAGACCCAAAACACGTACTTGCTAAAAATTTTCGCACCCGTTGATGAACCT
      P S V D P K H V L A K N F A P V D E L P
421 CCAACAAAGTGCAGTGAATTCAGGTGCCATTCCACCCTCCATTAATGGTGCTTACATC
      P T K C T V I Q G A I P P S I N G A Y I
481 CGCAACGGGCCAAACCCACAACATCTTCCACATGGACCTTACCATTATTTCGATGGAGAC
      R N G P N P Q H L P H G P Y H L F D G D
541 GGCATGCTTCACTCTCTCCTCATCTCTAATGGCACTGCAACTTTCTGTAGTCGATACGTT
      G M L H S L L I S N G T A T F C S R Y V
601 AAGACCTACAAATATACAGTTGAACGTGAACATGGCTCTTCCATATTTCCCTAATGTATTT
      K T Y K Y T V E R E H G S S I F P N V F
661 TCTGGTTTTAATGGCCTCACTGCTTCTGTTGCTCGTGGGGCTGTCACTGCTGCTAGGGTT
      S G F N G L T A S V A R G A V T A A R V
721 CTCTCTGGTCAGTATAATCCTGTTAATGGAATCGGTCTTGCAAATACAAGTCTTGCTTTC
      L S G Q Y N P V N G I G L A N T S L A F
781 TTTGGTGACAACTTTTGTCTTGGAGAATCTGATCTTCTTATGAAATCAAATTAAT
      F G D K L F A L G E S D L P Y E I K L T
841 CCTGATGGTGAAATTTACCTCGGTGCTCAGACTTCGATGGAAAATTTGTTATGCTC
      P D G E I V T L G R H D F D G K L F M S
901 ATGACTGCTCATCTAAAGTAGACCCAGCACAGGTGAAGCCTTCGCATTCCGATACGGC
      M T A H P K V D P S T G E A F A F R Y G
961 CCAATTCCTCCATTTTGTACCTTTTCCGGTTTAATTCATCCGGTTCGAAACAACCTGAT
      P I P P F L T F F R F N S S G S K Q P D
1021 GTACCCATTTTCTCCATGACACGACGACATTTCTTCATGACTTTGCTATCACCCTAAA
      V P I F S M T R P A F L H D F A I T Q K
1081 TTTGCCATATTTACAGAGATACAAATTGGGATGAATCCAATGGAGATGATTGTGGGTAAT
      F A I F T E I Q I G M N P M E M I V G N
1141 GGGTCACCTGTCGGGGCAGATCCGAGTGTAGTATCTAGGATTGGTGTGATTCCACGGTAT
      G S P V G A D P S V V S R I G V I P R Y
1201 GCCAAAGACGAATCAGATATGAAATGGTTCGACGTACCCGGGTTTAACATCATCCATGCA
      A K D E S D M K W F D V P G F N I I H A
1261 GTTAATGCATGGGATGAAGGTGAAGATGAAATAGTTTTAATGCACCAATATATTATCA
      V N A W D E G E D E I V L I A P N I L S
1321 GTAGAACATACTTTAGAAAGATGGAACCTCATTTCATGCGCTAATGGAGAAAGTACGTATC
      V E H T L E R M E L I H A L M E K V R I
1381 AATTTGAGAACGGGTATGGTTTCGCGACACCCGGTGTGCAAGAAATCTAGATTTTGGT
      N L R T G M V S R H P V S A R N L D F G
1441 GTGATTAATCAAACTTCACAGGGAAGAAACAGATTTGTTTATGCAGGAATTGGTGAC
      V I N Q N F T G K K N R F V Y A G I G D
1501 CCAATGCCTAAGATTTCAAGAGTAGTGAAATTGGATGTGGGAGATGAACATGAGCAGAAT
      P M P K I S G V V K L D V G D E H E Q N
1561 GATTGTACTGTGGGTGTCAGGATGTTCCGGTCTGGTTGTTATGGTGGTGAACCGTTTTAT
      D C T V G C R M F G S G C Y G G E P F Y
1621 GTTGCAAAAGAACCCGAGAACCTCGATGCCGATGAAGATGATGGGTATGTAGTGACATAC
      V A K E P E N L D A D E D D G Y V T Y
1681 GTACATGATGAGAATTTAGGGGAATCTAAGTTTTTGGTGATGGATGCTAAGTCAACCAACG
      V H D E N L G E S K F L V M D A K S P T
1741 CTTGATGTAGTGGCTGCTGTGACGTTGCCGGTTCGGGTTCCATACGGGTTTCATGGAATC
      L D V V A A V T L P G R V P Y G F H G I
1801 TTTGTGAGGGAAGTGAACCAAGAAGCTGATGTAAAAAGGGGTGGATGTTCATATTGAG
      F V R E S E L K K L M *
      TCCTAGTAAATCCTATTATATGTACATGGTAACCAACCATACCCATATTTAGGAACA +13

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**Figure S1M.** The nucleotide sequence and deduced amino acid sequences of CmCCD. An asterisk (\*) represents a stop codon.



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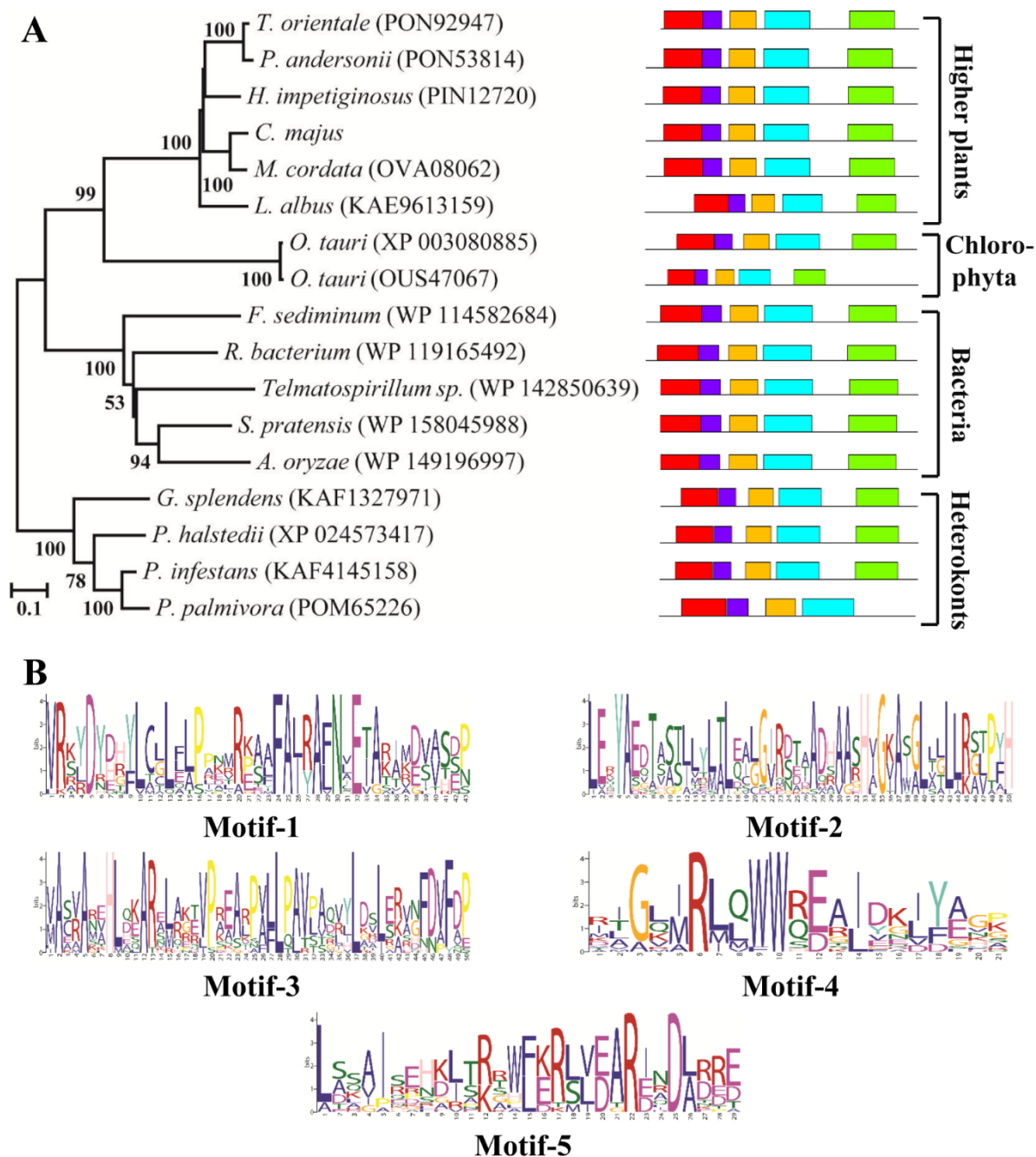
                                ATAAGCAAAAATCTACACTCCTTTTCACC
1  ATGCCTACTTCTTCAAGTACTACTTGGATTAATAAACCCCTCCATTTCCATAAACAAACCT 60
   M P T S S S T T W I N K P S I S I N K P
61 AGAAGAAGAAGTAGTAGTAGTACTCTGTCTTCATCTTTACAGTCTCCTTCTCTACTTCAC 120
   R R R S S S S T L S S S L Q S P S L L H
121 TTCCCTACCCAACGCCACCAATCTTCTCCTTCCACCACCACCTCCACCTCAGCTGCTATT 180
   F P T Q R H Q S S P S T T T S T S A A I
181 TCTACCTACACCCATACCCACACTCCAATCACTCTTCCCAAAGAGAAATCCAAAACACTA 240
   S T Y T H T H T P I T L P K E K S K T L
241 CACCCAATTTCTTCTCCTAATCCTAATCCTAATCCTACGCCAACAACAAAGACAATCCAA 300
   H P I S S P N P N P N P T P T T K T I Q
301 CACCCACCAAACTGGAATCCTTTCCAAAAAGCTGCATCCATGGCGTTAGATGCTTTTGAA 360
   H P P N W N P F Q K A A S M A L D A F E
361 ACAGCTTTACTCAACAAAGAACGTCAACACCCACTTCCCAAACAGCTGACCCCTTCCGTT 420
   T A L L N K E R Q H P L P K T A D P S V
421 CAAATCTCCGGTAACTTCGCTCCCGTTCCAGAACAACCTGTTTCGACAGAATCTCCCAGTC 480
   Q I S G N F A P V P E Q P V R Q N L P V
481 ACCGGCAGAATCCCTTGTTCCATTAGTGGATTTTACGTCCGTAACGGAGCTAATCCTTTA 540
   T G R I P C S I S G F Y V R N G A N P L
541 CACGAACCA
   H E P

```

**Figure S1N.** The nucleotide sequence and deduced amino acid sequences of CmNCED. An asterisk (\*) represents a stop codon.

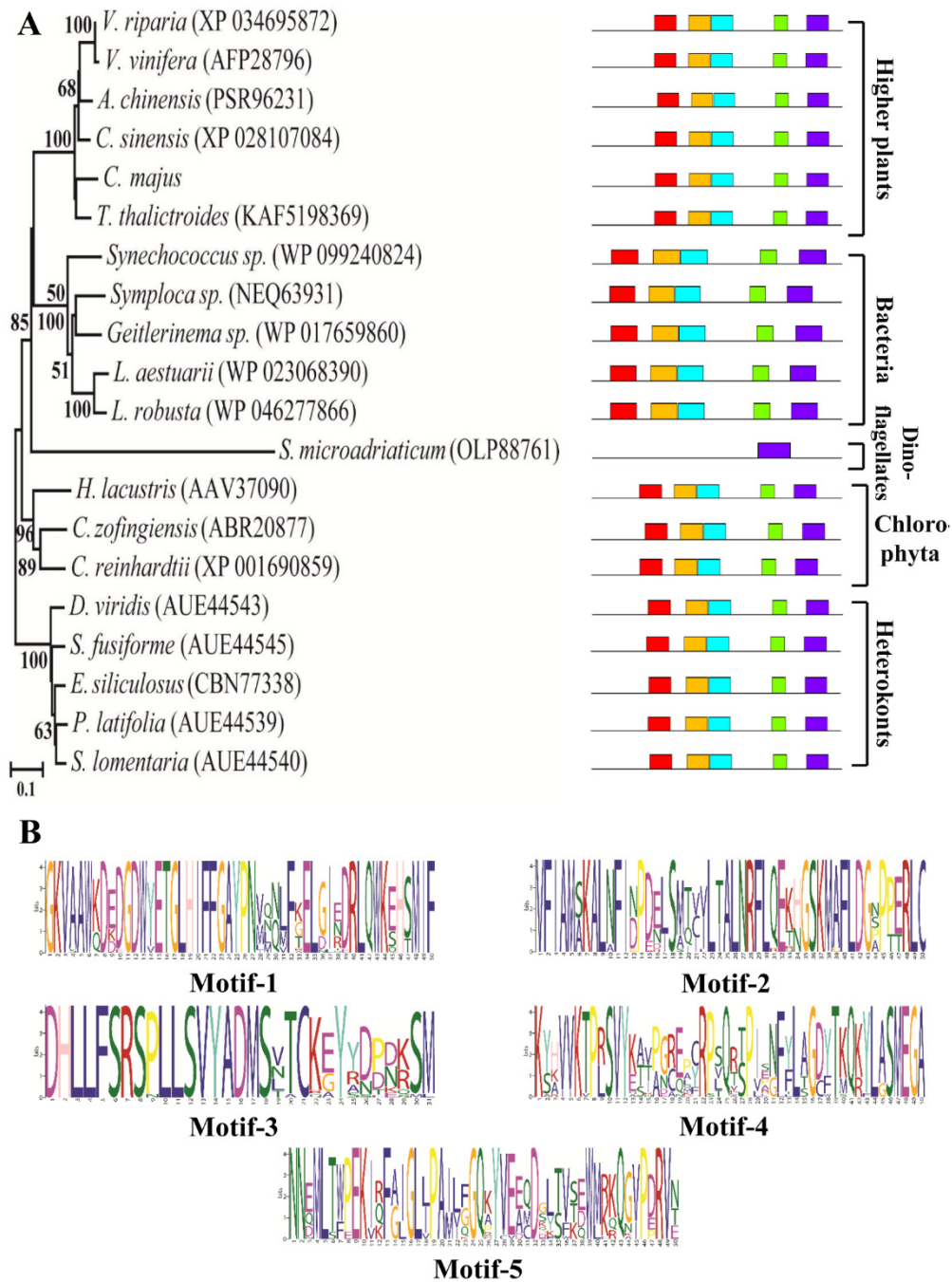
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G E R F E L S K I D P S T T V L E F L R  
121 ACCGAGACTCGTTTACTGGAACATAAGCTTAGCTGTGGAGAGGGTGGTTGGGGAGCTTGT  
T Q T R F T G T K L S C G E G G C G A C  
181 GTGGTTCTTCTGTCCAGATATGATCTGTACTTGACAAAGTTGAGGATTTTAAAGTGAGT  
V V L L S K Y D P V L D K V E D F K V S  
241 TCATGCTTAACCTTTGTTCAGATATACATGGATGTTCAATTACGACTACCGAAGGCCTT  
S C L T L V C S I H G C S I T T T E G L  
301 GGAATGTCAAGATGGGTTCACCCCAATCCACAAAGAATGTCTGGTTTTCATGCTTCT  
G N V K D G F H P I H K R M S G F H A S  
361 CAGTGTGGGTTCTGTACTCGGGAATGTGTATGTCCTCTCTCTCTCTCTGCTTGTAAATGCT  
Q C G F C T P F G M C M S L F S A L V N A  
421 GAGAAACTCAAAAGGACGATCCTCCTCTGATTTTGAAGCTCACAGATACAGAAGCT  
E K T Q K D D P F G F S K L T V S E A  
481 GAGATGGCTTTCAGGCAATCTTTCGCGGTGACAGGTACAGACCAATTCGCGATGCC  
E M A I S G N L C R C T G Y R P I A D A  
541 TGCAAGAGTTTTCAGTAATCGGACATGGAAGATCTAGGTCTGAATCTCTTTTGAAG  
C K S F A V N A D M E D L G L N S F W K  
601 AAGGGGACAAATGATAAAGCAAGTAATACCTTTTATACCCCAAAATGAAATTTGC  
K G D N D K A S K L P F Y T P Q N E I C  
661 ACCTTCCCTGAGTCTTAAAGCAGAGCTTAAGTCCAAACACTCTTGGATTTCGAAAGG  
T F P E F L K T E L K S K T L L D S K K  
721 CATTGTGGTATAGTCTCTGATTATGAGGAATTAAGGCCATTAAGGAATGCTTAGAA  
H C W Y S P V T I E E L K G L M E C L E  
781 AATGAAATGTAAACGGTTTAACTAGTTGTGTAAATACGGTACAGGCTATTACAAG  
N E N C N A L K L V V G N T T G T G Y Y K  
841 GAGCTAAACAGTACGACAGATATATTGATCTAAGCAATATTCTGAGCTCTCAGTGATC  
E L K Q Y D K Y I D L R H I P E L S V I  
901 AGAAGTGATAGCAGTGGTGTGAAATGGAAGCTGCTGTGACTATCTTAACACTATCCAT  
R S D S S G V E I G A A V T I S N T I H  
961 GCTTTGATGGAAGAAAGATGGGTATAACTCAACCAATAATCTGTGTTCAAGAAA  
A L M E E R K G D G Y N S T I N L V F R K  
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I S D H M N K V A S E F V R N T A S L G  
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1141 GCTGTGTTTCTGCTAGATATCTTAAAGGCTCCAAAGACTAAAGCTTACATTTGAG  
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1441 TTTGGTCTTATGGGACAAACATGCAATAAGGGCAAGAAATGTTGAGGAATCTTTGATT  
F G A Y G T K H A I R A R N V E E L L I  
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Y S K R P L A W I K S V E L V S P L P S  
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A V V E Y D T G N L E P P I L S V E E A  
2221 GTCATAGATGACAGCTTCTTTGACGTGCTCCATTCTTCCCGAAACAGGTAGGAGAT  
V N R C S F F D V P P F L S P K Q V G D  
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2401 TGATGGTGGTTTACAGCTCAACTCAGTGCCTGAGAAATGCACAGATTTGATTTGCTAAA  
C M V V Y S S T Q C P E N A Q I V I A K  
2461 TGCTTGGTCTTCTGAACATAACGTCGGTGTATTACAAGAAGTTGGAGGAGGATTC  
C L G L P E H N V R V T I T R V G G G F  
2521 GGTGGAAGGCTTAAAGCAATGCTCTGTCTACAGCATGCGAGTTGCTGCACACAAA  
G K A L K A M P V A T A C A V A A H K  
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L R H P V R V Y L S R K T D M I M A G G  
2641 AGACATCTTATGAAATAAAGTCAAGTGTGGTTTCAAGTCTGACGGAAGATCACTGGG  
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2881 TCCTTTATGCAAGGCTGTGATTGAGCATGATGATCATTTCTTTCTATGGAAGTGTAT  
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Y V R E R N I H T Y E S L K L F Y Q D T  
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A G E P I E Y T L P L V L D K L S K S  
3061 AACTTCTTCCAAAGGTTAGAAATATAAACAATTAATAGCTATAATAAGGAGGAGAAA  
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3121 AGAGGAATTTCTCGGCTGCCATCTTTCATCAAGTAATGCTTACAGTCACTCCAGGTAAA  
R G I S R V P I F H Q V M L R P T P G K  
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3241 GGGCTTTGCAAGAGTGAAGCAGATGGCGGCAATTTGCTCTCAGTCTGTAGATGTGAT  
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3421 TGCTGAATGCTTTGGTTGAAGACTTACCATCTTAAAGGAAGTTGCAAGAGCAGATG  
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3481 GGTCCAGTTTATGGGATATTTAATAATCCAGGCACATCTCCAATCTGTCACTTATCT  
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3601 GTGAGTGAAGTGGAGATTGATCTTCTACAGGAGCAACCAATATTGCGAAGCAATATT  
V S E V E I D L L T G A T T I L R T D I  
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3721 TTTGTTCAAGGAGTTGGGTTTTTATGCTGGAAGAGTACCTGACAACTCCGATGGAATTG  
F V Q G V G F F M L E E Y L T N S D G L  
3781 GTAGTATCTGAAGGAACATGACCTACAGATTTCCAACATAGACCACTCCCGAGACAG  
V S E G T W T Y K I P T I D T I P R Q  
3841 TTCAATGTTGAGCTACTGAACAGCGGACATCATCAAAACGTTGCTCTCTCTAAAGCT  
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S G E P P L L M A A S V H C A T R D A I  
3961 AAAGAAGCAAGAAAACAGGTCCTTTCTTGGAGTGGTCAAGTCTGATGATCATCTTAT  
K E A R K Q V L S W S G S E L D A S S Y  
4021 TCCACATTCCAATTGGATGCTCCTGCAACATGCTGTAGTGAAGGAGCTATGTGGAATC  
S T F Q L D V P A T M P V V K E L C G L  
4081 GATAGCGTTGAGCGGATTTAGAAAGTTTACCTTTCCCATTAAGAACTGT +155  
D S V E R Y L E S L L L S H \*

**Figure S10.** The nucleotide sequence and deduced amino acid sequences of CmAO. An asterisk (\*) represents a stop codon.

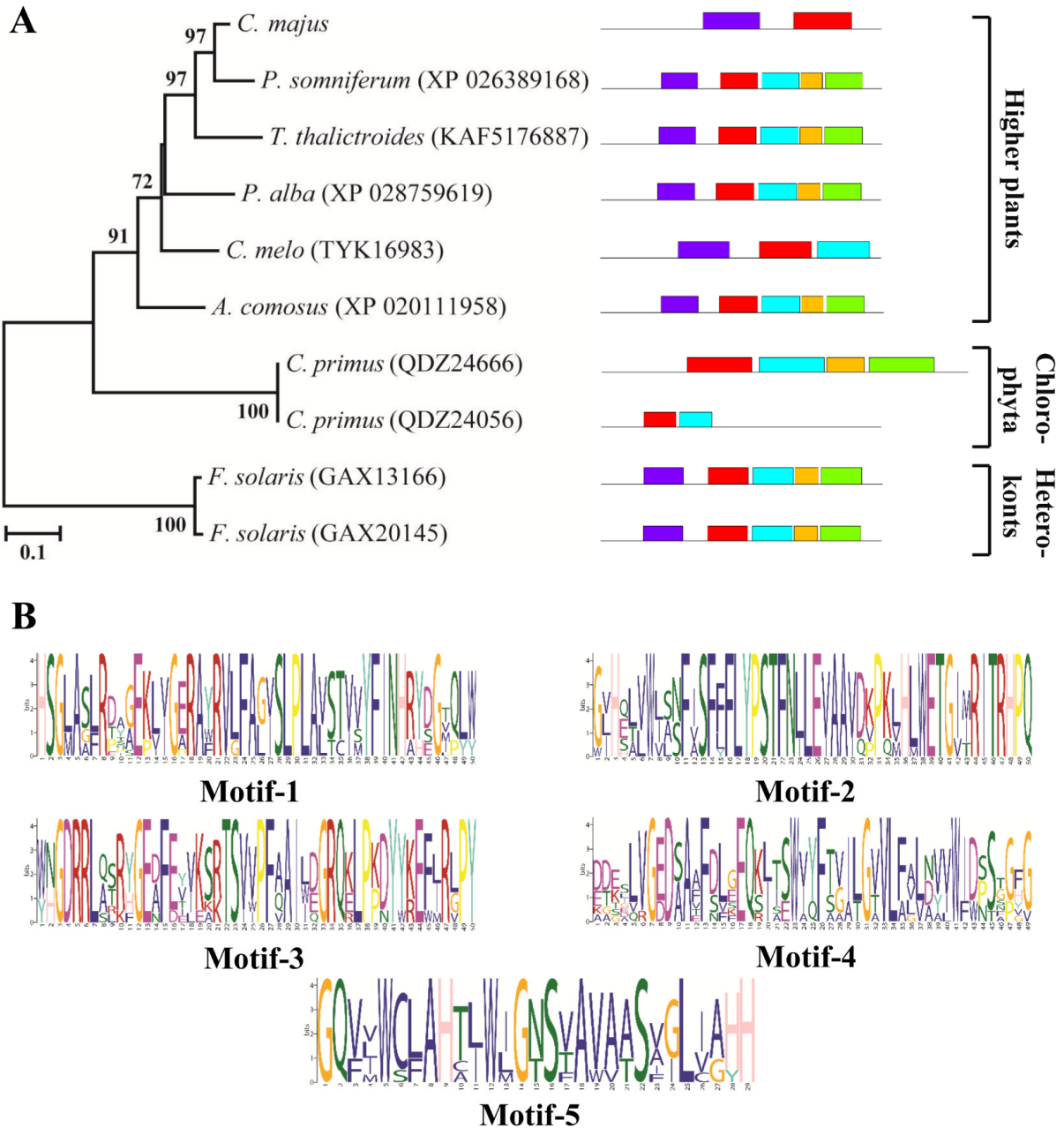


**Figure S2A:** Phylogeny of deduced CmPSY amino acid sequences along with other PSY sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to PSY sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmPSY gene. The height of the letters denotes the degree of conservation.

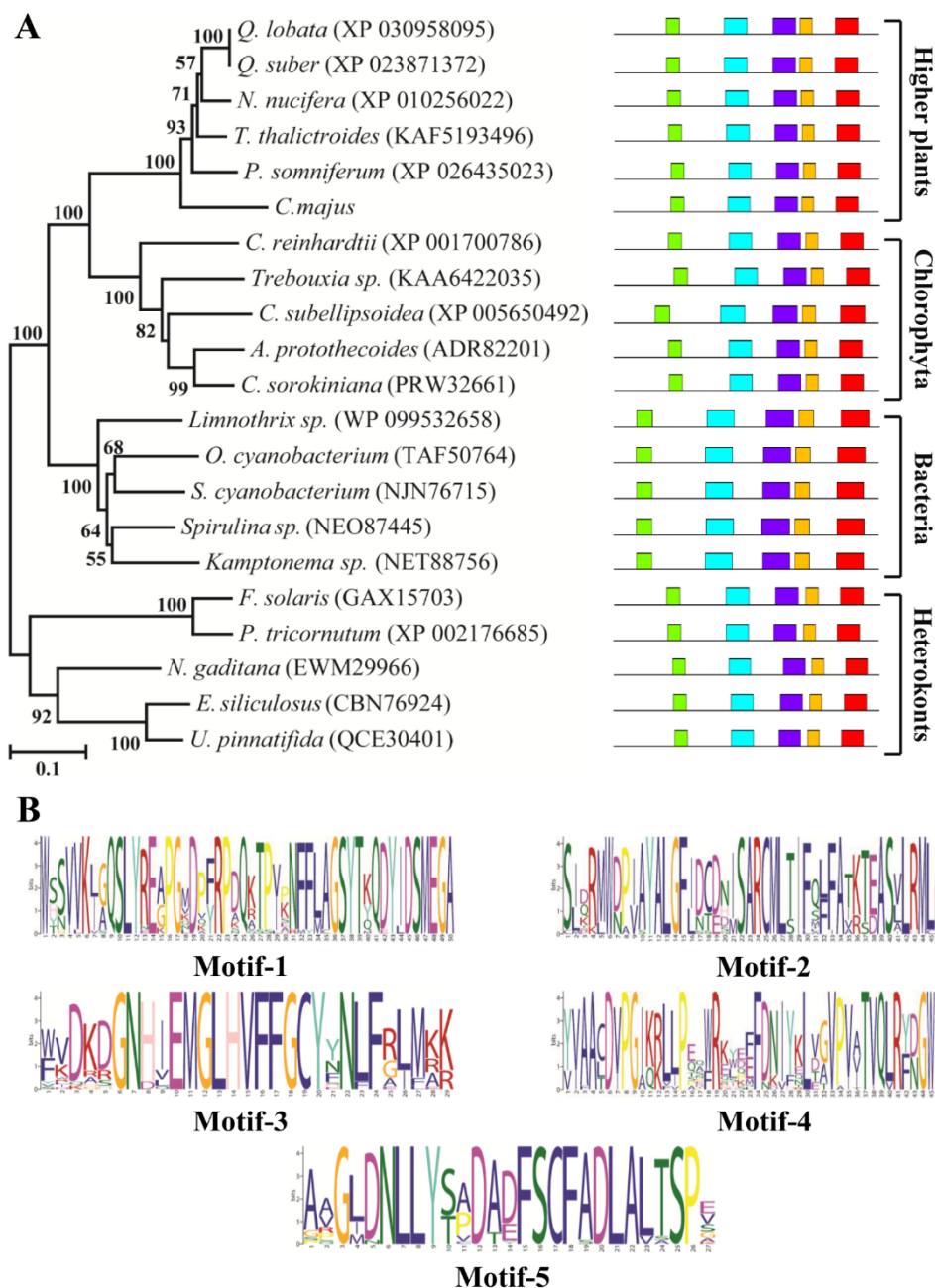




**Figure S2B:** Phylogeny of deduced CmPDS amino acid sequences along with other PDS sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to PDS sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmPDS gene. The height of the letters denotes the degree of conservation.

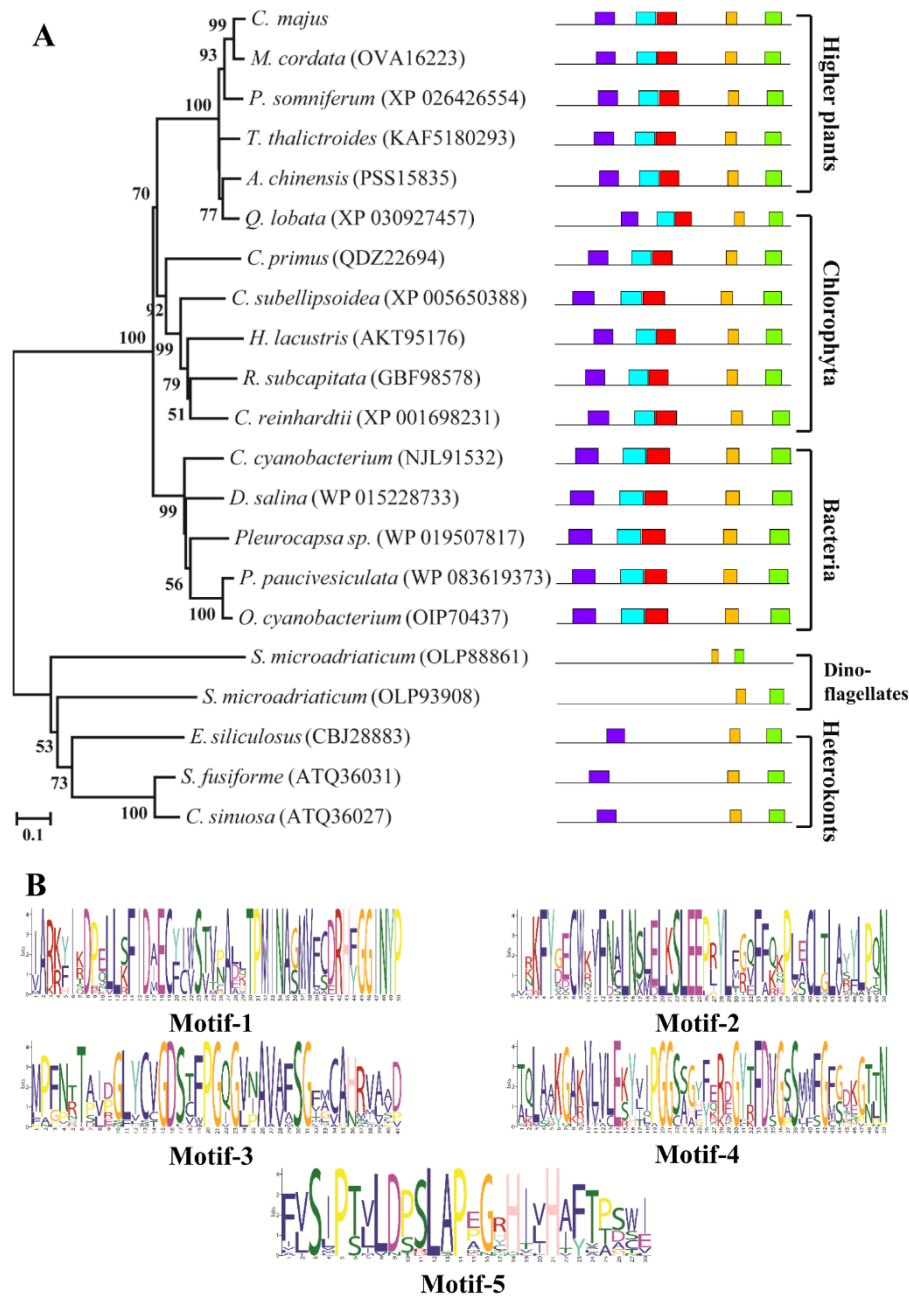


**Figure S2C:** Phylogeny of deduced CmZ-ISO amino acid sequences along with other Z-ISO sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to Z-ISO sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmZ-ISO gene. The height of the letters denotes the degree of conservation.

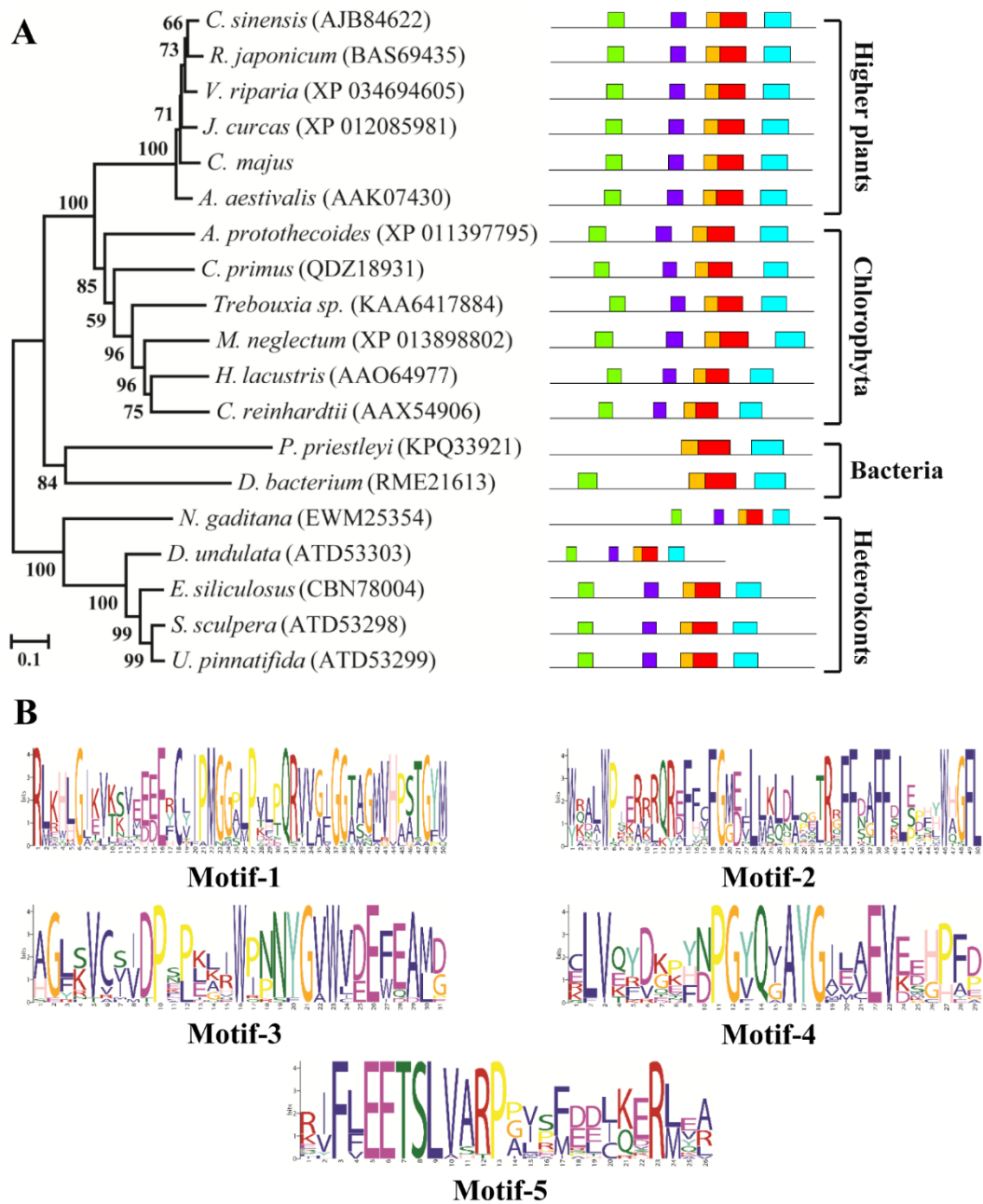


**Figure S2D:** Phylogeny of deduced CmZDS amino acid sequences along with other ZDS sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to ZDS sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmZDS gene. The height of the letters denotes the degree of conservation.





**Figure S2E:** Phylogeny of deduced CmCrtISO amino acid sequences along with other CrtISO sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to CrtISO sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmCrtISO gene. The height of the letters denotes the degree of conservation.

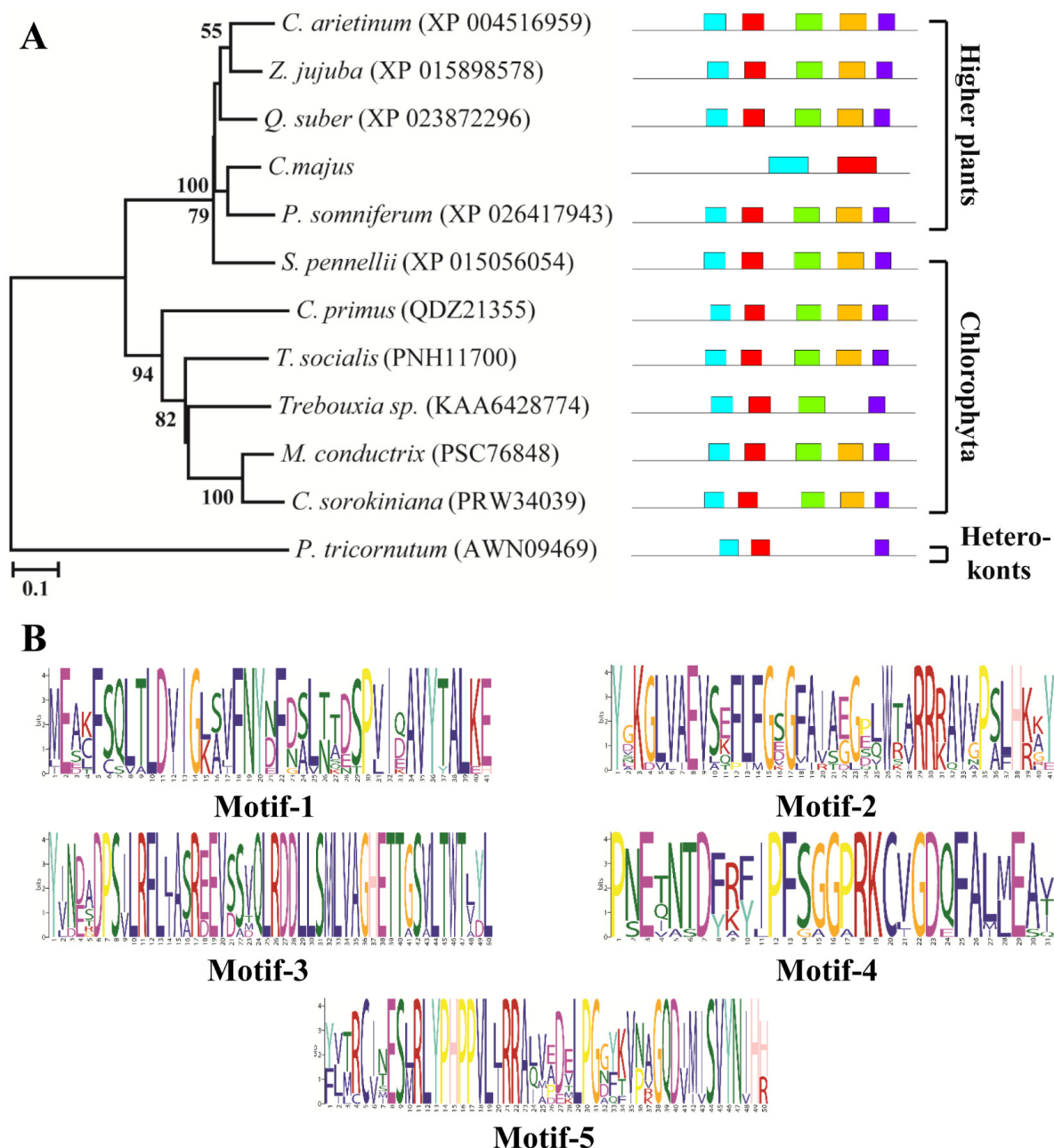


**Figure S2F:** Phylogeny of deduced CmLCYB amino acid sequences along with other LCYB sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to LCYB sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmLCYB gene. The height of the letters denotes the degree of conservation.

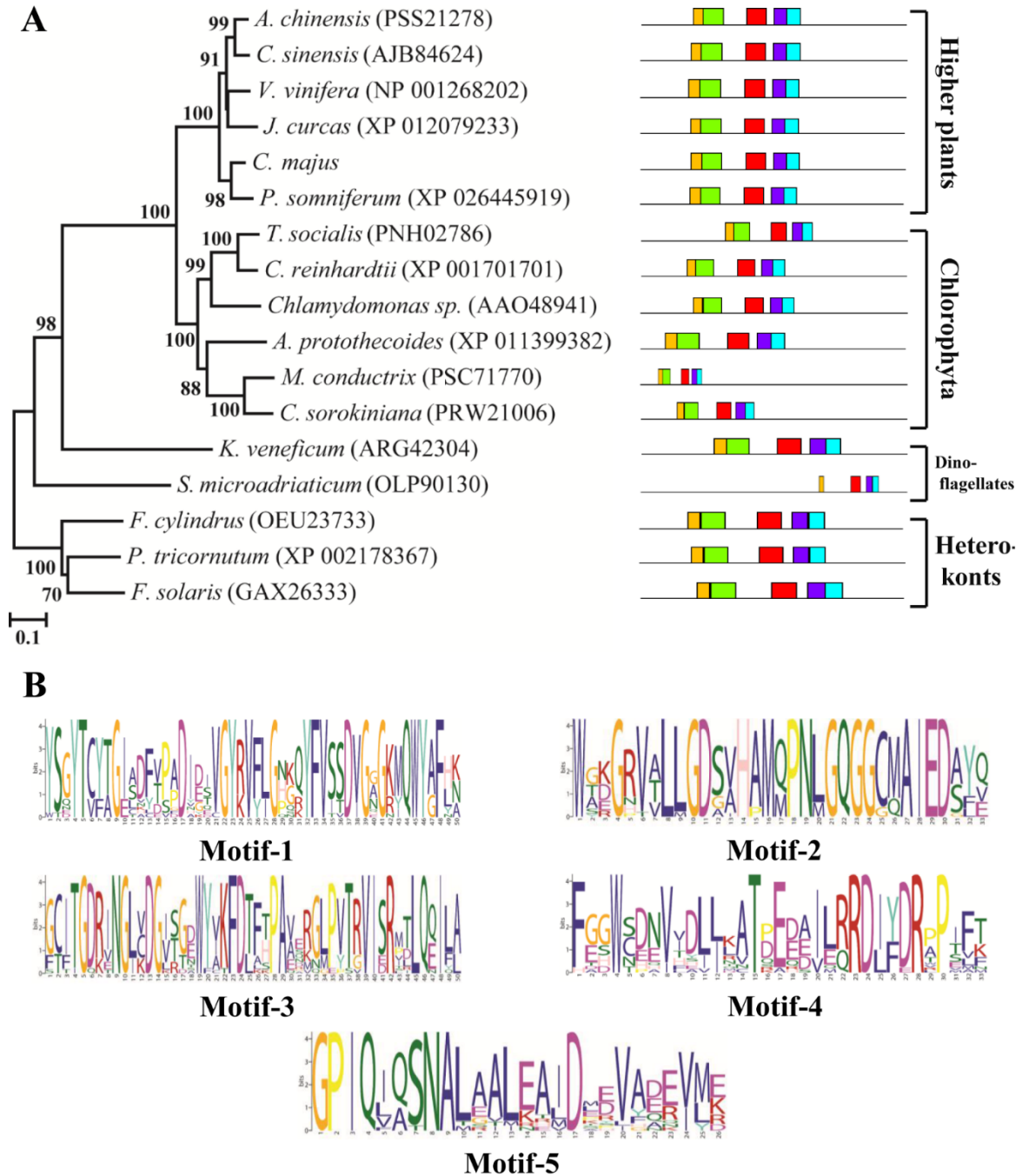








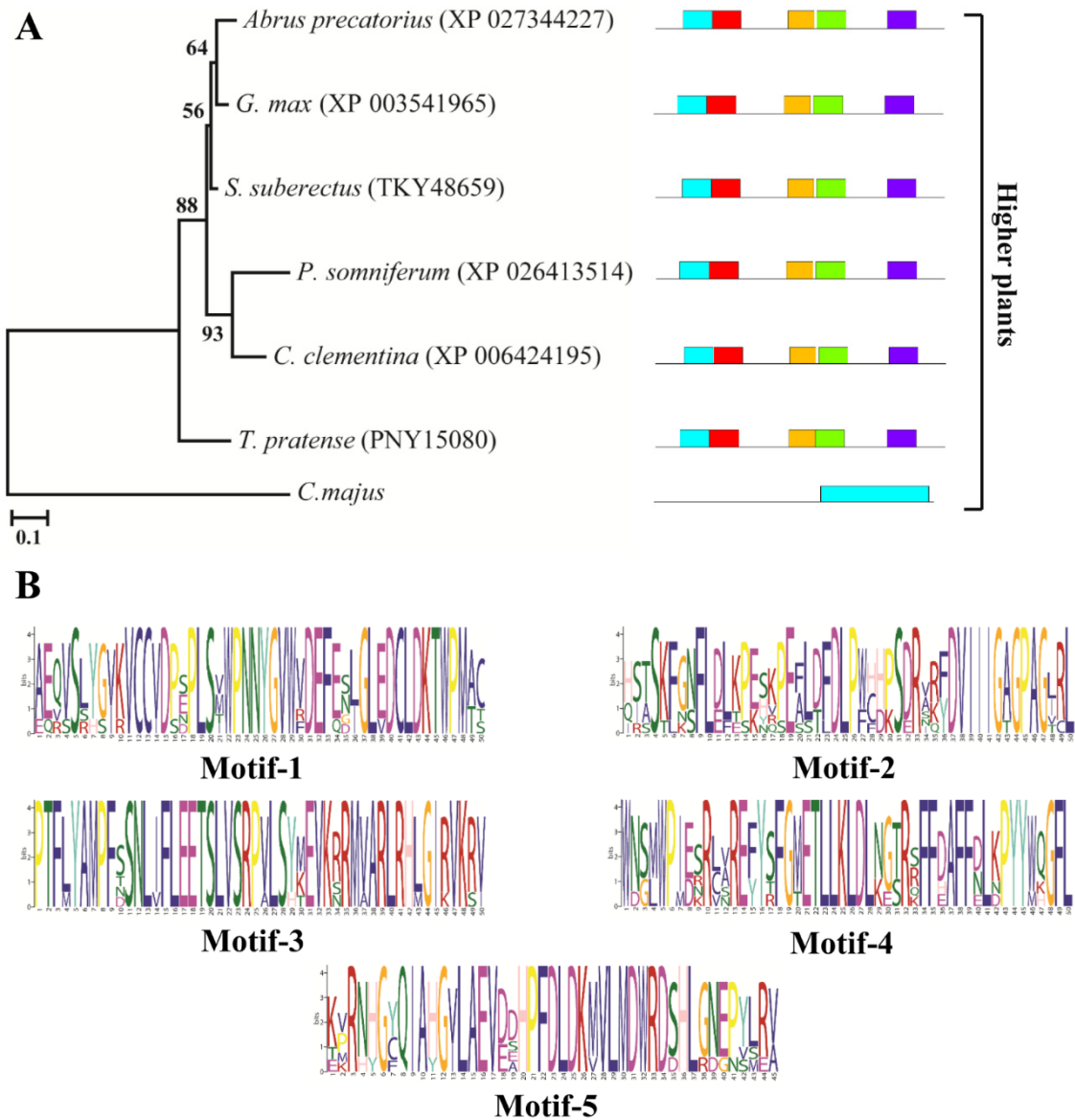
**Figure S2I:** Phylogeny of deduced CmCHXE amino acid sequences along with other CHXE sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to CHXE sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmCHXE gene. The height of the letters denotes the degree of conservation.



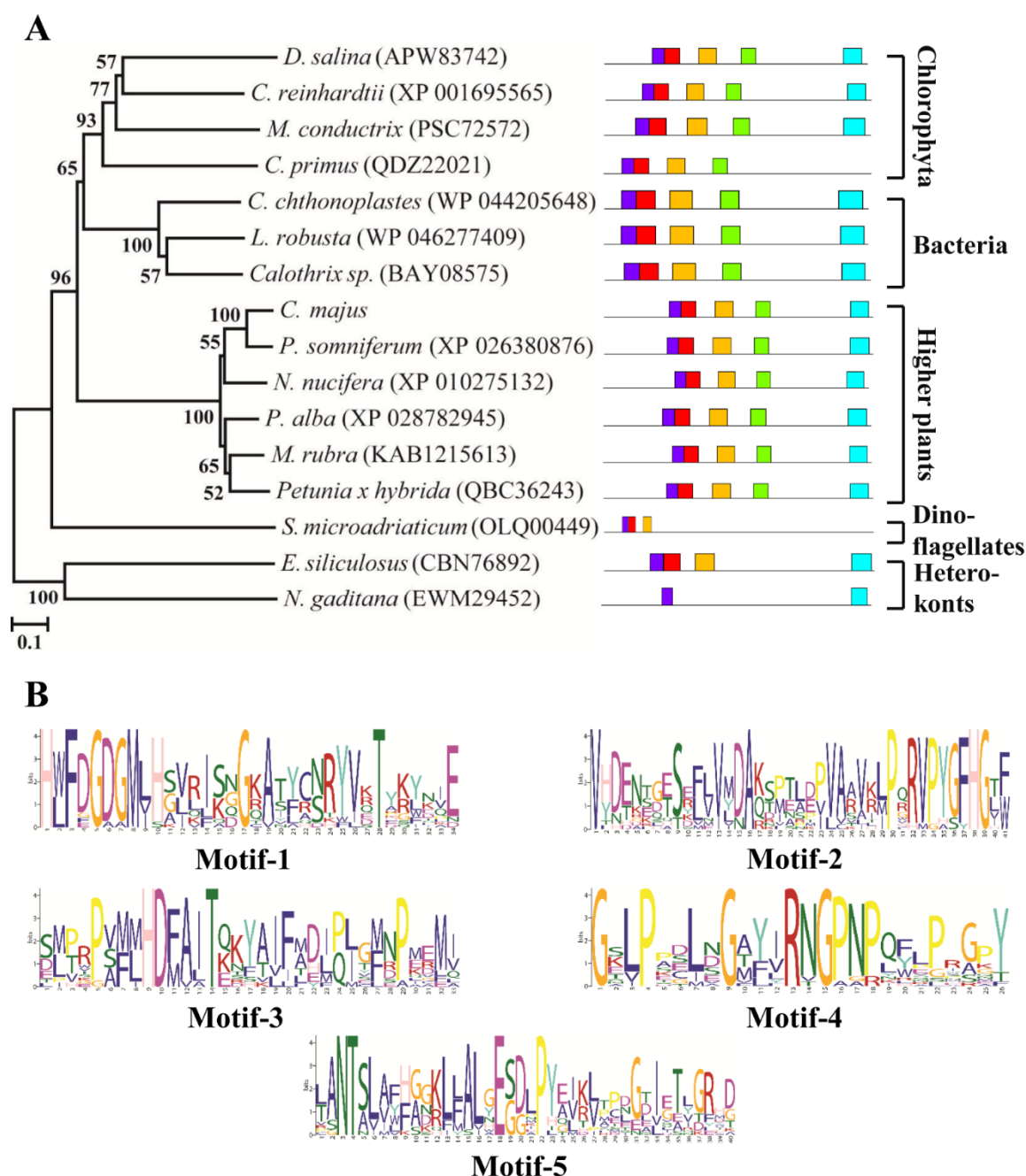
**Figure S2J:** Phylogeny of deduced CmZEP amino acid sequences along with other ZEP sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to ZEP sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmZEP gene. The height of the letters denotes the degree of conservation.





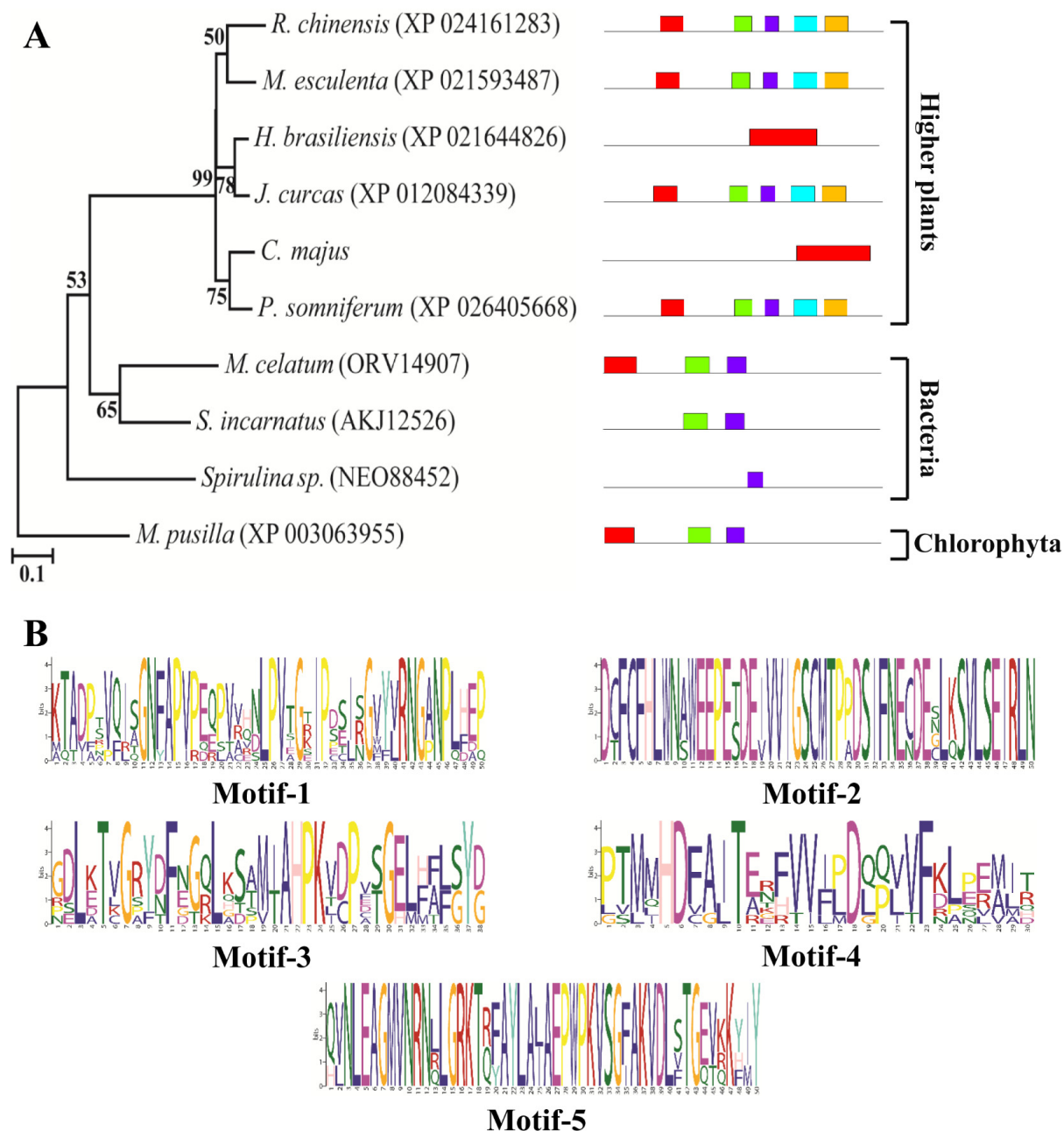


**Figure S2L:** Phylogeny of deduced CmCCS amino acid sequences along with other CCS sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to CCS sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmCCS gene. The height of the letters denotes the degree of conservation.

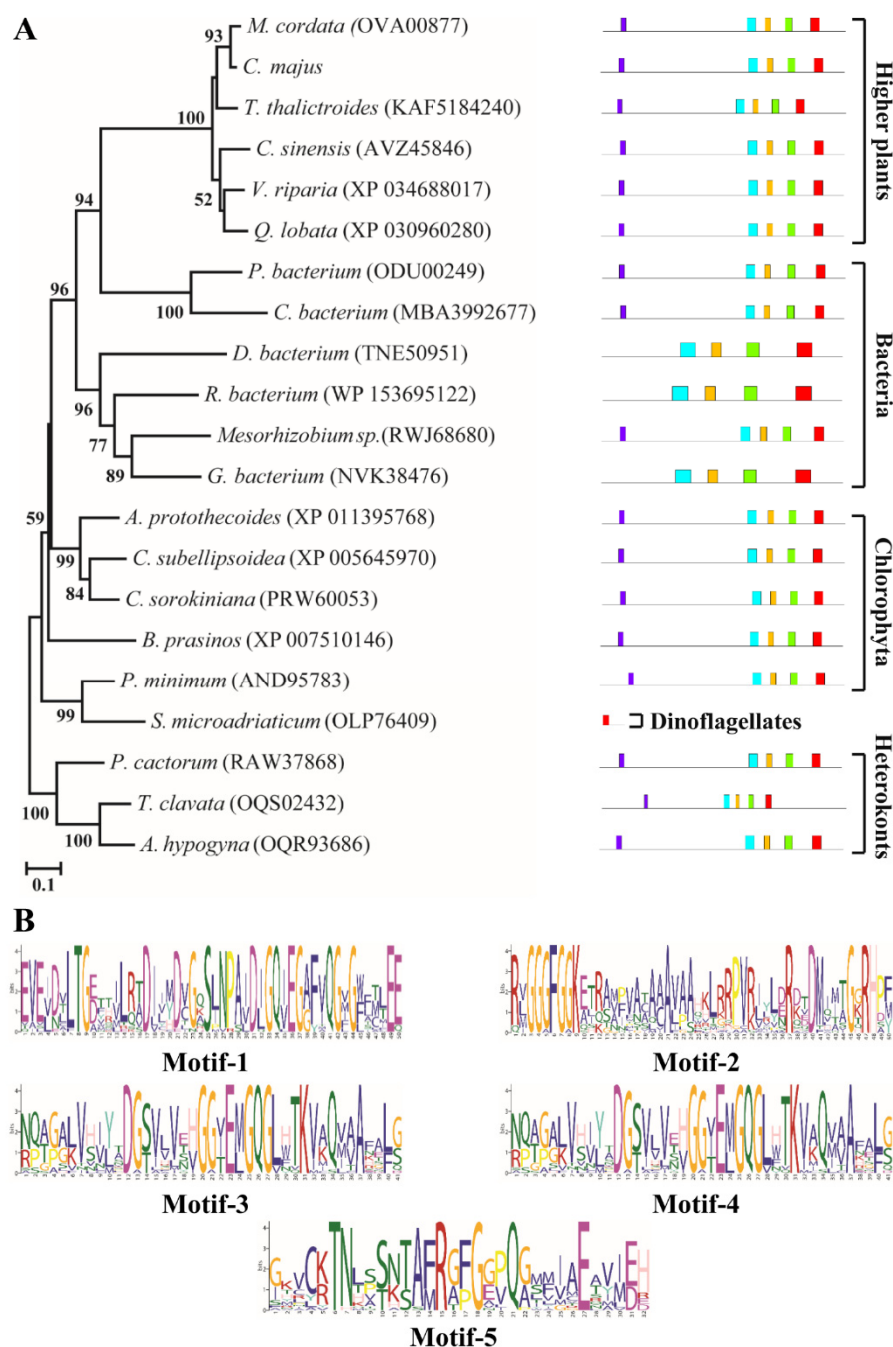


**Figure S2M:** Phylogeny of deduced CmCCD amino acid sequences along with other CCD sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to CCD sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmCCD gene. The height of the letters denotes the degree of conservation.





**Figure S2N:** Phylogeny of deduced CmNCED amino acid sequences along with other NCED sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to NCED sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmNCED gene. The height of the letters denotes the degree of conservation.



**Figure S2O:** Phylogeny of deduced CmAO amino acid sequences along with other AO sequences. The tree was constructed using MEGA 7 [116] on the basis of the Neighbor-Joining method [117]. Bootstrap values on the nodes indicate the number of times each group occurred within 1000 replicates [118]. On the right side, the analysis of conserved protein motifs using MEME software is presented, showing motifs and are ordered in colored boxes corresponding to AO sequence in the phylogenetic tree. Other protein sequence obtained from NCBI database as well as their accession numbers are provided in the bracket. (B) Conserved protein motif 1-5 present in the variable region of CmAO gene. The height of the letters denotes the degree of conservation.

*C. majus* ----- 1  
*M. cordata* ----- 1  
*T. orientale* ----- 1  
*H. impetiginosus* ----- 1  
*P. andersonii* ----- 1  
*L. albus* ----- 1  
*N. officinale* MSSVAVLVWAASSPNPDPLNNCGLVRVLESSRLLRQTTTWRSSSVMNRRRSGVSSLVASPSGEITLSSEEVYNVWLKQAALVNKQLRSSSD 100

*C. majus* -----MNGASTSSTIRAAFSHCVCQVRSYDHHYLCLLQLSPNMRKAFAFALRAFNVETARAMDVASDPKIGLMRLLWQEAIDKIFAHKKIEHPTAQ 92  
*M. cordata* -----MNGASTSSTIRAAFSHCVCQVRSYDHHYLCLLQLSPNMRKAFAFALRAFNVETARAMDVASDPKIGLMRLLWQEAIDKIFAHKKIEHPTAQ 92  
*T. orientale* -----MSGGASTSIRAAFSHCVCQVRSYDHHYLCLELPPNMRKSAFALRAFNVETARAMDVASDPKIGLMRLLWQEAIDKIFAHKKIEHPTAQ 92  
*H. impetiginosus* -----MSGGASTSIRAAFSHCVCQVRSYDHHYLCLELPPNMRKSAFALRAFNVETARAMDVASDPKIGLMRLLWQEAIDKIFAHKKIEHPTAQ 92  
*P. andersonii* -----MSGGASTSIRAAFSHCVCQVRSYDHHYLCLELPPNMRKSAFALRAFNVETARAMDVASDPKIGLMRLLWQEAIDKIFAHKKIEHPTAQ 92  
*L. albus* -----MSGGASTSIRAAFSHCVCQVRSYDHHYLCLELPPNMRKSAFALRAFNVETARAMDVASDPKIGLMRLLWQEAIDKIFAHKKIEHPTAQ 135  
*N. officinale* LDVKQDWLPGSLSLLEADRCEVCAEYAKTFYLGTLMTFERRKAIWAIVWCRRTDELVDGPNASHITFMALDRETREDLFRGRPDMLDA- 199

*C. majus* -----ALSSIIEHKKISKSWLKRSVEARINDARRENEIPOSEELEEK\*AE\*STVSTILYMTLQA---GGIRSTAADHAASHIKASGLLLLRS LPYHHSRNSQL 189  
*M. cordata* -----ALSSIIEHKKISKSWLKRSVEARINDARRENEIPOSEELEEK\*AE\*STVSTILYMTLQA---GGIRSTAADHAASHIKASGLLLLRS LPYHHSRNSQL 189  
*T. orientale* -----ALSSVINENKIKGWLKRSVEARINDARREVEIPEKIRELEQAE\*ASTILYMTLQA---GGIRSTIADHAASHIKASGLLLLRS LPYHHSRNSQL 189  
*H. impetiginosus* -----ALSAIIEHKKISKSWLKRSVEARINDARREVEIPEKIRELEQAE\*ASTILYMTLQA---GGIRSTIADHAASHIKASGLLLLRS LPYHHSRNSQL 189  
*P. andersonii* -----ALSAIIEHKKISKSWLKRSVEARINDARREVEIPEKIRELEQAE\*ASTILYMTLQA---GGIRSTIADHAASHIKASGLLLLRS LPYHHSRNSQL 189  
*L. albus* -----ALSSVIGENKIKGWLKRSVEARINDARRENEIPEKIRELEQAE\*ASTILYMTLQA---GGIRSTIADHAASHIKASGLLLLRS LPYHHSRNSQL 232  
*N. officinale* ALADTVARIPVDIQPRDMIEGMRDLRKSRYKNFDDLYLYCVAGTVGLMSVFMGIDPKSATTESVNAALALIANQLTNILEDVGEDARRG- 297

*C. majus* -----RYIPFEVASKHGLLSHEGGQNCVQLGYREGLPNAVFETIASVASVHLQKARELAKTVPAEALPVLPAVPAQVILDSLRVHFDVDFPRLMRG---ILGI 285  
*M. cordata* -----PYIPFEVASKHGLLVKEGGQNCVQLGYREGLPNAVFETIASVASVHLQKARELAKTVPAEALPVLPAVPAQVILDSLRVHFDVDFPRLTRG---VLGI 285  
*T. orientale* -----SYIPAEVAKHGLLVNHDGQIEVRVDSEGLCNVAFEMASVANVHLMQKARNLAGTVPAEALPVLPAVPAQVILDSLRANFDVDFPRLAKG---VFGI 285  
*H. impetiginosus* -----PYIPAEVAKHGLLVNHDGQIEVRVDSEGLCNVAFEMASVANVHLMQKARNLAGTVPAEALPVLPAVPAQVILDSLRANFDVDFPRLAKG---VFGI 285  
*P. andersonii* -----SYIPAEVAKHGLLVNHDGQIEVRVDSEGLCNVAFEMASVANVHLMQKARNLAGTVPAEALPVLPAVPAQVILDSLRANFDVDFPRLAKG---VFGI 285  
*L. albus* -----SYIPTAVASKHGLLVKGGGERRVDSEGLCNVAFEMASVANVHLMQKARNLAGTVPAEALPVLPAVPAQVILDSLRANFDVDFPRLTRG---VLGI 328  
*N. officinale* VYLPQDELAQAGLS-DEDIFAGKVTDKWRNFMRMLKRARMFDEAEKG-VIELSAASRMPVASLLLYRRILDEIANDYNNTKRAVGKAKIAAL- 394

*C. majus* SPLWFQKLKWNWAKSTY 303  
*M. cordata* SPLWFQKLKWNWAKSTY 303  
*T. orientale* PPLWFQKLKWNWAKSTY 303  
*H. impetiginosus* PPLWFQKLKWNWAKSTY 303  
*P. andersonii* PPLWFQKLKWNWAKSTY 303  
*L. albus* PPLWFQKLKWNWAKSTY 346  
*N. officinale* PLAYAKSVLKTSSR--- 409

**Figure S3A.** Amino acid alignment of CmPSY with selected corresponding genes was performed with the BioEdit program of ClustalW. The yellow highlighted box represents the substrate-binding pocket. Asterisks indicate catalytic residues, and those with a blue underline represent the conserved trans-isoprenyl diphosphate synthase domain. *M. cordata* (*Macleaya cordata*, OVA08062), *T. orientale* (*Trema orientale*, PON92947), *H. impetiginosus* (*Handroanthus impetiginosus*, PIN12720), *P. andersonii* (*Parasponia andersonii*, PON53814), *L. albus* (*Lupinus albus*, KAE9613159), and *N. officinale* (*Nasturtium officinale*, MT547989) were involved in amino acid alignment of CmPSY. A dash (–) represents an aligned gap.



*C. majus* -----MTLTSSVSVVNLSSGQGNIIINWNNSRRCCFSINSQDNNLLAFGGSDSMGLSLKSRKHAHVGRPRRK--VGPLQVWCVDYPRPELDNTVN 90  
*T. thalictroides* -----MTVAGSVSAAYLSIKGDLKNHGNLYPQQCCFSIHHNRKNLLAFRGSDAMGHQKCVSSSDHGRKIPQRDSRTS--KIVCVDYPRPELDNTVN 90  
*C. sinensis* -----MSQFGQVSTVSQGNNGISVWNPKSTWCGCGSPGSGPAKALSFRGSDSMGHRFKIPNAIYAVGTRPRK--VCPLKVCIDYPRPDLESTVN 90  
*V. riparia* -----MTQFRVSVAVNLSCQSNIIINFNQSQCTWRH--LYIDSDQTNLLFRGGDSMGLKLRIPNKHISIGTRRRK--FCPLQVWCMDYPRPELDNTVN 89  
*V. vinifera* -----MTQFRVSVVNLSCQSNIIINFNQSQCTWRH--LYIDSDQTNLLFRGGDSMGLKLRIPNKHISIGTRRRK--FCPLQVWCMDYPRPELDNTVN 89  
*A. chinensis* -----MLHIGFDFISQIGHVSAVNLGQINVRNFWNPQSTWRCGCHYNSRQLNALSFRGSDFMGHRFKIHDPHVSNGNRSRK--MRPLQVICMDYPRPDLDSTLN 98  
*N. officinale* -----MVVFGVSAANLPYQNGFLA-----LTSGGCDLMGHSFRVPTSRAPKIRTRRRSSAGPLQVWCVDYPRPELDNTVN 72

*C. majus* FIEAAHFSLSFRTSARPEKPLQVVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 190  
*T. thalictroides* FLEAAHFSSTFRAAPRPMKPLKTVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 190  
*C. sinensis* FLEAAHFSSTFRTSRRPKPLKVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 190  
*V. riparia* FLEAAHFSSTFRTSRRPKPLKVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 189  
*V. vinifera* FLEAAHFSSTFRTSRRPKPLKVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 189  
*A. chinensis* FLEAAHFSSTFRTSRRPKPLKVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 198  
*N. officinale* FLEAAHFSSTFRTSRRPKPLKVIAGAGLAGLSTAKYLADAGHKPILLEARDVLGGKAAWKDDGDWIEGLHIFPGAYPQNLFGEGLGINDRLQWK 172

*C. majus* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 290  
*T. thalictroides* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 290  
*C. sinensis* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 290  
*V. riparia* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 289  
*V. vinifera* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 289  
*A. chinensis* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 298  
*N. officinale* EHSIMFAMPSKPGFSSRFDFPDLPAPLNGIWAIRLNNEMLTWPEKVFAGILLPAMVGGQAYVEAQDGLTVKQWRRKQGVPRVTDVEFIAMSKALNFI 272

*C. majus* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 390  
*T. thalictroides* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 390  
*C. sinensis* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 390  
*V. riparia* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 389  
*V. vinifera* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 389  
*A. chinensis* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 398  
*N. officinale* NPDELSMQCILIALNRFLQEKHGSMAFLDGNPPERLCMPVVDHISQSLGGQVQLNSRIQKIELKSDGTVKRLILTNNGNAIEADAYVIAFPVDILKLLPE 372

*C. majus* DWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 490  
*T. thalictroides* EWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 490  
*C. sinensis* DWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 490  
*V. riparia* DWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 489  
*V. vinifera* DWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 489  
*A. chinensis* DWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 498  
*N. officinale* PWKETPYFKKLDKLVGVVINVHIWDRKLKNTYDHLFSSRPLLSVYADMSVTCKEYYDPNRSMLLVFAPAEWISCSDEIIEATMKE LAKLFPDEI 472

*C. majus* AADQSKAKILKYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLAARREKNRTTEASTA- 583  
*T. thalictroides* AADQSKAKILKYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLAARREKNRTTEASTA- 583  
*C. sinensis* SADQSKAKILKYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLVAREQG-KLAESV- 582  
*V. riparia* SEDQSKAKVLYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLVAREQG-KLAESV- 582  
*V. vinifera* SEDQSKAKVLYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLVAREQG-KLAESV- 582  
*A. chinensis* SADQSKAKILKYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLVAREQG-KLAESV- 590  
*N. officinale* AADQSKAKILKYHIVKTPRSVYKTPNCEPCRPQRSFVGGFYLAGDYTKQKYLASMEGAVLSGKLAQAIVQDYELLAASGPR-KLSEATVS- 564

**Figure S3B.** Amino acid alignment of CmPDS with selected corresponding genes was performed with the BioEdit program of ClustalW. The red, pink, green, and orange boxes represent the signal peptide, dinucleotide-binding motif, putative substrate carrier motif, and carotenoid binding motif, respectively. A highly conserved region of the PDS protein was highlighted in an ash color. The blue underline represents the FAD/NAD(P)-binding domain. *T. thalictroides* (*Thalictrum thalictroides*, KAF5198369), *C. sinensis* (*Camellia sinensis*, XP028107084), *V. riparia* (*Vitis riparia*, XP034695872), *V. vinifera* (*Vitis vinifera*, AFP28796), *A. chinensis* (*Actinidia chinensis*, PSR96231), and *N. officinale* (*Nasturtium officinale*, MT547988) were involved in amino acid alignment of CmPDS. A dash (–) represents an aligned gap.

C. majus	MASPLLSNSTFSF <del>SHHSHNGSSRPITSNRS</del> LTSSLNPIKIPNFD <del>SKLKRNP</del> K--TSFSLLQLHRRKVTVGASLGERETE <del>EKNSSSV</del> ADDEIQVGED	98
P. somniferum	MASSSSPILLTSNPNLIS <del>SNHKKPYKT</del> LT <del>LKR</del> -----IQIPNFTQFNKNS--LISFQLSRRKGVIVSASLGE <del>TEKEEKKNE</del> FPAAAAATSVVGED	89
T. thalictroides	MASS--PLFLSNPIFSF <del>SHRSKYKI</del> LAFYK-----PSKIP <del>IFKTL</del> SNQIPKNP <del>FVKS</del> YQIPIIRAR--ASVN <del>ETEGKSSSV</del> VDD---ELLVGED	86
P. alba	MAAPL--VLSNRFSSIP <del>PKTRHRS</del> LSQPSSLVSTAIFMNP <del>IQKPNKND</del> LFS <del>SKNP</del> --SKEV <del>LI</del> SRKFIAC--TSVGDTEAKD-----SSLVGED	83
C. melo	MAVAS--ATPPFSPPYLS <del>SPRHR</del> PD <del>AI</del> SLRP-----FSISAPNCLQLPLSLN---SLHI <del>FRPRFAAE</del> ASIGDRESGGSTSVSDD---EGLVGED	84
A. comosus	MAFSS--LLLTSTPL <del>LSHRR</del> TLPI <del>PSTR</del> P---LKSVPNPNFATNSSNPRS--IEPLFVSARVRARG-SSIGEAE <del>EEPIVD</del> GGDDEGGALRGED	89
C. majus	SAFFDLGE <del>QRIISW</del> YFTGILGVVLFALDVIWD <del>SS</del> TGVGLGKAFVD <del>SVSGISE</del> SH <del>IVMLILIFIFA</del> AVHSGLASF <del>RDIGEKLIGER</del> AF <del>RVLFAGISLP</del>	198
P. somniferum	SAFFDLGE <del>QRIISW</del> YFTGILGVVLFALDVIWD <del>STNG</del> FGLGKAFVD <del>SVSKVSE</del> SH <del>IVMLILIFIFA</del> AVHSGLASL <del>RESGEKLIGER</del> AF <del>RVLFAGISLP</del>	189
T. thalictroides	AATFNVE <del>QRIISW</del> YFTGILGVVLFALD <del>ALWD</del> SSFGFGY <del>GKAFID</del> VSGISE <del>SHIVMLVLI</del> FIFA <del>AVHSGMASL</del> ADPSEKLIG <del>PRAF</del> RVLFAGISLP	186
P. alba	SAEPDFKE <del>QRIISW</del> YFTVILGVVLFV <del>LVWV</del> WIONSS--GYGKAFIEAVSGLSD <del>SHIVMLILI</del> LIFASVHSGMASF <del>RD</del> TA <del>EKIIGER</del> AF <del>RVLFAGISLP</del>	181
C. melo	AAVFDLSE <del>QRIISW</del> YFTVILGVVLFV <del>LVWV</del> WIONSAG-GVGKAFIDAVSGISD <del>SHIVMLLLT</del> LIFAI <del>VHSGLASL</del> RDQGEKLIG <del>ERAF</del> RVLFAGVSLP	183
A. comosus	SAAFDLGE <del>QRIISW</del> YFTVILGVVLFV <del>LVWV</del> WIDPST--GFTA <del>FV</del> GA <del>VSS</del> LSS <del>SHIVMLILI</del> IIFA <del>AVHSGMASF</del> RDAGEKLIG <del>ERAF</del> RVLFAGISLP	187
C. majus	LAVSTWYF <del>FINIRYDGMQLWQLQSV</del> GLHQLLWIANFISFFFL <del>PS</del> -----	244
P. somniferum	LAVSTWYF <del>FINIRYDGMQLWQLQTL</del> LFGLHQLVWISNFSFFFL <del>PS</del> FFNLLEVA <del>AVDKPKLHLWETGIMRI</del> TRHPQMVGQV <del>MC</del> LAHTI <del>WIGNS</del> VAVATS	289
T. thalictroides	LAVSTWYF <del>FINIRYDGMQLWQLQNV</del> FWLHLLWVSNFISFFFL <del>PS</del> FFNLLEVA <del>AVDKPKLHLWETGIMRI</del> TRHPQMVGQV <del>WLC</del> LAHAI <del>WIGNS</del> VAVAAS	286
P. alba	LAVSTWYF <del>FINIRYDGLQLWQVQNV</del> SVHQLVWLANFISFFFL <del>PS</del> FFNLLEVA <del>AVDKPKLHLWETGIMRI</del> TRHPQMAGQV <del>WIC</del> LAHTI <del>WIGNS</del> VAVAAS	281
C. melo	LAVSTWYF <del>FINIRYDGMQLWQLQSV</del> GLHQLVWLSFVSFFFL <del>PS</del> FFNLLEVA <del>AVDKPKLHLWETGIMRI</del> TRHPQVAPSP <del>WNTVN</del> -----	270
A. comosus	LAVSTWYF <del>FINIRYDGTQLWQVQSV</del> GLHQLVWSSFISFFFL <del>PS</del> FFNLLEVA <del>AVDKPKLHLWETGIMRI</del> TRHPQMVGQV <del>WIC</del> LAHTI <del>WIGNS</del> VAVAAS	287
C. majus	-----	244
P. somniferum	IGLIGHHLFGVWNGDRRLSSRYGEAF <del>DI</del> VKSRTSWPFAAIDGR <del>OKLPD</del> Y <del>YKE</del> FIRLPYLTITGLTLGAYFAHPLMQAAS <del>FR</del> LHW	376
T. thalictroides	VGLIGHHLFGVWNGDRRLALRYGEAF <del>E</del> VKSRTSWPFAAIDGR <del>OKLPD</del> Y <del>YKE</del> FIRLPYLTITALTGAYFAHPLMQAAS <del>FR</del> LHW	373
P. alba	VGLIAHHLFGVWNGDRRLARRYGED <del>FE</del> TVKARTSV <del>P</del> FAAIDGR <del>OKLPD</del> Y <del>YKE</del> FIRLPYLTITAITLGAIFAHPLMQAAS <del>FR</del> LHW	368
C. melo	-----	270
A. comosus	VGLIAHHLFGVWNGDRRLASRYGEAF <del>E</del> VKSRTSVIPFAAIDGR <del>OKLPD</del> Y <del>YKE</del> FIRLPYLTITILTGLGAYFAHPLMQSSSYGLHW	374

**Figure S3C.** Amino acid alignment of CmZ-ISO with selected corresponding genes was performed with the BioEdit program of ClustalW. Green and brown boxes represent the cytoplasmic domain and predicted trans membrane (TM) helix, respectively. *P. somniferum* (*Papaver somniferum*, XP026389168), *T. thalictroides* (*Thalictrum thalictroides*, KAF5176887), *P. alba* (*Prosopis alba*, XP028759619), *C. melo* (*Cucumis melo*, TYK16983), and *A. comosus* (*Ananas comosus*, XP020111958) were involved in amino acid alignment of CmZ-ISO. A dash (-) represents an aligned gap.



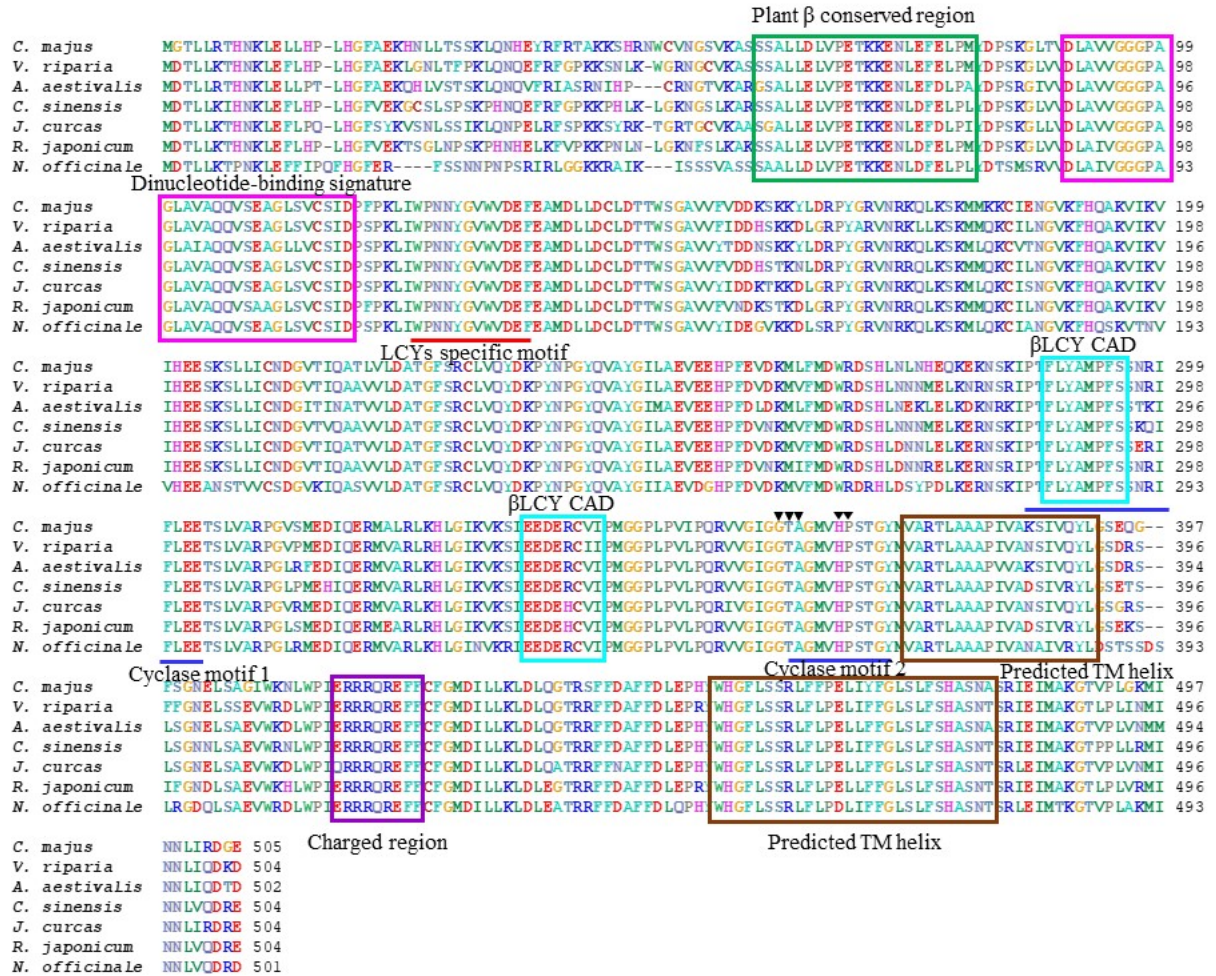
C. majus	MASFSSSTFLATSSASILVSQSSFCKEIRRGINGSSSFVYRCRGHKTPLKTRSFETKSSSSLD---TNVSDMRINAPKGLFPPEPECYRGPKLKVAI	GAG	97
P. somniferum	-MASSTSTPTATTATGSKTSANFCRDIMRNGIIGNSFVYRMRGKIQTTCRLQIN--S-LD---SNVSDMRINAPKGLFPPEPECYRGPKLKVAI	GAG	95
T. thalictroides	-MASSTSTPTSSSTSI GTTRFLRRCNLHRSIV-----LHRRRGVQMTMQSSDVL--S-LD---LNVS DMRINAPKGLFPPEPECYRGPKLKVAI	GAG	88
Q. lobata	--MASWVSPGASVTGTGSDKAGFLFWGRR-----SVAQVKSCRFWVR--S-LDSLETKVSDMRINAPKGLFPPEPECYRGPKLKVAI	GAG	83
N. nucifera	--MASSTCFSTTLTGRRNGFSSEMI GFSVRRP-----MVLDKGKIQLKTQRLVRS--S-LD---TNVSDMSINAPKGLFPPEPECYRGPKLKVAI	GAG	86
Q. suber	--MASWVSPGASVTGTRSDKAGLLFWGRR-----SVAQVKSCRFWVR--S-LDSLETKVSDMRINAPKGLFPPEPECYRGPKLKVAI	GAG	83
N. officinale	--MAASIVFAATPATGFLS-----VPLKARRLYVS--S-LD---TDVSDMSVNAKGLFPPEPVYKGPGLKLVSI	GAG	68
C. majus	LAGMSTAVE LLDQGHEVDIYDSRTLVGGKVGSEVDKHSNGHIEMGLHVFFGCYNNLFRMLMKVGADENLVKEDHTHTFINKGGQVGEVDFRFFI GAPLHG		197
P. somniferum	LAGMSTAVE LLDQGHEVDIYESRSF IGGRVGSFVDKS--GNHIEMGLHVFFGCYNNLFRMLMKVGADQNLVVDHTHTFVINKGGQIGELDFRFFV GAPLHG		194
T. thalictroides	LAGMSTAVE LLDQGHEVDIYESRPF IGGRVGSFVDKR--GNHIEMGLHVFFGCYNNLFRMLMKVGADKNLLVKDHTHTFINKGGQVGEVDFRFFI GAPLHG		187
Q. lobata	LAGMSTAVE LLDQGHEVDIYESRPF IGGRVGSFVDKR--GNHIEMGLHVFFGCYNNLFRMLMKVGADKNLLVKDHTHTFVINKGGQIGELDFRFFI GAPLHG		182
N. nucifera	LAGMSTAVE LLDQGHEVDIYESRSF IGGRVGSFVDKH--GNHIEMGLHVFFGCYNNLFRMLMKVGADKNLLVKDHTHTFVINKGGQIGELDFRFFV GAPLHG		185
Q. suber	LAGMSTAVE LLDQGHEVDIYESRPF IGGRVGSFVDKR--GNHIEMGLHVFFGCYNNLFRMLMKVGADKNLLVKDHTHTFVINKGGQIGELDFRFFI GAPLHG		182
N. officinale	LAGMSTAVE LLDQGHEVDIYDSRTF IGGRVGSFVDKR--GNHIEMGLHVFFGCYNNLFRMLMKVGADKNLLVKDHTHTFINKGGQIGELDFRFFV GAPLHG		167
C. majus	VNAFLNTQK LKAYDKARNALALSRSPVIRALVDPDGAMRDIRNLDSISFSDWFLSKGGTRMSICRMWDPVAYALGFDICDNMSARCMLTIFSLFATKTEA		297
P. somniferum	INAFPLTQQLKPYDKARNALALSRSPVIRALVDPDGALQDIRNLDSISFSTWFMSSKGGTRMSICRMWDPVAYALGFDICDNMSARCMLTIFALFATKTEA		294
T. thalictroides	INAFPLTQQLKTYDKARNAVALALSRPVRALVDPDGAMRDIRNLDSISFSDWFMSSKGGTRTSICRMWDPVAYALGFDICDNMSARCMLTIFSLFATKTEA		287
Q. lobata	IRAFPLTQQLKTYDKARNAVALALSRPVRALVDPDGAMRDIRNLDSISFSDWFLSKGGTRTSICRMWDPVAYALGFDICDNMSARCMLTIFSLFATKTEA		282
N. nucifera	IRAFPLATQQLKTYDKARNAVALALSRPVRALVDPDGAMDIRNLDSISFSDWFLSKGGTRMSICRMWDPVAYALGFDICDNMSARCMLTIFSLFATKTEA		285
Q. suber	IRAFPLTQQLKTYDKARNAVALALSRPVRALVDPDGAMRDIRNLDSISFSDWFLSKGGTRTSICRMWDPVAYALGFDICDNMSARCMLTIFSLFATKTEA		282
N. officinale	IRAFPLVTQQLKPYDKLRNSLALSRPVRALVDPDGAMRDIRNLDSISFSDWFMSSKGGTRASICRMWDPVAYALGFDICDNMSARCMLTIFSLFATKTEA		267
C. majus	SLLHMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREILYDKSADGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPDQWRELEFFDNIYKLVG		397
P. somniferum	SLLRMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREVLIDKTINGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPSEWRESEFFDNIYKLVG		394
T. thalictroides	SLLRMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREILYDVSTNGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPSQWRDLEFFDNIYELVG		387
Q. lobata	SLLRMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREILYDKSADGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPDQWRELEFFDNIYELVG		382
N. nucifera	SLLRMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREILYDKSADGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPDQWRELEFFDNIYKLVG		385
Q. suber	SLLRMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREILYDKSADGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPDQWRELEFFDNIYELVG		382
N. officinale	SLLRMLKGS PDVYLSGPPIKYYITDKGGRFHLRWGCREILYDKSADGDTYVGLAMSKATNKKTIVKADAVIAACDVP GIKRLIPDQWRELEFFDNIYELVG		318
C. majus	VPVVTQLRYNGWVTE LQD LERSRQLRQAAGLDNLLYS PDADFSCFADLALTSPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		497
P. somniferum	VPVVTQLRYNGWVTE LND LGKSRLKEAVGLDNLLYS PDADFSCFADLALTSPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		494
T. thalictroides	VPVVTQLRYNGWVTE LQD LGVSRQLRQAAGMDNLLYS PDADFSCFADLALTSPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		487
Q. lobata	VPVVTQLRYNGWVTE LQD LERSRQLRQAAGLDNLLYS PDADFSCFADLALTSPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		482
N. nucifera	VPVVTQLRYNGWVTE LQD LERSRQLRQAAGLDNLLYS PDADFSCFADLALASPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		485
Q. suber	VPVVTQLRYNGWVTE LQD LERSRQLRQAAGLDNLLYS PDADFSCFADLALTSPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		482
N. officinale	VPVVTQLRYNGWVTE LQD LERSRQLRQAAGLDNLLYS PDADFSCFADLALTSPEDEYYIEGGGSLQCCLVLTGDPYMPPLNDKIIERVAQVIALFPSSQ		318
C. majus	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICDAGEELVALRKKLAAIESQENTKAANVTDELST		597
P. somniferum	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICNGGEDLLALRKKLAAIESQENTKAANVTDELST		590
T. thalictroides	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICDAGEELVALRKKLAAIESQENTKAANVTDELST		587
Q. lobata	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICDAGEELVALRKKLAAIESQENTKAANVTDELST		582
N. nucifera	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICDAGEELVALRKKLAAIESQENTKAANVTDELST		585
Q. suber	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICDAGEELVALRKKLAAIESQENTKAANVTDELST		582
N. officinale	GLEVTWSSVVKIGQSLYREAPGNDPFRPDQKTFVKNFFIAGSYTKQDYIDSMEGATLSGRQAAAYICDAGEELVALRKKLAAIESQENTKAANVTDELST		318
C. majus	V 598		
P. somniferum	V 591		
T. thalictroides	V 588		
Q. lobata	V 583		
N. nucifera	V 586		
Q. suber	V 583		
N. officinale	- 318		

**Figure S3D.** Amino acid alignment of CmZDS with selected corresponding genes was performed with the BioEdit program of ClustalW. The red, pink, and orange boxes represent the signal peptide, dinucleotide-binding motif, and carotenoid binding motif, respectively. *P. somniferum* (*Papaver somniferum*, XP026435023), *T. thalictroides* (*Thalictrum thalictroides*, KAF5193496), *Q. lobata*, XP030958095 (*Quercus lobata*), *N. nucifera* (*Nelumbo nucifera*, XP010256022), *Q. suber* (*Quercus suber*, XP23871372), and *N. officinale* (*Nasturtium officinale*, MT547991) were involved in amino acid alignment of CmZDS. A dash (-) represents an aligned gap.



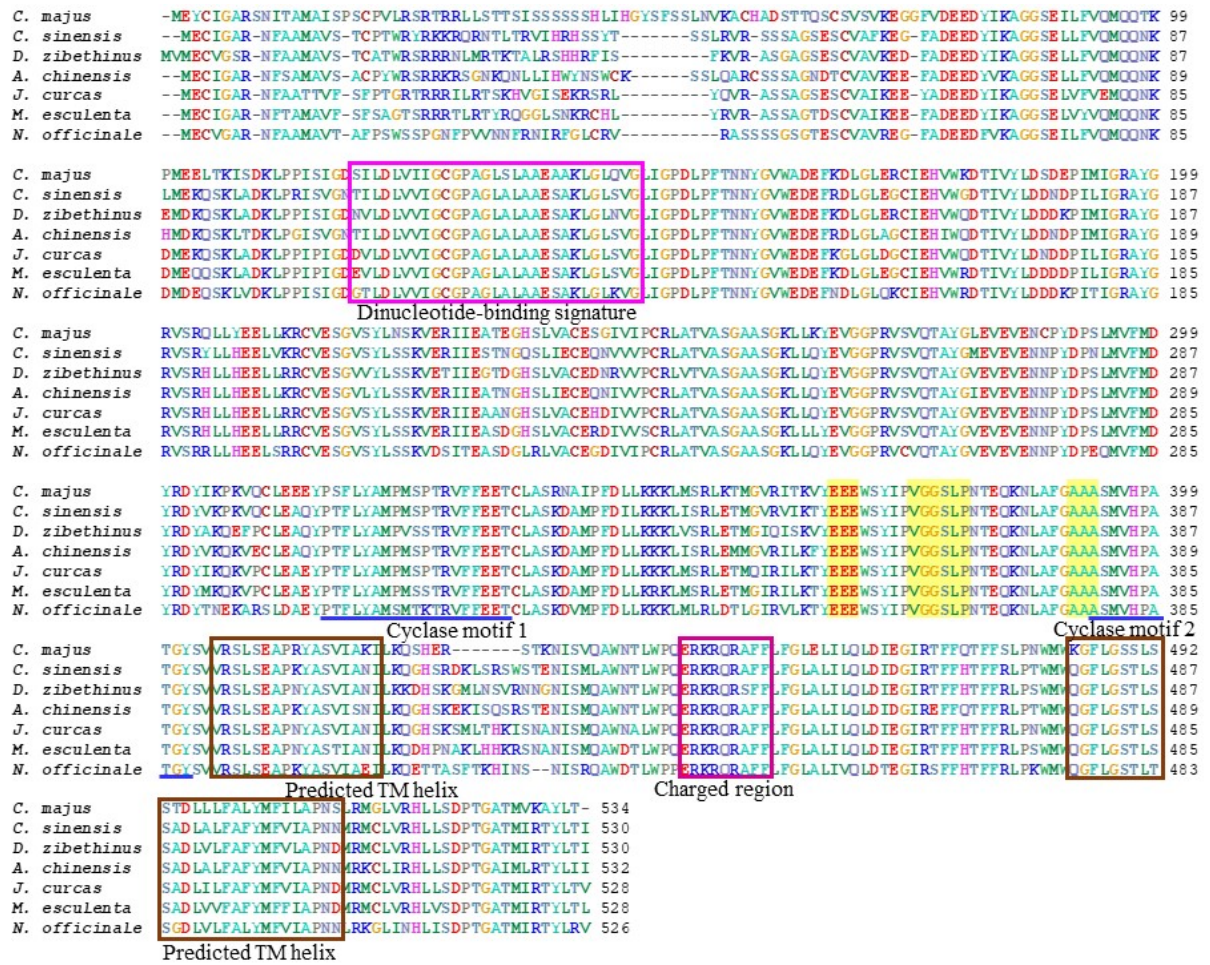
C. majus	-----MAELGRSP--SLTYSLPSLSHPFKTLP-----	26
M. cordata	-----MAELGRSP--SLIHSLSPSFSHPKTLA-----	26
P. somniferum	-----MAISQSTPPMALIHSLSVPH-HKTLA-----	27
T. thalictroides	-----MALPIFSQS-TFTTTQNFPSLHKNP-----	27
A. chinensis	MFLSHPN-----FMRQ-----LGASPLSP-----	47
Q. lobata	MPVSHLTLSMPLPGHNSQFFIHQNTTRLGTITPTNQNHKQFFPTTQNCVGLSGHKLC-----	100
N. officinale	-----LNSQFFDECYAKKSNRIRPSQKHLLSLRHAKTLWANDYQPN-----	1
C. majus	-----FNTLNLCCFWKP-----IEGFELRKSCKLGLL--NKRRIGSL--TKSVLSVEKEVSRSGSE--SGERDNFDAIVIGSGIGG	97
M. cordata	-----FSSFNRCCKPID-----FBGFELRKSCKLGLILKENNRKRVRSFVKSKSVLSVEKEVGTGG--SGERDYDAIVIGSGIGG	102
P. somniferum	-----FSSLTPTMFKSVSL-----TRFBGFELORRKKLGLKE--RQRRTGGG--TTKSVLSVEKNVSSSDSG--NEKRSTYDAIVIGSGIGG	104
T. thalictroides	-----FSVFSNN-----FQSFQTR-NCKLGNLK--KRWNENYTLRLNSALSLEKEVGSSGNGGIDNREKSYDAIVIGSGIGG	96
A. chinensis	-----CFDPINSHEPS-----GETKLGFSQR--KGSDFIVGSKSVLSVGEVLESDGGER-HNRNVCYDAIVIGSGIGG	112
Q. lobata	SMELCFHSITQLGFSRPRNLESKFLSGGPLRTSNKSYKLGSRIGFSEGN--MRNGKFIVRPKSVLSVEKAVEREG--IGREASYDAIVIGSGIGG	193
N. officinale	-----	1
C. majus	LVAQTQLAVKGARVLVLEKIVIPGGSSGFYQKDGITFDVGSVMFGGSDKGNLNLITRALAAVGCCKLDMLPDSTVHYHLPDNLVSRVHREYSDFVME LI	197
M. cordata	LVAATQLAVKGARVLVLEKIVIPGGSSGFYQKDGITFDVGSVMFGGSDKGNLNLITRALAAVGCCKLDMLPDSTVHYHLPDNLVSRVHREYSDFITE LT	202
P. somniferum	LVAQTQLAVKGANVLVLEKIVIPGGSSGFYQKDGITFDVGSVMFGGSDKGNLNLITRALAAVGCCKLDMLPDSTVHYHLPDNLVSRVHREYSDFITE LT	204
T. thalictroides	LVAQTQLAVKGARVLVLEKIVIPGGSSGFYQKDGITFDVGSVMFGGSDKGNLNLITRALAAVGCCKLDMLPDSTVHYHLPDNLVSRVHREYSDFITE LT	196
A. chinensis	LVAATQLAVKGARVLVLEKIVIPGGSSGFYQKDGITFDVGSVMFGGSDKGNLNLITRALAAVGCCKLDMLPDSTVHYHLPDNLVSRVHREYSEFITE LI	212
Q. lobata	LVAATQLAVKGARVLVLEKIVIPGGSSGFYQKDGITFDVGSVMFGGSDKGNLNLITRALAAVGCCKLDMLPDSTVHYHLPDNLVSRVHREYSEFVAE LT	293
N. officinale	-----MFGFSDKGNLNLITQALKAVERKMEVDPPTTVHFHLPNNLSVQIHREYDDFITE LT	57
C. majus	NRFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALRTPMINASMV	297
M. cordata	NRFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALRTPMINASLV	302
P. somniferum	NKFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALQTPMINASMV	304
T. thalictroides	NKFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALRTPMINASMV	296
A. chinensis	NKFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALQTPMINASMV	312
Q. lobata	NKFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALQTPMINASMV	393
N. officinale	NKFPHKEKGIHKFYGECKWIFNALNSLEKSLLEP LYLFGQFFQKPLECLTLAYLNPQNAIARKFIQDQLLSFIDAECEFIIVSTVNALQTPMINASMV	143
C. majus	MCERHFGGINYPVGGVGRIAKSLAKGLLDKGSNIYKANVT SIILEDKAVGVKLSGDREFFSKTIIISNATRWDTFKLLKQKELPKKEENFQKLYVKSP	397
M. cordata	VCEERHFGGINYPVGGVGRIAKSLAKGLLDKGSNIYKANVT SIILEDKAVGVKLSGDREFFSKTIIISNATRWDTFKLLKQKELPKKEENFQKLYVKAP	402
P. somniferum	LCDRHFHFGGINYPVGGVGRIAKSLAKGLLDKGSNIYKANVT SIILEDKAVGVKLSGDREFFSKTIIISNATRWDTFKLLKQKELPKKEENFQKLYVKAP	404
T. thalictroides	LCDRHFHFGGINYPVGGVGRIAKSLAKGLLDKGSNIYKANVT SIILEDKAVGVKLSGDREFFSKTIIISNATRWDTFKLLKQKELPKKEENFQKLYVKAP	396
A. chinensis	LCDRHFHFGGINYPVGGVGRIAKSLAKGLLDKGSNIYKANVT SIILEDKAVGVKLSGDREFFSKTIIISNATRWDTFKLLKQKELPKKEENFQKLYVKAP	412
Q. lobata	LCDRHFHFGGINYPVGGVGRIAKSLAKGLLDKGSNIYKANVT SIILEDKAVGVKLSGDREFFSKTIIISNATRWDTFKLLKQKELPKKEENFQKLYVKAP	493
N. officinale	LNLRKF---LYPIL---	154
C. majus	SFLSIHMAVEAKVLPPDTHCHHFILENDWTKLEPYGSIFLSIPTVLDSSLAPEGRHILHIFTTSSIEDWGGLPKQDYDAKKEHVADEIISRLKELKLPFG	497
M. cordata	SFLSIHMAVEAKVLPPDTHCHHFILENDWTKLEPYGSIFLSIPTVLDSSLAPEGRHILHIFTTSSIEDWGGLPKQDYDAKKEHVADEIISRLKELKLPFG	502
P. somniferum	SFLSIHMAVEAKVLPPDTHCHHFILENDWTKLEPYGSIFLSIPTVLDSSLAPEGRHILHIFTTSSIEDWGGLPKQDYDAKKEHVADEIISRLKELKLPFG	504
T. thalictroides	SFLSIHMAVEAKVLPPDTHCHHFILENDWTKLEPYGSIFLSIPTVLDSSLAPEGRHILHIFTTSSIEDWGGLPKQDYDAKKEHVADEIISRLKELKLPFG	496
A. chinensis	SFLSIHMAVEAKVLPPDTHCHHFILENDWTKLEPYGSIFLSIPTVLDSSLAPEGRHILHIFTTSSIEDWGGLPKQDYDAKKEHVADEIISRLKELKLPFG	512
Q. lobata	SFLSIHMAVEAKVLPPDTHCHHFILENDWTKLEPYGSIFLSIPTVLDSSLAPEGRHILHIFTTSSIEDWGGLPKQDYDAKKEHVADEIISRLKELKLPFG	593
N. officinale	-----	154
C. majus	LKSSIVFKEVGTPTKTHRRFLARDSGTYGPMRGTTPKGLLGMPFNNTAIDGLYCVGDSCFPGQGVIAVAFSGIMCAHRAADI GLEERSPILDGALLRLLG	597
M. cordata	LKSSIVFKEVGTPTKTHRRFLARDSGTYGPMRGTTPKGLLGMPFNNTAIDGLYCVGDSCFPGQGVIAVAFSGIMCAHRAADI GLEERSPILDGALLRLLG	602
P. somniferum	LKSAIVFKEVGTPTKTHRRFLARDSGTYGPMRGTTPKGLLGMPFNNTAIDGLYCVGDSCFPGQGVIAVAFSGIMCAHRAADMGLEKNSPILDAALLRLLG	604
T. thalictroides	LKSSIVFKEVGTPTKTHRRFLARDSGTYGPMRGTTPKGLLGMPFNNTAIDGLYCVGDSCFPGQGVIAVAFSGIMCAHRAADI GLEERSPILDSALLRLTG	596
A. chinensis	LKSSIVFKEVGTPTKTHRRFLARDSGTYGPMRGTTPKGLLGMPFNNTAIDGLYCVGDSCFPGQGVIAVAFSGIMCAHRAADI GLEERSPILDAALLRLLG	612
Q. lobata	LRSSIVFMEVGTPTKTHRRFLARDSGTYGPMRGTTPKGLLGMPFNNTAIDGLYCVGDSCFPGQGVIAVAFSGIMCAHRAADI GLEERSPILDAALLRLLG	693
N. officinale	-----	154
C. majus	WLRITIA 603	
M. cordata	WLRITIA 608	
P. somniferum	WFRSMA 610	
T. thalictroides	WLRITIA 602	
A. chinensis	WLRITIA 618	
Q. lobata	WLRITIA 699	
N. officinale	----- 154	

**Figure S3E.** Amino acid alignment of NoCrtISO with selected corresponding genes was performed with the BioEdit program of ClustalW. The red box represents the signal peptide. *M. cordata* (*Macleaya cordata*, OVA16223), *P. somniferum* (*Papaver somniferum*, XP026426554), *T. thalictroides* (*Thalictrum thalictroides*, KAF5180293), *A. chinensis* (*Actinidia chinensis*, PSS15835), *Q. lobata* (*Quercus lobata*, XP030927457), and *N. officinale* (*Nasturtium officinale*, MT547983) were involved in amino acid alignment of CmCrtISO. A dash (–) represents an aligned gap.



**Figure S3F.** Amino acid alignment of CmLCYB with selected corresponding genes was performed with the BioEdit program of ClustalW. The green, pink, light blue, brown, and purple boxes represent plant  $\beta$  conserved region, dinucleotide-binding motif,  $\beta$ LCY catalytic domain (CAD), predicted trans membrane (TM) helix, and charged region, respectively. The red underlined indicates LCY specific motif, whereas the blue underlined indicates cyclase motif 1 and 2. The highlighted arrowheads indicate the regulatory motif conserved in all  $\beta$ -bicyclase. *V. riparia* (*Vitis riparia*, XP034694605), *A. aestivalis* (*Adonis aestivalis*, AAK07430), *C. sinensis* (*Camellia sinensis*, AJB84622), *J. curcas* (*Jatropha curcas*, XP012085981), *R. japonicum* (*Rhododendron japonicum*, BAS69435), and *N. officinale* (*Nasturtium officinale*, MT547985) were involved in amino acid alignment of CmLCYB. A dash (–) represents an aligned gap.





**Figure S3G.** Amino acid alignment of CmLCYE with selected corresponding genes was performed with the BioEdit program of ClustalW. Pink, brown, and purple boxes represent the dinucleotide-binding motif, predicted trans membrane (TM) helix, and charged region, respectively, and those with a blue underline represent cyclase motif 1 and 2. Yellow highlighted box indicate the conserved motif. *C. sinensis* (*Camellia sinensis*, XP028074216), *D. zibethinus* (*Durio zibethinus*, XP022751743), *A. chinensis* (*Actinidia chinensis*, PSS20792), *J. curcas* (*Jatropha curcas*, XP012076949), *M. esculenta* (*Manihot esculenta*, XP021596942), and *N. officinale* (*Nasturtium officinale*, MT547986) were involved in amino acid alignment of CmLCYE. A dash (–) represents an aligned gap.



*C. majus* ---MAAGFSVAISARTFRFGQNPFIGSKPNSLINPSSFLSPSIRRNPKFTTAKKS-TFTVYFVLEEKQGISRFIEEEDKAEADVSSSSSEELNRVSV 95  
*A. aestivalis* MLASMAAATSTSSSRAFRFRGLFNTKPNIRNPPCLLFSPLLMR-----NRNGAG-ALTICFVAERTCRGRIPIQIEDEK---NMDEVFEQMNSSASV 90  
*V. vinifera* ---MATGISASLNSMSCRLGRNFTATGPSSVISLSFSLTPVTHLKGNIFFLQRRR-SLRVCLVLEKEIEDG---IEIEDD-----SPSSN----- 80  
*T. wilfordii* ---MAASLSTATASERLRLPLTLASKPN--FTP--FFSPSIRFRNKIFNKISKRPSLAICFVVEDKKQGVQIEAQNEKEEN---SEHSIPQILTP 88  
*A. chinensis* ---MAAGISVAASSRSFRLGRGPFGLGOKPNSMISPTYLFSLPIRRHDSMIOGRRK-TTTCFVVEDEKL-SAQFEPERGEAE-----IEKQISVA 86  
*I. nil* ---MAVGISIAASSRTVISQCFSLVRPATHSASPPSLLFSPLSRRFRSSVLSRRKPSLTVCFVLEDEKLESGGVIRAEETIER---A---IEKQISAS 90  
*N. officinale* ---MAAGLSTAVT---FNPLHRSFSSSFRLLHFKSVAGFPFSLRFG-----FVCVVEERKQSSPIDNDEPFESTR---STAIDPELLAL 78

*C. majus* RVAEKLARKKSERITYLVAAIMSTLGITSMVAAYVYRFSWQM--EGGEVPVSEMPGTFALAVGAAGVMEFWARWAKALWHASLWHEESHQPREGGPF 193  
*A. aestivalis* RVAEKLARKKSERITYLIAALMSMGITSMALVAVYRFSWQM--EGGDIPTVEMLGTFALSVGAAGVMEFWARWAKALWHASLWHEESHQPREGGPF 188  
*V. vinifera* RASERLARKKSERITYLVAAMMSLGITSMALVAVYRFSWQM--EGGEIPTVEMLGTFALSVGAAGVMEFWARWAKALWHASLWHEESHQPREGGPF 178  
*T. wilfordii* RVAERLARKKSERITYLVAAMMSLGITSMAMVAVYRFAWQM--EGGEVPLSEMPGTFALSVGAAGVMEFWARWAKALWHASLWHEESHQPREGGPF 186  
*A. chinensis* RVAEKMSRKSERITYLVAAMMSLGITSMAMVAVYRFSWQM--GGGEVPTSEMPGTFALSVGAAGVMEFWARWAKALWHASLWHEESHQPREGGPF 184  
*I. nil* RLAEKLARKKSERITYLVAAMMSLGITSMALVAVYRFAWQM--EGGEVPTSEMPGTFALSVGAAGVMEFWARWAKALWHASLWHEESHQPREGGPF 188  
*N. officinale* RLAEKLERKKSERITYLVAAMMSLGITSMAMVAVYRFSWQMDMEGGEISMEMPGTFALSVGAAGVMEFWARWAKALWHASLWHEESHQPREGGAF 178

*C. majus* ELVDFAIINAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IANVPYFRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 293  
*A. aestivalis* ELVDFAIINAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IANVPYFRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 288  
*V. vinifera* ELVDFAIINAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IANVPYLRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 278  
*T. wilfordii* ELVDFAIINAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IANVPYFRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 286  
*A. chinensis* ELVDFAITNAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IAKVPYLRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 284  
*I. nil* ELVDFAITNAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IADVPYFRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 288  
*N. officinale* ELVDFAITNAVPAIALLSYGTFEKLIPGLCFGAGLGITVFGMAYMFVHDGLVHRRFPVGP IADVPYFRKVAARHQLHSDKFNQVPIYGLFLGPKLEEE 278

*C. majus* VGGNEELEKEISRRIKSNDNR----- 315  
*A. aestivalis* VGGNEELEKEISRRIKRMNAL----- 309  
*V. vinifera* VGGNEELEKEISRRIKSDSS----- 299  
*T. wilfordii* VGGNEELEKEISRRIKSYKS----- 306  
*A. chinensis* VGGNEELEKEISRRIKSNGS----- 305  
*I. nil* VGGNDELEEVNRRIKSSTGR----- 310  
*N. officinale* VGGNEELEKEISRRIKSYRKSNGSSS 306

HX<sub>4</sub>H      HX<sub>2</sub>HH

**Figure S3H.** Amino acid alignment of CmCHXB with selected corresponding genes was performed with the BioEdit program of ClustalW. The brown boxes indicate the transmembrane region. The histidine domain of the CHXB protein was highlighted in pink color. Blue and red underlined indicate the fatty acid hydroxylase domain and highly conserved region (motif 1). *A. aestivalis* (Adonis aestivalis, ABL67481), *V. vinifera* (*Vitis vinifera*, AAM77007), *T. wilfordii* (*Tripterygium wilfordii*, KAF5731165), *A. chinensis* (*Actinidia chinensis*, PSS04390), *I. nil* (*Ipomoea nil*, BAI47580), and *N. officinale* (*Nasturtium officinale*, MT547981) were involved in amino acid alignment of CmCHXB. A dash (–) represents an aligned gap.

*C. majus* MTS SSSCTS LTLSSLSLSPNHQILQNKPIFFPR-NPSQ-ILSIKSSIKKESSYSSS-----NGSWVSPDWLTS LTKSLTISTSQDDSGIPIASAK 91  
*P. somniferum* MTS SAS--LLSLSSLCSLAPQOQTILKPIFTSSRKNPQ-ILSIKSSKGEET--NNK-----NGSWVSPDWLTS LTKSLSN-TSNDSDSGIPIASAK 87  
*Q. suber* -----MPSSLSLSTFSLLP LLLKPTTRSTLS SSRPTSHT--LTIKSTDKNSTSNSKPTNTNKA GSWVSPDWLTS LTRS LTI-SKDDSDSGIPIASAK 92  
*C. arietinum* -----MCHCSLS-PSHLS LSFLS--TTPFTLPKPYPIHR--YSIKSSINKNQSTTTK-----QSWVSPDWLTS LSKSLTT-RKDDSDSGIPIASAK 81  
*S. pennellii* -----MPSVTISSESLTTPHHR---TTVLRPNPQNRSQTIKSIDKKKPPSTK-----PTSWVSPDWLTKLTRS LTL-QNDDSDSGIPIASAK 83  
*Z. jujuba* -----MSCSCSYS-LSHLS SPFLKPI TSAFTFSSPLRS PFRSLSVKSIDKNSTNSKLSTK--PSWVSPDWLTS LARS LTI-SKDDSDSGIPIASAK 90  
*N. officinale* -----RLESPKPK-----FTFSIKS-----SIEKPKPKLETNSK-----SQSWVSPDWLTS LTRTIS-SKNDSDSGIPIASAK 63

Signal peptide

*C. majus* LDDVSDLLGGALFLPLFKWMNEYGP IYRLAAGPRNFVWSDPAIAKHVLRNYG-KYKGLVAEVSEFLFGSGFAIAEGPLWTARRRAVVP SLHKYLSIM 190  
*P. somniferum* LDDVSDLLGGALFLPLFKWMKEYGP IYRLAAGPRNFVWSDPAIAKHVLRNYGTYKSKGLVIEVSEFLFGSGVAIAEGSLWTARRRAVVP SLHKAYLSII 187  
*Q. suber* LDDVSDLLGGALFLPLFKWMNDYGP IYRLAAGPRNFVWSDPAIAKHVLRNYG-KYKGLVAEVSEFLFGSGFAIAEGPLWTARRRAVVP SLHKYLSVI 191  
*C. arietinum* LDDVSDLLGGALFLPLFKWMNEYGP IYRLAAGPRNFVWSDPAIAKHVLRNYG-KYKGLVAEVSEFLFGSGFAIAEGPLWTARRRAVVP SLHKYLSIM 180  
*S. pennellii* LDDVSELGGALFLPLYRWMLYGP IYRLAAGPRNFVWSDPAIAKHVLRNYG-KYKGLVAEVSEFLFGSGFAIAEGPLWTARRRAVVP SLHKYLSVI 182  
*Z. jujuba* LDDVSDLLGGALFLPLFKWMNDYGP IYRLAAGPRNFVWSDPAIAKHVLRNYG-KYKGLVAEVSEFLFGSGFAIAEGSLWTARRRAVVP SLHKYLSVI 189  
*N. officinale* LDDVSDLLGGALFLPLFKWMNEYGP IYRLAAGPRNFVWSDPAIAKHVLRNYG-KYKGLVAEVSEFLFGSGFAIAEGPLWTARRRAVVP SLHKYLSVI 162

*C. majus* VDRVFSKCAQRLVEQLKTDADNGSPVNMEAKFSQTLTDVIGLSVFNYNFDALTADSPVIDAVITALKAEARSTDLLPWKIDALCKIIPRQIKAQNAV 290  
*P. somniferum* VDRVFSKCAERLVEKIKTDADNGTPVNMEAKFSQTLTDVIGLAVFNYNFDSLTADSPVIEAVITALKAEARSTDLLPWKIDLLRRVIFRQIKAEKAVT 287  
*Q. suber* VDRVFSKCAERLVEKIKPDALSGTPVNMEKFCQTLTDVIGLSIFNYNFDSLTDSVIDAVITALKAEARSTDLLPWKIKALCKIIPRQIKAEKAVN 291  
*C. arietinum* VDRVFSKCAERLVEKIQPDALNGTAVNMEKFSQTLTDVIGLSVFNYNFDALNDSPVIEAVITALKAEARSTDLLPWKYNFLCKIIPRQIKAEKAVT 280  
*S. pennellii* VDRVFSKCAERMVEKILLDAISGSAVNMEAKFSQTLTDVIGLALFNYNFDSLTDSVIDAVITALKAEARSTDLLPWQIKALCKIIPRQIKAEKAVS 282  
*Z. jujuba* VDRVFSKCAERMVEKIQPKALDGTAVNMEATFSQTLTDVIGLSVFNYNFDSLNADSPVIDAVITALKAEARSTDLLPWKVKALCKIIPRQIKAEKAVT 289  
*N. officinale* VDRVFSKCAERLVEKIQPYALDGRAVNMEKFSQTLTDVIGLSVFNYNFDSLTDSVIDAVI----- 225

*C. majus* VIR----- 293  
*P. somniferum* VIRQTVIELIAKCKIVEAEGEQIDGEEYVNDADPSIIRFLLASREEVSSVQLRDDLLSMIVAGHETTGSVLTWTLYLLSKDPPSLMRAQEEVDVRLQGR 387  
*Q. suber* EIRRTVEELIAKCKOMVEAEGERINEEYVNDADPSIIRFLLASREEVSSVQLRDDLLSMIVAGHETTGSVLTWTLYLLSKDSSSLVKAQEEVDVRLQGR 391  
*C. arietinum* VIRKTVEDLIVCKEIVESEGERIDAEYVNDADPSIIRFLLASREEVSSVQLRDDLLSMIVAGHETTGSVLTWTLYLLSKDSSSLAKAQEEVDVRLQGR 380  
*S. pennellii* LIRQTVIELIAKCKREIVETEGERINEEYVNDADPSIIRFLLASREEVSSVQLRDDLLSMIVAGHETTGSVLTWTLYLLSKDPPSSLEKAQEEVDVRLQGR 382  
*Z. jujuba* VIRQTVIELIAKCKEIVEAEGERIDEEYVNDADPSIIRFLLASREEVSSVQLRDDLLSMIVAGHETTGSVLTWTLYLLSKDSSSKMAQEEVDVRLQGR 389  
*N. officinale* ----- 225

*C. majus* ----- 293  
*P. somniferum* SPKYADIKELKYVTRCINE SLRLYPHPFVLLRRALVLPDVLPGNYKVNAQQDQIMISVNIHRSSEVMDRAEEFPERFLEGGVPVNETNTDFRIFPSSGGP 487  
*Q. suber* PPAYEDIKNLKFLTCCIME SLRLYPHPFVLIIRRAQVAEMLPDGYKVNAQQDQIMISVNIHSSKVMERAEYVPERFLEGGVPVNETNTDFRIFPSSGGP 491  
*C. arietinum* RPTYEDIKNLKFLTRCITE SLRLYPHPFVLIIRRAQVADLPDGYKVNAQQDQIMISVNIHRSSEVMDRAEEFPERFLEGGVPVNETNTDFRIFPSSGGP 480  
*S. pennellii* SPTYEDMKNLKFLTRCITE SLRLYPHPFVLIIRRAQVADLPDGYKVNAQQDQIMISVNIHSSSEVMDRAEEFPERFLEGGVPVNETNTDFRIFPSSGGP 482  
*Z. jujuba* PPSYEDVDKFLTRCITE SLRLYPHPFVLIIRRAQADLPDGYKINAGQDQIMISVNIHSSKVMERAEYVPERFLEGGIPNETNTDFRIFPSSGGP 489  
*N. officinale* ----- 225

*C. majus* ----- 293  
*P. somniferum* RKCLGDQFAMMEATVALAIFLQRMNFE LVPDQNI SMTTGATIHHTNGLYMTLSQRQVQPTFASAASR 554  
*Q. suber* RKCVGDQFALMEATVALAVFLQHMNFE LVPNQNI SMTTGATIHHTNGLYMTLSQRQPKSAFVSSRL 558  
*C. arietinum* RKCVGDQFALLEATVALAVFLQNMNFE LVPNQNI SMTTGATIHHTNGLYMKLNRLK----- 537  
*S. pennellii* RKCVGDQFALLEATVALAIFVQNFSEFLIPDQTI SMTTGATIHHTNGLYMKVKQREKVS/LAAAP-- 547  
*Z. jujuba* RKCVGDQFALLEATVALAIFLQHFNFE LVPDQNI SMTTGATIHHTNGLYMKLSSRQTKSLSA----- 551  
*N. officinale* ----- 225

**Figure S3I.** Amino acid alignment of CmCHXE with selected corresponding genes was performed with the BioEdit program of ClustalW. The red boxes represent the signal peptide. The blue, yellow, and pink color highlighted denotes signal peptide C, N, and H regions of the CHXE protein, respectively. *P. somniferum* (*Papaver somniferum*, XP026417943), *Q. suber* (*Quercus suber*, XP023872296), *C. arietinum* (*Cicer arietinum*, XP004516959), *S. pennellii* (*Solanum pennellii*, XP015056054), *Z. jujuba* (*Ziziphus jujuba*, XP015898578), and *N. officinale* (*Nasturtium officinale*, MT547982) were involved in amino acid alignment of CmCHXE. A dash (–) represents an aligned gap.



*C. majus* -MALTAIYSSL--NPSSTIFSKTHLPIPTAKD~~FS~~EEILPSLHYNIL-FRSKPF~~Q~~DKRRKPKV~~KI~~SAWAP--EAVTSTQNGINGGGGL-SKKLRI~~LI~~AGGGI 93  
*P. somniferum* -MSSVTIYSTN--NPSVTIFSRTHLPKQTSRAFS~~EE~~ISPC~~LH~~NYL-FRSKPIETKKRKPLTPVAWAA~~PN~~KEAVNS~~DS~~GIDQS--KKKLRI~~LI~~AGGGI 93  
*A. chinensis* -MVS~~SV~~LHNSI--YPS~~TN~~LF~~SR~~THFPPIPSKH~~FP~~VEFLYSVNYIS-FR~~PK~~PIGQTRKTPKVRATIT~~ES~~PPPLTGGAEINGKLPP~~Q~~KKLRL~~LV~~AGGGI 96  
*V. vinifera* -MASAVFYSSV--QPS--IFSRTHIPIPIS~~KD~~SE~~EE~~FGHSIN~~YK~~Y-FRSNPGQKKRVAQVKATL~~AE~~ATPAP~~P~~APS~~LPS~~-----KKVRI~~LV~~AGGGI 86  
*C. sinensis* -MTSTVFIY~~TS~~L--NPS~~TT~~LF~~SR~~THFPPIPS~~RD~~FSLE~~LL~~HVPNSNYG-FRT~~KE~~NGRMKRM~~TK~~PKVSVSEAPPE-RSSAA~~EV~~DGNS-----KKLRL~~LV~~AGGGI 91  
*J. curcas* MASSTLFCNLI--NPSISVFSRTHLPFPVSS~~SM~~ELSS~~SA~~HCN~~FI~~H-FRSKKS~~Q~~KKKLTQVKAV~~TE~~STSV~~AS~~QSD~~EQ~~QPEQ-----RKPRI~~LV~~AGGGI 91  
*N. officinale* -MGSTPFCYSINQSPSKLD~~FT~~RT~~HF~~VFN~~PA~~YILD~~SS~~FTGKSGVGLSGFR~~RR~~--TLVG~~KA~~ATALV~~EE~~KKREAV~~TE~~K-----KKSRI~~LV~~AGGGI 87

*C. majus* GGLVFALAAKKRGFDVLVFERDVS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDMEVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GAWIYK~~FD~~TTPAVERGLPVT~~RV~~I 193  
*P. somniferum* GGLVLALAA~~LR~~KGFSVLVFERDVS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDMEVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GSWYIK~~FD~~TTPAVQRGLPVT~~RV~~I 193  
*A. chinensis* GGLVFALAAKKRGFEVLVFERDLS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDMEVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GSNWYIK~~FD~~TTPAERGLPVT~~RV~~I 196  
*V. vinifera* GGLVLALAAKKRGFDVVFEDKMS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDMEVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GSNWYIK~~FD~~TTPAERGLPVT~~RV~~I 186  
*C. sinensis* GGLVFALAAKKRGFDVVFEDKLS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDLEVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GSNWYIK~~FD~~TTPAERGLPVT~~RV~~I 191  
*J. curcas* GGLVFALAAKKRGFEVLVFERDLS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDLEVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GSNWYIK~~FD~~TTPAERGLPVT~~RV~~I 191  
*N. officinale* GGLVFALAAKKRGFDVLVFERDLS~~AI~~RGGQYRGPIQISNALA~~AE~~LAIDTVA~~EE~~VLKAGCITGDRINGLVDG~~IS~~GSNWYIK~~FD~~TTPAASRGLPVT~~RV~~I 187

*C. majus* SRMTLQEIFAKAVGQDSIINDSNVVD~~F~~EDDGNKVTVLENGQRYEGD~~LL~~VGADG~~IS~~WVKRKNLFGPKDAQYSGYTCTY~~G~~ICDFVE~~PI~~ESVGYRVFLG~~HK~~ 293  
*P. somniferum* SRMTLQQLLAKAVGQDSIINDSNVVD~~F~~EDDGNKVTAVLENGQRYEGD~~LL~~VGADG~~IS~~WVKRKNLFGPKDAQYSGYTCTY~~G~~ICDFVE~~PI~~ESVGYRVFLG~~HK~~ 293  
*A. chinensis* SRMTLQQLLCAVGEDVIMNESNVVD~~F~~EDDGNKVTVLENGQRYEGD~~LL~~VGADG~~IS~~WVKRKNLFGSQEASYSGYTCTY~~G~~IADFVE~~PI~~ESVGYRVFLG~~HK~~ 296  
*V. vinifera* SRMTLQQLLARAVGEDIIMNGSNVVD~~F~~EDDGNKVTVLENGQRYEGD~~LL~~IADG~~IS~~WVKRKNLFGPKDAQYSGYTCTY~~G~~IADFVE~~PI~~ESVGYRVFLG~~HK~~ 286  
*C. sinensis* SRMTLQQLLCAVGEDVIMNDSNVVD~~F~~EDDGNKVTVLENGQRYEGD~~LL~~VGADG~~IS~~WVKRKNLFGSTEA~~Y~~SGYTCTY~~G~~IADFVE~~PI~~ESVGYRVFLG~~HK~~ 291  
*J. curcas* SRMTLQQLLALAVGEDVIRNESNVVD~~F~~EDDGNKVTVLENGQRYEGD~~LL~~VGADG~~IS~~WVKRKNLFGPKDATYSDYTCTY~~G~~IADFVE~~PI~~ESVGYRVFLG~~HK~~ 291  
*N. officinale* SRMTLQQLLCAVGEVIRNESNVVD~~F~~EDSGDKVTVLENGQRYEGD~~ML~~VGADG~~IS~~WVKRKNLFGPKDAQYSGYTCTY~~G~~ICDFVE~~PI~~ESVGYRVFLG~~HK~~ 249

*C. majus* QIFVSSDVGAGKMQWYAFHNEPAGGTDAPNGKKE~~RL~~LQIFGSCWCDNV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 393  
*P. somniferum* QIFVSSDVGGKMQWYAFYNEPAGGTDAPNAKKE~~RL~~LKIFGSCWCDNV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 393  
*A. chinensis* QIFVSSDVGAGKMQWYAFHNEPAGGVDGPAKKE~~RL~~LKIFEGWCNDV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 396  
*V. vinifera* QIFVSSDVGAGKMQWYAFYNEPAGGVDGPEKKE~~RL~~LKIFEGWCNDV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 386  
*C. sinensis* QIFVSSDVGAGKMQWYAFHNEPAGGVDGSTGKK~~RL~~LKIFEGWCNDV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 391  
*J. curcas* QIFVSSDVGAGKMQWYAFHKEPPGGVDPRNGKKE~~RL~~LKIFEGWCNDV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 391  
*N. officinale* QIFVSSDVGAGKMQWYAFHNEPAGGVDGPAKKE~~RL~~LKIFEGWCNDV~~DL~~LNATDEDAI~~LR~~RDIDYDRVPIFTW~~GK~~GRVTL~~LG~~DSVHAMQPNMGQGGCMAI 249

*C. majus* EDSYQLAVELEKSWNESVESGISIDVTSALKRYE~~KE~~RRRLRVAVIYGMARMAAIMASTYKPYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 493  
*P. somniferum* EDSYQLAVELDKAWKE~~S~~VDSGSPVDVFSALKRYE~~KE~~RRRLRVAVIYGMARMAAIMASTYKPYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 493  
*A. chinensis* EDSYQLALELDKAWKQSI~~ES~~GPSIDVVS~~SL~~KSYE~~KE~~RRIRVAVIYGMARMAAIMASTYKAYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 496  
*V. vinifera* EDSYQLAMELDKAWEQSI~~KS~~GTPIDVVS~~CL~~KSYE~~KE~~RRIRVAVIYGMARMAAIMASTYKAYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 486  
*C. sinensis* EDSYQLAMELDKAWERSVESGPSIDVVS~~SL~~RYE~~ED~~ARRLRVAVIYGMARMAAIMASTYKAYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 491  
*J. curcas* EDGYQLALEIEKAWKQSI~~ES~~GTPIDIVVS~~SL~~KSYE~~KE~~RRIRVAVIYGMARMAAIMASTYKAYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 491  
*N. officinale* EDSYQLALEIEKAWKQSI~~ES~~GTPIDIVVS~~SL~~KSYE~~KE~~RRIRVAVIYGMARMAAIMASTYKAYLGVLG~~PL~~SFITK~~RI~~PHPGRVGGRRFFIDI~~GM~~PLMSWV 249

*C. majus* LGGNSSKLEGRSVCCRLSDKANDQLRRWFEDDDALERAL~~NG~~EWFLFSPENN-SGSQEP~~I~~HLSRDNKPC~~LI~~GNVSHADVAGTSIA~~IP~~SPQIS~~KM~~HARISY 592  
*P. somniferum* LGGNSEKLGRSLCRLSDKANDQLRRWFEDDDALERAL~~NG~~EWFLFSPDDNLDGSAQPIHLSRDNKPC~~LI~~GNVSHADVAGTSIA~~IP~~SPQIS~~KM~~HARISY 593  
*A. chinensis* LGGNGSKLEGRSLCRLTDKANDQLRRWFEDDDALERAL~~NG~~EWCLLPYGNP-DGSLNPIFLSRDNKPC~~LI~~GNVSHADVAGTSIA~~IP~~SPQIS~~KM~~HARISY 595  
*V. vinifera* LGGNSSKLEGRPPSCRLSDKANDQLRRWFEDDDALERAL~~NG~~EWFLFSPG---ESGLQPICLSKDNKPC~~LI~~GNVSHADVAGTSIA~~IP~~SPQIS~~KM~~HARISY 583  
*C. sinensis* LGGNGSNLDGRSLCRLSDKANDQLRRWFEDDDALERAL~~NG~~EWCLLPYGNA-DGALKPIFLSRDEKQ~~PI~~IGSVSHADIPGMSVTL~~LP~~QVSKMHARISY 590  
*J. curcas* LGGNSSKLEGRSQCCRLSDKASDQLRTWFE~~DD~~DALERAL~~NG~~EWFLFPLGNK-VVSEPICLSRDNKPC~~LI~~GNVSHADVAGTSIA~~IP~~SPQIS~~KM~~HARISY 590  
*N. officinale* LGGNSSKLEGRSVCCRLSDKANDQLRRWFEDDDALERAL~~NG~~EWFLFSPENN-SGSQEP~~I~~HLSRDNKPC~~LI~~GNVSHADVAGTSIA~~IP~~SPQIS~~KM~~HARISY 249

*C. majus* KDGAFFYLTDLQSEHG~~TW~~ITDIEGRRYRVPPN~~LP~~SRFRPSDVIEFGS--EATFKV~~KV~~LAVPSNI~~PD~~KKUTP-VLSAT- 665  
*P. somniferum* KDGFYFYTDLRSEHG~~TW~~ITDIEGRRYRVPPN~~LP~~SRFRPSDVIEFGSDQKAA~~FR~~VK~~LA~~APTNI~~PK~~EEETP-LLNAV- 668  
*A. chinensis* KDGAFFYLTDLQSEHG~~TW~~ITADNEGKRYRVSPN~~FP~~PTFRPTDII~~EF~~FGSDRKVAF~~RV~~K~~MD~~PKRIAE~~KK~~ETSEILQAV- 671  
*V. vinifera* KDGAFFYLTDLQSEHG~~TW~~ITDINVGRRQVSPN~~FP~~PTFRPTDIE~~FG~~SDRKVAF~~RV~~K~~MD~~PKRIAE~~KK~~ETSEILQAV- 658  
*C. sinensis* KNGAFFYVTLRSEHG~~TW~~ITDINVGRRQVSPN~~FP~~PTFRPTDIE~~FG~~SDRKVAF~~RV~~K~~MD~~PKRIAE~~KK~~ETSEILQAV- 667  
*J. curcas* KDGAFFYVTLRSEHG~~TW~~ITDINVGRRQVSPN~~FP~~PTFRPTDIE~~FG~~SDRKVAF~~RV~~K~~MD~~PKRIAE~~KK~~ETSEILQAV- 665  
*N. officinale* KDGAFFYVTLRSEHG~~TW~~ITDINVGRRQVSPN~~FP~~PTFRPTDIE~~FG~~SDRKVAF~~RV~~K~~MD~~PKRIAE~~KK~~ETSEILQAV- 249

**Figure S3J.** Amino acid alignment of CmZEP with selected corresponding genes was performed with the BioEdit program of ClustalW. The yellow and red boxes represent the short motifs of lipocalin family proteins and forkhead-associated (FHA) domains, respectively. The phosphopeptide binding site of the ZEP protein was highlighted in green color. The blue underline represents the FAD-binding domain. *P. somniferum* (*Papaver somniferum*, XP\_026445919), *A. chinensis* (*Actinidia chinensis*, PSS21278), *V. vinifera* (*Vitis vinifera*, NP\_001268202), *C. sinensis* (*Camellia sinensis*, AJB84624), *J. curcas* (*Jatropha curcas*, XP\_012079233), and *N. officinale* (*Nasturtium officinale*, MT547990) were involved in amino acid alignment of CmZEP. A dash (–) represents an aligned gap.

C. majus MASAAYSTCLSYDKN-VVTCIE LLKQSNERFLRRSNWQHGLIKMLWSNTIDSKITQWTRSYKNYFOLKSRGSHVILGGKDHASASRSGNTBGRCPVW 99  
 M. cordata MASAAYSTCLSYDKN-VGAYIE SLTKSNGFLRRSNWQKQCSI KMLKRPNIIDSKTTPQWTRSYKNYFQLSSRDSPLILGGKDNDSACSVNTDGHCPVD 99  
 P. somniferum MASAAYSIYLSYDKK-VLARI E SLPKSDGRFLQGTWNQHR LFKMKYRPNRLVSRIPKQARSFKTYLQCKTRDLHLSLDGEDTASDSTVTIGEHCSVN 99  
 V. riparia MALAAHP TCFSDHDESTSSCC-ASWLKRGERFLRKGPVVRGVVMIKVSSKCRSRNSKLLRSYRNCIQVEFKYPNFLSHRTKISPMCG--SNNIIPEVE 97  
 H. umbratica MAQAARS LCFSDHKGQVLCRTSGLSNERFHRRCVAHFHGVIVLVKIQSGRKARCSQLNKSNNLYAASDLRCSNQLSRRKVRNFSSCS--CNRRRPKTE 98  
 M. esculenta -----MPVMKPAISSSSSYFRPGIASYERIHGRGLNYQSIVLVNFWPNSRKRYVQLMRTBKNYHGIKLRCSHSGWTKKFSFPCR--TGANVTAK 92

C. majus EA-DFFDPM LGLVMQWRQMVMVAVGLVTCIFLWPSADAVDALKT CACLLKECRVE LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFENKVV 198  
 M. cordata EV-DFFNPM LRVLMQWRQMVMVAVGLVTCIFLWPSADAVDALKT CACLLKECRVE LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFENSVW 198  
 P. somniferum EV-DVWG SVLSHLTKHLKQTQVTVAAVGLACIFLVLPTADAVDALKT CGCLLKECRVE LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFENRW 198  
 V. riparia EVFEFPVATVNLNLKRWSQLHFMKVGVGLACTMLLIPSANAVDALKT CTCLLKECRLE LAKCIANPSCAANVACLQTCNNRPDETECQIKCGDLFENNVS 197  
 H. umbratica EVFAFLVPTISNVLNEWSQSKIVKVGGLACAYLVI PSARAVDALKT CTCLLKECRLE LAKCIANPSCAANIACLQTCNDRPDETECQIKCGDLLENSV 198  
 M. esculenta EVLNF LMFVSNNLKEKSH LQFLKVASILACVLLFIPSA DAVDALKT CTCLLKECRLE LAKCIANPACANIACLQTCNNRPDETECQIKCGDLFENTVV 192

C. majus DEFNECAVSRRKCVPKSDVGEFPVPDPAALVKNFNVGDFSGKWISSGLNPTDFDQCQLHEFHMEBGNKLVGNLSWRIRTPDGGFFTRTATQKVFQDPL 298  
 M. cordata DEFNECAVSRRKCVPKSDVGEFPVPDPGALVKNFNIIGDFSGKWISSGLNPTDFDQCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSATQKVFQDPL 298  
 P. somniferum DEFNECAVSRRKCVPKSDVGEFPVPDPALVKNFNIIDFTGKWIITSGLNPTDFDQCQLHDFHMEANKLVGNLSWRIRTPDGGFFTRTAVQKVFQDPL 298  
 V. riparia DEFNECAVSRRKCVPKSDIGEFPVPDPAVLVKNFNIADFSGKWIITSGLNPTDFDQCQLHEFHTEENKLVGNLSWRIRTPDGGFFTRSTMQRVFQDPL 297  
 H. umbratica DEFNECAVSRRKCVPKSDIGEFPVPSPAVLVENFNIADFSGKWIITSGLNPTDFDQCQLHEFHAEAGKLVANLSWRIGTFDGGFFTRSTLQRFQDPL 298  
 M. esculenta DEFNECAVSRRKCVPKSDVGEFPVPDPAVLVKNFNIADFNKGWIITRGLNPTDFDQCQLHEFHVESNKLGVNLSWRIRTPDGGFFTRSTVQRFQDPL 292

C. majus QPGILYNHDNEFLHYQDDWYILSSKIENNPDYIVFYIRGRNDADWDGYGGAFLYTRSAVLPSIVPELERAAKSVGRDFNTFIRTDNTCGPEPPLVERLE 398  
 M. cordata QPGILYNHDNEFLHYQDDWYILSSKIENNPDYIVFYIRGRNDADWDGYGGAFLYTRSAVLPSIVPELERAAKSVGRDFNTFIRTDNTCGPEPPLVERLE 398  
 P. somniferum QPGILYNHDNEFLHYQDDWYILSSKIENNADDYIVFYIRGRNDADWDGYGGAFLYTRSAVLPSIVPEIERATKSVGRDFSTFIRTDNTCGPEPPLVERIE 398  
 V. riparia QPGILYNHDNEFLHYQDDWYILSSKIENKPDYIVFYIRGRNDADWDGYGGAFLYTRSAVLPSIVPELEKAAKSVGRDFNKFIRTDNTCGPEPPLVERLE 397  
 H. umbratica YPGILYNHDNEFLHYQDDWYILSSKIENKDDYIVFYIRGRNDADWDGYGGAFLYTRSAVLPSIVPELEKAAKNIORDFNKFIRTDNTCGPEPPLVERLE 398  
 M. esculenta QPGILYNHDNEFLHYQDDWYILSSKVENKSDYIVFYIRGRNDADWDGYGGAFLYTRSAVLPSIAPPELERAAKSVGRDFSKFIRTDNTCGPEPPLVERLE 392

C. majus KTVEEGERTIIREVEEIEGEIESEVERVEKTEMNLLQRLFDGFKE LQODEENL LKGLSQEEMEILNDLKMEAEVEKLFQGAIPLRKLR 487  
 M. cordata KTVEEGERTIIREVEEIEGEGE-----EVEKVEKTEMNLLQRLFDGFKE LKODEENL LKGLSEEMEILNDLKMEANEVEKLFQGAIPLRKLR 483  
 P. somniferum KTVEEGERTIIREVEEIEGEIVNEVEKVERTERTLLERLFDGFKE LKODEENL LKGLSEEMAILNDLKMEANEVEKLFQGAIPLRKLR 487  
 V. riparia KTVEEGERTIIREVEEIEGELG-----KTEKTFETLMGFGKE LRKDEEYFLKELSKDEMDLLSELKMEASEVEKLFGRALPLRKLR 479  
 H. umbratica KKVEEGERTIIREVEEIEGEVEKEVKRIEKTETMLFQRLAEGFGKE LQQGEANFLRGLSKDEMDLLSELKMEASEVEKLFSEALPLRKLR 487  
 M. esculenta KTVEEGEKSIIREVQIEGEGEVEKVG-----KTEMTLFQRLAEGFGKE LQODEEILRLKLSKEEMELFNDLKMEASEVEKLFQGAIPLRKLR 477

**Figure S3K.** Amino acid alignment of CmVDE with selected corresponding genes was performed with the BioEdit program of ClustalW. Blue, ash, and red underlined represent the VDE cys-rich, lipocalins, and Glu-rich domains, respectively. Asterisks indicate the important residues for pH switch, and those with black boxes represent the putative active site. *M. cordata* (*Macleaya cordata*, OVA03356), *P. somniferum* (*Papaver somniferum*, XP026400851), *V. riparia* (*Vitis riparia*, XP034683443), *H. umbratica* (*Herrania umbratica*, XP021282368), and *M. esculenta* (*Manihot esculenta*, XP021623227) were involved in amino acid alignment of CmVDE. A dash (–) represents an aligned gap.



C. majus ----- 1  
 P. somniferum MATFLRCPMPSPFKAPIIKAPP----NPFPLTETNS-----RKQTKPMTQITSTLKSFLDLKPESEKPESTFDLPFDKSEKRVKIDVIIIGAGPAG 87  
 S. suberectus MGTTF--VLFSPPPPPTKPHQPLHS-TTPPSLLPQTHY-TTS---RKLIIRKRIHSASKFNGFLELEPKHRPEALDFLPWCHPSPDRARFDVIIIGAGPAG 93  
 A. precatorius MGTTC--MLFSPPPTKTHHPLNS-PTPSFPLPPTHY-TTSPSTSRKTRG-RIHSASKFNGFLELDKPEHQPEALDLDLPWCHPSPDRARFDVIIIGAGPAG 95  
 T. pratense MNTSL--MLFSPVITTT-----TISTFPFKTHHTTSLQSSRKQHGRIHSSTKFGNFDLKSKESEALDFLPWHHPSPDRSQFDVIIIGAGPAG 89  
 G. max MGTTF--MLFSPPPLKPHQVP--LTFPLPQTHH-TAS-----RNRKRVHSTSKFNGFLELDKPESEKPESTFDLPWCHPSPDRARFDVIIIGAGPAG 87  
 C. clementina MATLL--SPFSPLAKVSQIIDSTSSPFSPLPLGR-QNACSRKADHHHHRRITSKFGNFDLETPESVPEFDLPWCHPSPDRIRIDVIIIGTGPAG 97

C. majus ----- 1  
 P. somniferum LRLAEQVS-SYGIRVCCIDSSPLSMWPNNGVWDEPQSLGLEDCLDKTPWMTTIFLDGRRTKYLDRIPIGRVNRKGLKTKLEKSVLNGVKPFESKVNMI 186  
 S. suberectus LRLAEQVS-LYGKVCVCDPEPLSVWPNNGVWDEPBNGLLEDCLDKTPWMACVIINDSKIKYLGRCYGRVSRKRLKQKLEGGCVSHGVRFHAKAWQV 192  
 A. precatorius VRLAEQVS-LYGKVCVCDPEPLSMWPNNGVWDEPBNGLLEDCLDKTPWMACVIINN SKIKYLGRCYGRVSRKRLKQKLEGGCVSHGVRFHAKAWQV 194  
 T. pratense ICLAEQVS-LYGKVCVCDPNPLSIWPNNGVWDEPFGLEGLLEDCLDKTPWMAIYIDNNNTKYLDRCYGRVNRKGLKTKLEKSVLNGVKPFESKVNMI 188  
 G. max LRLAEQVS-LYGKVCVCDPEPLSVWPNNGVWDEPBNGLLEDCLDKTPWMACVIINDSKIKYLGRCYGRVSRKRLKQKLEGGCVSHGVRFHAKAWQV 186  
 C. clementina LRLAEQVSRHSVKVCVCDPSPLSTWPNNGVWDEPBDIGLVDCLDKTPWMTCFIINDHKTKYLDRIPIGRVSRNLIKTKLENCVSHGVRFHAKAWQV 197

C. majus -----DSFLFI 6  
 P. somniferum EHHFEFSVVICEDGVELTGSLLVDASGFSFPVQFNEP---RNHGYQIAHGILAEVEEHPFDLDKMLVMDWRDHLGNEPVLRVKNKHPTFLYAMPFS 282  
 S. suberectus KHQEFESTVLCDGTELGKSLIVDASGFSFTIAYDKV---RNHGYQIAHGILAEVDDHPFDLDKMLVMDWRDHLGNEPVLRVSNRPFLLYAMPFS 288  
 A. precatorius EHQEFESTVLCDGTELGKSLIVDASGFSFTIAYDKM---RNHGYQIAHGILAEVDDHPFDLDKMLVMDWRDHLGNEPVMRVSNRPFLLYAMPFN 290  
 T. pratense KHQEFESIWCDDGTNLKGSLLVDASGYGSNFIYDIDLTLTKRNYGYQIAYGVLAEDVADHPFDLDKMLVMDWRDHLRQ----GNSSEVPFTFYAMPFT 283  
 G. max QHQEFESKVLCDGTELGKSLIVDASGFASNFVAYDKV---RHHGYQIAHGILAEVDDHPFDLDKMLVMDWRDHLGNEPVLRSNRPFLLYAMPFS 282  
 C. clementina NHQEFESSTVCDGNEIKASLIVDASGFASFPVEYDKP---RNHGYQIAHGILAEVEEHPFDLDKMLVMDWRDHLGNEPVLRSNKLPTFLYAMPFD 293

C. majus PLKIFLSSHLINIRTWLVFSKFSH----FSLHRLFMSTLLRS-----PMLSTLTVPFLKTA----- 59  
 P. somniferum SNLIFLEETLIVSRFVLSYTEVKNRMVARLRHLGIRVKRVIIDEKCLIPMGGPLPTIPQSI LCHGATAGLVHPSTGYMVAQTLARSTILADVIAECLGST 382  
 S. suberectus SNLIFLEETLIVSRFVLSYMEVKRRMVARLRHLGIRVKRVIIDEKCLIPMGGPLPMIPQDVMAIGGTSGVHPSTGYMVARMTAVAPWAAIAECLGST 388  
 A. precatorius SNLIFLEETLIVSRFVLSYMEVKRRMVARLRHLGIRVKRVIIDEKCLIPMGGPLPMIPQDVMAIGGTSGVHPSTGYMVARMTAVPWAIAECLGST 390  
 T. pratense SNLIFLEETLIVSRFVLSHKEVKRRMVARLRHLGIRVKRVIIDEKCLIPMGGSLPKIPQNVIAFGGNSGLVHPSTGYLMARTMTLAPIVASSINECLGST 383  
 G. max SNLIFLEETLIVSRFVLSYMEVKRRMVARLRHLGIRVKRVIIDEKCLIPMGGPLPMIPQDVMAIGGTSGVHPSTGYMVARMTAVAPWAFITQCLGST 382  
 C. clementina SNLIFLEETLIVSRFVLSYKEVKRMAARLRHMGIRVKRVIIDEKCLIPMGGPLPMIPQDVMAIGGTSGGLIHPATGYMVARMTALAPALADAIAECLGST 393

C. majus -----SFFPITSTNSRK-----LKQPRIQISSKFNFLDLKPESEKPEFLTFDLP-----FHKSDRVKIDVIIIGAGPAG 124  
 P. somniferum RMIRGSGMHQR-VWNGLWPMDCRSREYRFGTETLLKLDLKGTRKFHAFDFLDLPYWGQFLSSRLNIMELGMLSLSLFSGHASRSTRIDIVTKCPLPLA 481  
 S. suberectus RMIRGKQLHAK-VWNSMWPIESRLVREFYSGMETLLKLDLNGSRFFDAFFDLKPYWGQFLSSRLTLKELVWLSISLFGHASNPSRLDIVTKCPLPLA 487  
 A. precatorius RMIRGKQLHAK-VWDSMWPIESRLAREFYSGMETLLKLDLNGSRFFDAFFDLKPYWGQFLSSSLTLKELVWLSISLFGHASNPSRFDIVTKCPLPLA 489  
 T. pratense RMIRGKQLYAKEIWNSMWPIESRVAREYTFGMEETLLKLDLNETRQFFEAFFELKPYWMKGLSSSLTLNDIIWLSMSLFAHSSNSSLRAIVTKCTILEA 483  
 G. max RMIRGKQLHDK-VWNSMWPINRLVREFYSGMETLLKLDLNGSRFFDAFFDLKPYWGQFLSSRLTLNELWLSISLFGHASNPSRFDIVTKCPLPLA 481  
 C. clementina RMIRGRPLHQR-VWNGLWPIDRRCNREFYSGMETLLKLDLKGTRRFFDAFFDLNPHYWGQFLSSRLSLAELAGLSLFGHASNSSLRAIVTKCPLPLV 492

C. majus LRLAE----- 129  
 P. somniferum KMIGKLVNSAI- 492  
 S. suberectus KMMGNIALEYIG 499  
 A. precatorius KMMGNIALEYIG 501  
 T. pratense EMVANI CRELIR 495  
 G. max KMMGNIALEYIG 493  
 C. clementina KMMGNIALETTI- 503

**Figure S3L.** Amino acid alignment of CmCCS with selected corresponding genes was performed with the BioEdit program of ClustalW. The brown boxes indicate the conserved FLEET motif essential for  $\beta$  and  $\kappa$ -cyclase activity. *P. somniferum* (*Papaver somniferum*, XP\_026413514), *S. suberectus* (*Spatholobus suberectus*, TKY48659), *A. precatorius* (*Abrus precatorius*, XP\_027344227), *T. pratense* (*Trifolium pratense*, PNY15080), *G. max* (*Glycine max*, XP\_003541965), and *C. clementina* (*Citrus clementina*, XP\_006424195) were involved in amino acid alignment of CmCCS. A dash (–) represents an aligned gap.

*C. majus* -----MDSLSSFFTKFHP-----HKLI LSPSP-TKNPLFYISAVNVEDRLTINDPKPTPSS-----PLSQNPNTNRTPTITSSVA 70  
*P. somniferum* -----MDAFSSSFCTKFPY-----TNKLAFSPSTSSQTHLYFISAVNVEER-----PKRTTNS-----SSSTINTETPVLG--- 65  
*N. nucifera* MKSVSSEFLNTRERMDAFSSSFQHPNLLS-----PPNKS TTAFTVTPSPHSPLFTISAVRIEER-----SQSTTKTKPATRQPKPPTPLSSSTTTTT 91  
*M. rubra* -----MDAFSSSFLSTLAMFKLLSVTMKTQKAFRTPPSSANGVPLVSVRIEER-----PQQTSTAKPSPSRTTTKTSPQRPETQGT 80  
*P. alba* -----MVPKPFIVSSSS-----SSFS SP--SPVVR LSVSVRIEDK-----PPSQTVT-----TTSPKPPAEITPSPP 58  
*P. hybrida* -----MDAFSSSTFLSTLSQ-----HPKSLSPNSPNTATSSPSLVYSVRIEER-----PQKTTTT-----TSTKPAQLPQKPNPS 67  
*N. officinale* ----- 1

*C. majus* TKAQVGD PKKSTITRRRSIT--TDLSPVPTSFNADFSIINNFDIPAIRSPVDPKHVLAKNFAPVDELPTTKCTVIQGAIPPSINGAYIRNGPNPQ 167  
*P. somniferum* -----GDHAKKPVLTKRKPSRSFVETPSQSTIFNTFNVNFDIPPTPRSPVDPQHVLA TNFAPVDEFPPTKCTVIEGELPE SINGAYIRNGPNPQ 159  
*N. nucifera* RIASPTTSPTRIQTTPVGTTSATRTPELSIPFTIFNADDDIINNFDIPLRSPVDPKIVLADNFAPVDELPTTDCPVIEGKLPCLNGVYIRNGPNPQ 191  
*M. rubra* RLSPLSSSQKSATSLKAPLASEAKRPELSVPVAVIFNVDDIINNFDIPLRSPVDPKIVLADNFAPVDELPTTDCPVIEGKLPCLNGVYIRNGPNPQ 180  
*P. alba* PTTTAKTAGSRRVWKR-----PTEQSLPSLIFNSFTIINNFDIPKPSVDPKIVLADNFAPVDELPTTDCPVIEGKLPCLNGVYIRNGPNPQ 150  
*P. hybrida* PYTPPKATPKRQLPIKPK-----QVEPSFPAVIFNADDDIINNFDIPLRSPVDPKHVLAKNFAPVDELPTTDCPVIEGKLPCLNGVYIRNGPNPQ 159  
*N. officinale* ----- 1

*C. majus* HLPFGPYHLFDGDMHLSLISNGTATFC SRVYKTKYTVEREHGSSIFPNVFSGFNGLTASVARGAVTAARVLSGQYNFVNGIGLANTS LAFFGDKLFA 267  
*P. somniferum* YLPRGPYHLFDGDMHLSLISNGQATFC SRVYKTKYKIEHKGSLPFPNVFSGFNGLTASAARGAITAARVLSGQYNFINGIVANTS LAFFSKLFA 259  
*N. nucifera* YLPRGPYHLFDGDMHLSLRFSGGRATFC SRVYKTKYKINVERQLHGVPLPNVFSGFNGLTATVARGAVSAGRILTGQYNFINGIGLANTS LAFFGNRLFA 291  
*M. rubra* YLPRGPYHLFDGDMHLSIKISQKATLC SRVYKTKYKINERDAGYPLLPNVFSGFNGLAASAARGALSAARVSGQYNFANGIGLANTS LAFFANRLFA 280  
*P. alba* YLPRGPYHLFDGDMHLSIKISQKATLC SRVYKTKYKINERDAGYPLLPNVFSGFNGLIASAARGSLTAARVLTGQYNFANGIGLANTS LAFFGNRLFA 250  
*P. hybrida* YLPRGPYHLFDGDMHLSIKISQKATFC SRVYKTKYKIVEREAGFQVLPNVFSGFNGLTASAARGAITAARVSGQYNFANGIGLANTS LAFFGDKLFA 259  
*N. officinale* ----- 1

*C. majus* LGE SDLPYEIKLTPDGEIVTLGRHDFDGKLFMSMTAHPKVDPTGEAFAPRYGPIPPFLTFFRFNSSGSKQPDVPFISMTRPAPLHDFAITTKYAIPTFEI 367  
*P. somniferum* LGE SDLPYEIKVTPDGEILTVGRDFDGKLFMSMTAHPKVDPTGEAFAPRYGVPVFFLTFFRFDSSGVKQADVPFISMTRPAPLHDFAITTKYAIPTFEI 359  
*N. nucifera* LGE SDIPYQVRLTPEGD IQTIGRWDSDGKLFMSMTAHPKIDADTGEAFAPRYAPVPPFLTYFYFDANGVKQPDVPFISMTRPAPLHDFAITTKYAIPTFEI 391  
*M. rubra* LGE SDLPYTRVRLTSGDIEITLGRHDFDGKLFMSITAHKVDPTGEAFAPRYGAPVPPFLTYFYFDANGVKQPDVPFISMTRPAPLHDFAITTKYAIPTFEI 380  
*P. alba* LGE SDLPYEVKVPNGDIEITLGRHDFDGKLFMSMTAHPKIDPTGEAFAPRYSPVPPFLTYFYFDANGVKQPDVPFISMTRPAPLHDFAITTKYAIPTFEI 350  
*P. hybrida* LGE SDLPYAVKLA PDGDIITLGRHDFDGKLFMSMTAHPKIDPTGEAFAPRYGMPVPPFLTYFYFDANGVKQPDVPFISMTRPAPLHDFAITTKYAIPTFEI 359  
*N. officinale* ----- 1

*C. majus* QIGMNPMEIVGSGSPVGADPSVSRIGVIPRYAKDESDMKWFDVPGFNIHAINAWDE-GEDEIVLIAPN---ILSVEHTLERMELIHALMEKVRINL 462  
*P. somniferum* QIGMNPMEIVGSGSPVGADPSAVSKI GVIPIRYAKDESEMKNWFDVPGFNIHAINAWDE-GEDEIVLIAPN---ILSVEHTLERMELVHALMEKVRINL 454  
*N. nucifera* QIGMNPMEIVGSGSPVGADPSAVSRIGVIPRYAKDESEMKNWFDVPGFNIHAINAWDEEDDEDAIVLIAPN---ILSVEHTLERMELVHALMEKVRIDL 487  
*M. rubra* QIGMNPMEIVGSGSPVGADPSKVRIGVIPRYAKDESEMKNWFDVPGFNIHAINAWDEEDDRAIVMVAPE---ILSVEHTMERMDLVHALMEKVRIDL 476  
*P. alba* QIGMNPDLMLAGG-SPVGS DSKVSRIGVIPRYAKDESQIKWFDVPGFNIHAINAWDEEDGNEIVLIAPN---ILSVEHTLERMELVHALMEKVRIDL 445  
*P. hybrida* QIGMNPIDFITGG-SPVSSDSKVPRIGVIPRYAKDESEMKNWFDVPGFNIHAINAWDEEDGGDITVMVAPE---ILSVEHTLERMDMIHASVEKVRIDL 454  
*N. officinale* -----MIRWFLPNCPIFNANAWEEDEWVLTICLENPDLDVSGNVKEKLENFNNELYEMFRNM 62

*C. majus* RTGMVSRHPVSARNLDFGVINQFTGKKNRFVYAGIDPMFKISGVVKLVMSGEDEH-----EQNDCTVSCRMFGSGCYGGEFFVAKPENLD-ADDD 554  
*P. somniferum* RTGMVSRQPLSARNLDFGVINQFTGKKNRFVYAGIDPMFKISGVVKLVMSGEDEH-----EHDCTVSCRMFGSGCYGGEFFVAREPNNPD-ADDD 546  
*N. nucifera* RTGIVSRFPVSARNLDFGVINQFTAKKSRVYLVGDPMPKISGVVKLVMSGEQ-----RQDCTVSCRMFGSGCYGGEFFVANSPESSRPADEDD 579  
*M. rubra* NTGIVTRHPISARNLDFAVINPAVYGGKKNRYVYAAIGDPMFKISGVVKLVMSKRE-----RQDCTVSCRMFGSGCYGGEFFVAREPNNPE-ADDD 567  
*P. alba* RTGIVTRHPISARNLDFAVINQAVYGGKKNRYVYAAIGDPMFKIAGVVKLVMSKGE-----ERRDCTVSCRMFGSGCYGGEFFVARDPEDPE-ADDD 537  
*P. hybrida* RTGMVSRHPVSTRNLDFGVINPAVYGGKKNRYVYAAIGDPMFKVAGIAKLVMSAES-----DRRDCTVSCRMFGSGCYGGEFFVAKDPNNLE-ADDD 547  
*N. officinale* RTGSASQKKLSASAVDFPRINEFYTGKKQRYVYGTILDSIAKVGTIKRILHABAE TGRKILEVGGNIRIYDLGGGRYGEAFIVPR-----EAAEDN 157

*C. majus* GYVVTYVHDENLGSKFLVMDAKSPTLDVVAATLPGRVPIYGFHGFVRESE LKKLM- 611  
*P. somniferum* GYVVTYVHDENLGSKFLVMDAKSPTLDIVA SVKLPGRVPIYGFHGFVRESE LKKL-- 602  
*N. nucifera* GYVVS YVHDENLGSKFLVMDAKSPTLEVVAVKLPRRVPIYGFHGLFVRESEDLRCKV 637  
*M. rubra* GYLVSYVHDEKESGSRFLVMDAKSPNLDIVA VKLPRRVPIYGFHGLFVRESEDLKML-- 623  
*P. alba* GYVVTYVHDENLGSKFLVMDAKSPLELDVVAARLPRRVPIYGFHGLFVRESEDLRKL-- 594  
*P. hybrida* GYVVS YVHDENLGSKFLVMDAKSPNLDIVA VKLPRRVPIYGFHGLFVRESEDLRKL-- 603

**Figure S3M.** Amino acid alignment of CmCCD with selected corresponding genes was performed with the BioEdit program of ClustalW. Asterisks indicate histidine residues involved in the coordination of the catalytic Fe<sup>2+</sup>. The yellow highlighted boxes represent aspartate or glutamate residues which are predicted to be fixing the iron atom. The conserved amino acids present in the hydrophobic patches are shown in black boxes. *P. somniferum* (*Papaver somniferum*, XP\_026380876), *N. nucifera* (*Nelumbo nucifera*, XP\_010275132), *M. rubra* (*Morella rubra*, KAB1215613), *P. alba* (*Prosopis alba*, XP\_028782945), *P. hybrid* (*Petunia x hybrid*, QBC36243), and *N. officinale* (*Nasturtium officinale*, MT547984) were involved in amino acid alignment of CmCCS. A dash (–) represents an aligned gap.



*C. majus* MPTSSST-----TWIN-KPSSISINKPRRSSSSSTLSSSLQSPSLHFPQTHQSSPSTTTSTSAASTYTHHTPTITLPKEKSKTLHPISSPNPNPN 91  
*P. somniferum* MSSSSVS-----SWVTNKPSSMSRNQRRSRNLLSSSLQSPSLVQTTSS--SSSTASISTYTHHTSSSSRTAQITLPKEKTKTLHLQSS-----PT 85  
*R. chinensis* MATPNSWAHTAQIQHLLSSSSSFSSSLVNMG-FPTRSIALNRRSSSTIHSALQ--SPSVLHFPKQPIHPRVITKEATITPSPPTKTVTTTQOPF----- 91  
*H. brasiliensis* MASS-----AISMSSSISLDAFRA-SKLNISSSSLHTPSILHFPKQ--SPRTTSFPPSPSISTTIPNKVTLPPAPSVDKSLAPEIN----- 78  
*M. esculenta* MASSSSSPA-----AAISMSSSVSLDRP-----SIISSSLQTPSILHFPKQ--SSTATSPSPSISTTIPKKIATT-LPSVDKSLAPVQN----- 79  
*J. curcas* MASTAP-----PAITMSSSISIGRP--SRKPNVTCSLQTPSILHFPKQ--STRTATYPPSSAISTSTTSPINK-SSSTDISVPP----- 75  
*N. officinale* MVSSPAK----- 7

*C. majus* PTPTTKTIQHPPNWNPFQKAASMALDAFETALLNKEQHPLPKTADPSVQISGNFAPVP-EQPVQRNLPVTVGRIPCSISGFYVRNGANPLHEP----- 183  
*P. somniferum* ATPKTTKPNQ-NWNIIQKVASMALDACETALLSKEKQQLPKTADPSVQISGNFAPVP-EQPVCONLPVTVGSIPSSINGVIVRNGANPLHEPLSGHHLF 183  
*R. chinensis* -----HWNLLQRAASTALDMLBGLVSRSESONPLPKTADPRVQIAGNFAPVP-EQPVRLSLPVSCTIPECISGVIVRNGANPLHEPVAGHHFF 178  
*H. brasiliensis* -----QLNLLQRAAAMALDAVESALVSHENQYPLPKTADPTVQISGNFAPVP-EQPVHNLPLVAGKIPDSIRGVILRNGANPLHEPVAGHHFF 165  
*M. esculenta* -----QWNLLQKAAAMALDAVESALVSHERRPLPKTADPAVQIAGNFAPVP-ERPWHNLPLVTVGTIPDTIRGVIVRNGANPLHEPVAGHHFF 166  
*J. curcas* -----EWNLLQKAAAMVLDKVENVLVSHERRPLPKTADPTVQISGNFAPVP-EQPVWRDLPLVTVGTIPDSIRGVILRNGANPLHEPVAGHHFF 162  
*N. officinale* -----QRPEMTLATALPTTVEDVINTFIDPPSRPSVDPKHVLSDNFAPVLDLPLPTNCEIIGSLPPLSDGAIYIRNGPNQFLRGPYHLF 93

*C. majus* ----- 183  
*P. somniferum* DGDGMHNAVNIQGSVSYSCRFTEHRLVQEKSLGRFVFPKAIHELHGHSG-IARLMLFYVRGAFGLVDPNQIGVANAGLVYFNRLLLAMSEDDLPYQV 282  
*R. chinensis* DGDGMHNAVSIINDGAASYACRFTEHRLVQEREIGRFVFPKAIHELHGHSG-IARLALFYARGALGLVDPHIGVANAGLVYFNRLLLAMSEDDMPYQV 277  
*H. brasiliensis* DGDGMHNAVRFEGSVSYACRFTEHRLVQERKLRFDI----- 204  
*M. esculenta* DGDGMHNAVRFEGSVSYACRFTEHRLVQEREIGRFVFPKAIHELHGHSG-IARLLLFCARGLFGTVDSHGTGVANAGLVYFDRLLAMSEDDLPYHV 265  
*J. curcas* DGDGMHNAVRFEGSVSYACRFTEHRLVQERKLRGPIFPKAIHELHGHSG-IARLLLIFYARGIFDIVDPHIGLVANAGLVYFNRLLLAMSEDDLPYHV 261  
*N. officinale* DGDGMLHAIRIHGGKATLCSRIVKTYKYNVEKQSGAFVMVNVFSGFGVGTASVARGALTAARVLGQYFNPNVIGLANTSLAFFSNRLPALGESDLPYAV 193

*C. majus* ----- 183  
*P. somniferum* RLTPDGGDLTVGRDFEQLKSAMIAHPKLDPVSGLEFALSIDVVQKPYLKYFRFSKNGEKSPDVEIP-LAQPTMMHDFAITENFWIPDQQVVFKLK 379  
*R. chinensis* RLTPDGGDLTVGRDFEQLKSAMIAHPKLDPVSGLEHLSIDVVQKPYLKYFRFSADGEEKSPDVEIP-LAAPTMHDFAITENFWIPDQQVVFKLK 374  
*H. brasiliensis* ----- 204  
*M. esculenta* RVLPSGDLKTVGRYFNFGQLKSAMIAHPKLDPVSGLEFALSIDVVQKPYLKYFRFSKNGEKSPDVEIP-LDQPTMMHDFAITENFWIPDQQVVFKLK 362  
*J. curcas* RVLPCGDLKTVGRYFNFGQLKSAMIAHPKLDPVSGLEFALSIDVVQKPYLKYFRFSKNGEKSPDVEIP-LDQPTMMHDFAITENFWIPDQQVVFKLK 358  
*N. officinale* RLTPDGGDLTVGRDFEQLKSAMIAHPKLDPEGTETAFRIGFVP-PFLTYFRDSSGKKQDVFIFSMSTSPSFIHDFAITENFWIPDQQVVFKLK 292

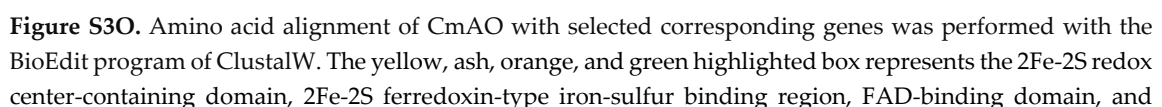
*C. majus* ----- 183  
*P. somniferum* -EMIRGGSPVYDKNKVRFGLVNLKAKDSSDMKVEVPDCCFHLNNAWEEPETDEIVVIGSCMTTPDPSIFNECEDEGLQSVLSEIRLNLKTGKSTRRPI 478  
*R. chinensis* -EMIRGGSPVYDKNKSRFGILAKNATNADDIIVWECDDTFCFHLNNAWEEPETDEIVVIGSCMTTPDPSIFNECEDEGLQSVLSEIRLNLKTGKSTRRPI 473  
*H. brasiliensis* ----- 204  
*M. esculenta* -EMIRGGSPVYDKNKSRFGILDKKANDASKIIVWVAPDCCFHLNNAWEEPETDEIVVIGSCMTTPDPSIFNECEDEGLQSVLSEIRLNLKTGKSTRRPI 461  
*J. curcas* -EMIRGGSPVYDENKISRFGLDKKANDSSKIRWVAPDCCFHLNNAWEEPETDEIVVIGSCMTTPDPSIFNECEDEGLQSVLSEIRLNLKTGKSTRRPI 457  
*N. officinale* DLMIEGGSPVGTDTGKIRLGLVQIRIAGDESEMKVEFVGFNITHAINAWDEDDGNSIVLIAFNIMSEHTLER-MDLVHALVKVKIDLVTVGIVTRHPI 391

*C. majus* ----- 183  
*P. somniferum* ISEENQLN-LEAGMVNRNLGRKTRPAYLALAEWPVKVSGIAKVDLVTVG-----EVQKFIYGDNKTFGGEPYFVFN--SSSDREDDGHILAFMHDETTSK 569  
*R. chinensis* ISDESEHVNLEAGMVNRNLGRKTRPAYLALAEWPVKVSGIAKVDLVTVG-----QVKKHIYGDNRKTFGGEPFFLPS--GSCGEEDGGYILSFVHDEKTVK 565  
*H. brasiliensis* ----- 204  
*M. esculenta* ISE-SEQVNLEAGMVNRNLGRKTRPAYLALAEWPVKVSGIAKVDLVTVG-----EVRKIMYG-NKYGGEPLFLPSDSSNSGKEDSGYILCFVHDEKQK 554  
*J. curcas* ISD-KHQVNLEAGMVNRNLGRKTRPAYLALAEWPVKVSGIAKVDLVTVG-----ETKKIYGDNKYGGEPLFLPD--SNSGKEDDGFLCFVHDEKQK 548  
*N. officinale* SAR-----NLDFGVINAPLRRSRIVYAGVDGMPKISGVVKLDVSKGDRDCTVARMYGPCTYGGEPFVAKDPGNPEABEDDGIVVTVHDEASGE 486

*C. majus* ----- 183  
*P. somniferum* SELLVINAMN--LELEASVKLPSRVYPYGFHGTFINSMLENQA 610  
*R. chinensis* SELQIVNAMN--LKLEATVTLPSRVYPYGFHGTFTDSKDLKNOA 606  
*H. brasiliensis* ----- 204  
*M. esculenta* SELQIVNAMN--LKLEATVKLPSRVYPYGFHGTFTISAKOLEKQA 595  
*J. curcas* SELQIVNAKN--LQLEATVKLPSRVYPYGFHGTFTITAKOLEKQA 589  
*N. officinale* SKFLVMDAKSPLEIVAVALPRRVYPYGFHGLFVKERDLNKL- 528

**Figure S3N.** Amino acid alignment of CmNCED with selected corresponding genes was performed with the BioEdit program of ClustalW. *P. somniferum* (*Papaver somniferum*, XP026405668), *R. chinensis* (*Rosa chinensis*, XP024161283), *H. brasiliensis* (*Hevea brasiliensis*, XP021644826), *M. esculenta* (*Manihot esculenta*, XP021593487), *J. curcas* (*Jatropha curcas*, XP012084339), and *N. officinale* (*Nasturtium officinale*, MT547987) were involved in amino acid alignment of CmNCED. A dash (–) represents an aligned gap.







hammer-head domain, respectively. Asterisks indicate the eight conserved cysteine residues of [2Fe-2S] centers, and those with a red and pink rectangle box represent 2Fe-2S ferredoxin-type iron-sulfur binding domain and FAD-binding domain. The dotted blue and red underlined indicates that motif corresponding two non-identical [2Fe-2S] redox centers and molybdenum cofactor and substrate-binding domain. The putative motifs involved in Moco and substrate binding (MocoI-MocoV) are underlined in black continuous line. *M. cordata* (*Macleaya cordata*, OVA00877), *V. riparia* (*Vitis riparia*, XP\_034688017), *Q. lobate* (*Quercus lobate*, XP\_030960280), *T. thalictroides* (*Thalictrum thalictroides*, KAF5184240), and *C. sinensis* (*Camellia sinensis*, AVZ45846) were involved in amino acid alignment of CmAO. A dash (-) represents an aligned gap.

**Table S1** List of primers designed and used in the qRT-PCR analysis to determine mRNA expression levels of *C. majus* CBP, XBP, and ABP genes

Primer names	Primer sequence (5'→3')	PCR product length (bp)
CmPSY-F	TGTTGAAGCTCGGATTATCGATG	102
CmPSY-R	AATATGGTGGAAACAGTGGATTCTG	
CmPDS-F	AAGACCTGAACCTTGACAATACCG	130
CmPDS-R	AGATAGACCAGCCAAGCCTG	
Cm-Z-ISO-F	GGTAATTGTAGGAGCATCGCTTG	109
Cm-Z-ISO-R	ATCAAAGAAAGCTGAATCCTCACC	
CmZDS-F	AGTGGGTTCCTTTGTCGATAAAC	106
CmZDS-R	GCCACCTTTCTCATCAAGC	
CmCrtISO-F	TGACTTCGTCATGGAATCATC	117
CmCrtISO-R	AGTGACTTCAATTCCAGCGAG	
CmLCYB-F	TGATCTGGCCTAACAATTACGG	148
CmLCYB-R	TTAACCCTTCCATAAGGTCTGTC	
CmLCYE-F	ATCTTGGGCTAGAAAGGTGTATTG	106
CmLCYE-R	CGACTAACTCTTCCATAAGCACG	
CmCHXB-F	GTACGAGTTGCAGAGAAATTAGCC	115
CmCHXB-R	TGTAATAAACAGCAGCAACAGCC	
CmCHXE-F	GTCAAGATGATTCAGGGATACCC	131
CmCHXE-R	AGCTGCAAGACGATAAATGGG	
CmZEP-F	TCACAAGGGTTATTAGCCGAATG	150
CmZEP-R	CTTCATATCGCTGTCCGTTCTC	
CmVDE-F	CTGTTGGGTGTTATGCAGCAG	141
CmVDE-R	CCTGCACTCTTTCAATAAACAAGC	
CmCCS-F	CATTCTTCCCAATCACTTCCAC	104
CmCCS-R	TTTGATTGAGGCTTCAGATCTAGG	
CmCCD-F	TCTAATGGCACTGCAACTTTCTG	129
CmCCD-R	AGCAACAGAAGCAGTGAGGC	
CmNCED-F	CACTCCAATCACTCTTCCCAAAG	103
CmNCED-R	GTGTTGGATTGTCTTTGTTGTTGG	
CmAOF-F	TGAAATTGGAGCTGCTGTGAC	128
CmAOF-R	ACGCAACCTTGTTTCATATGGTC	
Cm $\alpha$ -tubulin-F	TCCATCCTGAACAACTCATAAGTG	112
Cm $\alpha$ -tubulin-R	TTTCTGATCCGATCAAGACACAG	

**Table S2** Analysis of CBP gene sequences using the SignalP program

<b>Gene names</b>	<b>Original shearing site (C score)</b>	<b>Synthesized shearing site (Y score)</b>	<b>Signal peptide (S score)</b>
CmPSY	0.278	0.190	0.218
CmPDS	0.111	0.125	0.154
CmZ-ISO	0.119	0.124	0.183
CmZDS	0.250	0.265	0.515
CmCrtISO	0.635	0.260	0.221
CmLCYB	0.120	0.125	0.151
CmLCYE	0.194	0.141	0.186
CmCHXB	0.118	0.133	0.167
CmCHXE	0.128	0.176	0.304
CmZEP	0.116	0.118	0.135
CmVDE	0.158	0.124	0.144
CmCCS	0.116	0.158	0.400
CmCCD	0.107	0.126	0.156
CmNCED	0.107	0.106	0.126
CmA0	0.108	0.112	0.122