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CmZDS MASGILFSPV--SFSGKH--NCRDRLPARN--S-VILKGCDFLYVSSLLRQVSDMSVNAKGLFPPEPERYRGPRLKVAIIAGLAGMSTAVELLDQGHEV 97
CsZDS MASGILFSPV--SFSGKH--NCRDRLPARN--S-VILKGCDFLYVSSLLRQVSDMSVNAKGLFPPEPERYRGPRLKVAIIAGLAGMSTAVELLDQGHEV 97
CmoZDS MASGILFSPV--SFSGKH--NCRDRLPARN--S-VILKGCDFLYVSSLLRQVSDMSVNAKGLFPPEPERYRGPRLKVAIIAGLAGMSTAVELLDQGHEV 94
VvZDS1 MESSILFPAAGSRPFKGTIVGLFLSGGRRPMPSCLLKGRQLVVRSSLLSIVSDMSVNAKGLFPPEPERYRGPRLKVAIIAGLAGMSTAVELLDQGHEV 100
CuZDS MESSILFPAAGSRPFKGTIVGLFLSGGRRPMPSCLLKGRQLVVRSSLLSIVSDMSVNAKGLFPPEPERYRGPRLKVAIIAGLAGMSTAVELLDQGHEV 86

CmZDS DYESRTEFIGGKVGSPVDKRGNHIEMGLHVFFGTCYNNLFRMLMKKVGAEKNLLVKDHTHTFVNKGGEGIGELDFRFPVGAPIHGIRAFIATNQIGTYDKARN 197
CsZDS DYESRTEFIGGKVGSPVDKRGNHIEMGLHVFFGTCYNNLFRMLMKKVGAEKNLLVKDHTHTFVNKGGEGIGELDFRFPVGAPIHGIRAFIATNQIGTYDKARN 197
CmoZDS DYESRTEFIGGKVGSPVDKRGNHIEMGLHVFFGTCYNNLFRMLMKKVGAEKNLLVKDHTHTFVNKGGEGIGELDFRFPVGAPIHGIRAFIATNQIGTYDKARN 194
VvZDS1 DYESRTEFIGGKVGSPVDKRGNHIEMGLHVFFGTCYNNLFRMLMKKVGAEKNLLVKDHTHTFVNKGGEGIGELDFRFPVGAPIHGIRAFIATNQIGTYDKARN 200
CuZDS DYESRTEFIGGKVGSPVDKRGNHIEMGLHVFFGTCYNNLFRMLMKKVGAEKNLLVKDHTHTFVNKGGEGIGELDFRFPVGAPIHGIRAFIATNQIGTYDKARN 186

CmZDS ALALALSPVVKALVDPDAAMKDIRNLDLSISFSEWFLSKGGTRASIQRMDPVAYALGFIDCDNISARCMILTFSLFATKTEASLLRMLKGSFDPVFLSGPI 297
CsZDS ALALALSPVVKALVDPDAAMKDIRNLDLSISFSEWFLSKGGTRASIQRMDPVAYALGFIDCDNISARCMILTFSLFATKTEASLLRMLKGSFDPVFLSGPI 297
CmoZDS ALALALSPVVKALVDPDAAMKDIRNLDLSISFSEWFLSKGGTRASIQRMDPVAYALGFIDCDNISARCMILTFSLFATKTEASLLRMLKGSFDPVFLSGPI 294
VvZDS1 ALALALSPVVKALVDPDAAMKDIRNLDLSISFSEWFLSKGGTRASIQRMDPVAYALGFIDCDNISARCMILTFSLFATKTEASLLRMLKGSFDPVFLSGPI 300
CuZDS ALALALSPVVKALVDPDAAMKDIRNLDLSISFSEWFLSKGGTRASIQRMDPVAYALGFIDCDNISARCMILTFSLFATKTEASLLRMLKGSFDPVFLSGPI 286

CmZDS RKYITDRGGRFHLRWGCREVLYDKFADGETYIISGLAMSKATNKKIVKADAYVAACDVPGIRKRLIPSQWREWEFFDNIYKLGVPVVTVQLRYNGWVTELQ 397
CsZDS RKYITDRGGRFHLRWGCREVLYDKFADGETYIISGLAMSKATNKKIVKADAYVAACDVPGIRKRLIPSQWREWEFFDNIYKLGVPVVTVQLRYNGWVTELQ 397
CmoZDS RKYITDRGGRFHLRWGCREVLYDKFADGETYIISGLAMSKATNKKIVKADAYVAACDVPGIRKRLIPSQWREWEFFDNIYKLGVPVVTVQLRYNGWVTELQ 394
VvZDS1 RKYITDRGGRFHLRWGCREVLYDKFADGETYIISGLAMSKATNKKIVKADAYVAACDVPGIRKRLIPSQWREWEFFDNIYKLGVPVVTVQLRYNGWVTELQ 400
CuZDS RKYITDRGGRFHLRWGCREVLYDKFADGETYIISGLAMSKATNKKIVKADAYVAACDVPGIRKRLIPSQWREWEFFDNIYKLGVPVVTVQLRYNGWVTELQ 386

CmZDS DLERSRQLRQAVGLDNLNLYTPDADFSCFADLALTSPEYIIEGQGSLLQCVLTPGDPYMPLLNDEIIRVAKQVILFLFPSSQGLEVIWSSVVKIGQSLYR 497
CsZDS DLERSRQLRQAVGLDNLNLYTPDADFSCFADLALTSPEYIIEGQGSLLQCVLTPGDPYMPLLNDEIIRVAKQVILFLFPSSQGLEVIWSSVVKIGQSLYR 497
CmoZDS DLERSRQLRQAVGLDNLNLYTPDADFSCFADLALTSPEYIIEGQGSLLQCVLTPGDPYMPLLNDEIIRVAKQVILFLFPSSQGLEVIWSSVVKIGQSLYR 494
VvZDS1 DLERSRQLRQAVGLDNLNLYTPDADFSCFADLALTSPEYIIEGQGSLLQCVLTPGDPYMPLLNDEIIRVAKQVILFLFPSSQGLEVIWSSVVKIGQSLYR 500
CuZDS DLERSRQLRQAVGLDNLNLYTPDADFSCFADLALTSPEYIIEGQGSLLQCVLTPGDPYMPLLNDEIIRVAKQVILFLFPSSQGLEVIWSSVVKIGQSLYR 486

CmZDS EAPGKDFPRDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRCSAYICDAGEELMMLREKIDAFES----ETAKGS--DELSLV 576
CsZDS EAPGKDFPRDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRCSAYICDAGEELMMLREKIDAFES----ETAKGS--DELSLV 576
CmoZDS EAPGKDFPRDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRCSAYICDAGEELMMLREKIDAFES----ETAKGS--DELSLV 573
VvZDS1 EAPGKDFPRDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRCSAYICDAGEELMMLREKIDAFES----ETAKGS--DELSLV 583
CuZDS EAPGKDFPRDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRCSAYICDAGEELMMLREKIDAFES----ETAKGS--DELSLV 570

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Figure S1. Multiple alignments of the amino acid sequences of CmZDS with other ZDSs. Identical residues are indicated by a black background, and similar residues are shaded with a gray background. The solid underline indicates the dinucleotide-binding domain, and the dotted underline indicates the carotenoid-binding domain. CsZDS, *Cucumis sativus* (XM_004142474); CmoZDS, *Cucurbita moschata* (JN253179); VvZDS1, *Vitis vinifera* (JQ319636); CuZDS1, *Citrus unshiu* (AB072343).

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CmLCYE  MEQCGLAARNFAAMAASNTSNTASIGTRRLQLLQRTESRQFRLRRPSVLAM-----ASAGSESCIAVREGFADIEDYIKGGSELLFVQMCKKMEMQS 95
CsLCYE  MEQCGLTARNFAAMASNTSNTASIGTRRLQLLQRTESLQFRLRRPSVFM-----ASAGSESCIAVREGFADIEDYIKGGSELLFVQMCKKMEMQS 95
CsaLCYE MEQCG--ARNFAAMAVS--TCTHWRYRKRRCNTLTVIHRHSSYTSSTRVRS-----SSAGSESCVAFREGFADEEDYIKAGGSELLFVQMCKKMEMQS 93
GmLCYE  MECVA--ARNLAAMAFV--VSPHSRLRFRFRKFRRRRTASSSSCGGRVRCCLKVBAFAGSESCVATFEDFADEEDYIKAGGSELLFVQMCKKMEMQS 97
VvLCYE  MECIC--AFNFAAMAVS--TSAPWRFRFRFRMFPENACFNHSDCYLPSVRFV-----ASAGSESCVAVREGFADEEDYIKAGGSELLFVQMCKKMEMQS 92

CmLCYE  KLADLPPISIGNGLDLVVIGCGPAGLALAAESAPLGLKVLIGPDLPTNNGVWDEDFKDLGEGCIEHVMDTIVYLDDKDFVLLIGRAYGRVSR 193
CsLCYE  KLADLPPISVNGVLDLVVIGCGPAGLALAAESAPLGLKVLIGPDLPTNNGVWDEDFKDLGEGCIEHVMDTIVYLDDKDFVLLIGRAYGRVSR 193
CsaLCYE KLADKLPPIVGNLTLDLVVIGCGPAGLALAAESAKLGLSVGLIGPDLPTNNGVWDEDFDLGEGCIEHVMDTIVYLDNDFVLLIGPCFIRGRVSR 193
GmLCYE  KLADKLP--FICDLDLVVIGCGPAGLALAAESAKLGLKVLIGPDLPTNNGVWDEDFKDLGEGCIEHVMDTIVYLDNDFVLLIGRAYGRVSR 193
VvLCYE  KLADKLPQISTEFGHLDLVVIGCGPAGLALAAESAKLGLSVGLIGPDLPTNNGVWDEDFKDLGEGCIEHVMDTIVYLDNDFVLLIGRAYGRVSR 190

CmLCYE  HLLHEELLKRCIKSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEVNNPYDPSLMVFMFYDRD 292
CsLCYE  HLLHEELLKRCIKSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEVNNPYDPSLMVFMFYDRD 292
CsaLCYE HLLHEELLKRCVSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEVNNPYDPSLMVFMFYDRD 292
GmLCYE  HLLHEELLKRCVSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEVNNPYDPSLMVFMFYDRD 292
VvLCYE  HLLHEELLKRCVSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEVNNPYDPSLMVFMFYDRD 290

CmLCYE  YARHENSLEAQYPTFLYAMPMSPTKVFEEETCLASKDAMPFDLLKKKLSRLDTMGIRIVKTYEEEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
CsLCYE  YARQENSLEAQYPTFLYAMPMSPTKVFEEETCLASKDAMPFDLLKKKLSRLDTMGIRIVKTYEEEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
CsaLCYE YARFRVQCLEAQYPTFLYAMPMSPTKVFEEETCLASKDAMPFDLLKKKLSRLDTMGIRIVKTYEEEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
GmLCYE  YARQNVQCLEAQYPTFLYAMPMSPTKVFEEETCLASKDAMPFDLLKKKLSRLDTMGIRIVKTYEEEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
VvLCYE  HARQVQCLEAQYPTFLYAMPMSPTKVFEEETCLASKDAMPFDLLKKKLSRLDTMGIRIVKTYEEEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 390

CmLCYE  SVVRSLSLEAPKYASVIAPKILKQGHSEDLRSWSTENISMIAWNTLWPEERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQFGLGTLSSAD 492
CsLCYE  SVVRSLSLEAPKYASVIAPKILKQGHSEDLRSWSTENISMIAWNTLWPEERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQFGLGTLSSAD 492
CsaLCYE SVVRSLSLEAPKYASVIAPKILKQGHSEDLRSWSTENISMIAWNTLWPEERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQFGLGTLSSAD 492
GmLCYE  SVVRSLSLEAPKYASVIAPKILKQGHSEDLRSWSTENISMIAWNTLWPEERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQFGLGTLSSAD 492
VvLCYE  SVVRSLSLEAPKYASVIAPKILKQGHSEDLRSWSTENISMIAWNTLWPEERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQFGLGTLSSAD 490

CmLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTA 533
CsLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTA 533
CsaLCYE LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTA 532
GmLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTA 532
VvLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTA 530

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Figure S2. Multiple alignments of the amino acid sequences of CmLCYE with other LCYEs. Identical residues are indicated by a black background, and similar residues are shaded with a gray background. The solid underline indicates a dinucleotide binding motif, and the dotted underlines indicate two cyclase motifs. CsLCYE, *Cucumis sativus* (XM_004141124); CsaLCYE, *Camellia sinensis* var. *assamica* (HM536196); GmLCYE, *Glycine max* (XM_003533727); VvLCYE, *Vitis vinifera* (NM_001281164).

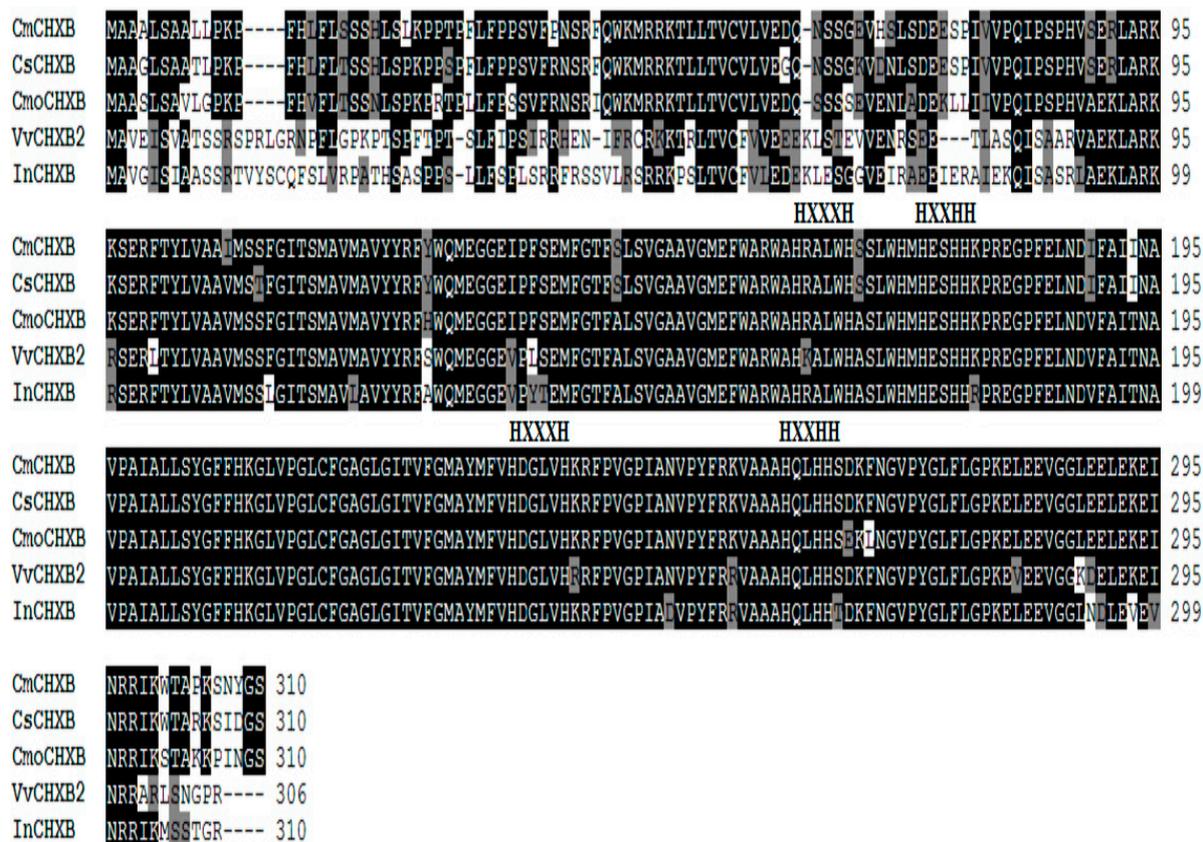


Figure S3. Multiple alignments of the amino acid sequences of CmCHXB with other CHXBs. Identical residues are indicated by a black background, and similar residues are shaded with a gray background. HXXXH and HXXHH, where X encodes for any amino acid, represent 4 conservatively spaced histidine motifs. CsCHXB, *Cucumis sativus* (XM_004140710); CmoCHXB, *Cucurbita moschata* (JN253180); VvCHXB2, *Vitis vinifera* (XM_002273545); InCHXB, *Ipomoea nil* (AB499058).

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CmCHXE -----1
CsCHXE -----60
VvCHXE -MPSLMSLSSEFALLTPTFTFNFKPTTLEINPSLPY---LSITCSSDNNPKPTRSSSWVSPDWLTSLSRSLTMCQDDSGIPVATAKLDVSELLGGALFLP 95
FvCHXE MLCSLHSFSSLTLLPSESS---PKPTTFHHSFSI---RSTNKDLENNSKPTSTSWVSPDWLTSLSRSLTTHSKNDDSGIPVATAKLDVSELLGGALFLP 94
DcCHXE --MYPHHSISLSLPLPIRQNLKSHHPEFHQPPHSLPLSIKSSLDLKKPKNSGQSWVSPDWLTSLSRSLTTHSKNDDSNIPVATAKLDVSELLGGALFLP 97

CmCHXE -----1
CsCHXE LFKWMNRYGPIYRLAAGPRNFVVVSDPALAKHVLRNRYGKYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVP SLHKKYLSVIIVDRVFCKCAERLVEKL 160
VvCHXE LFKWMNRYGPIYRLAAGPRNFVVVSDPALAKHVLRNRYGKYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVP SLHKKYLSVIIVDRVFCKCAERLVEKL 195
FvCHXE LFKWMNRYGPIYRLAAGPRNFVVVSDPALAKHVLRNRYGKYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVP SLHKKYLSVIIVDRVFCKCAERLVEKL 194
DcCHXE LFKWMNRYGPIYRLAAGPRNFVVVSDPALAKHVLRNRYGKYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVP SLHKKYLSVIIVDRVFCKCAERLVEKL 197

CmCHXE -----1
CsCHXE EKDALNNSVNMEERFSQTLTDVIGLSVFNYSFDSLSTDSVPIDAVYTALKEAEARSTDILPYWKTALCKIIPRQIKAEAVTVIRKKTVEELIAKCKE 260
VvCHXE RTDALNGSAVNMEERFSQTLTDVIGLSVFNYNFDSLTDSPVIDAVYTALKEAEARSTDILPYWKTALCKIIPRQIKAEAVTVIRKKTVEELIAKCKE 295
FvCHXE QADALSCAVNMEERFSQTLTDVIGLSVFNYNFDSLTDSPVIDAVYTALKEAEARSTDILPYWKTALCKIIPRQIKAEAVTVIRKKTVEELIAKCKE 294
DcCHXE EISALNGSAVNMEERFSQTLTDVIGLSVFNYNFDSLTDSPVIDAVYTALKEAEARSTDILPYWKTALCKIIPRQIKAEAVTVIRKKTVEELIAKCKE 297

CmCHXE -----1
CsCHXE VEEGERINDEEYVNDADPSILRFLASREEVSSQLRDDL SMLVAGHETTGSVLTWTLTYLLSKNSSSLKACNEVDRVLQGRSBSYEDIKLKLTRC 360
VvCHXE VEEGERINDEEYVNDSDPSILRFLASREEVSSQLRDDL SMLVAGHETTGSVLTWTLTYLLSKNSSSLKACNEVDRVLQGRSBSYEDIKLKLTRC 395
FvCHXE VEEGERINDEEYVNESDPSILRFLASREEVSSQLRDDL SMLVAGHETTGSVLTWTLTYLLSKNSSSLKACNEVDRVLQGRSBSYEDIKLKLTRC 394
DcCHXE VEEGERINDEEYVNEADPSILRFLASREEVSSQLRDDL SMLVAGHETTGSVLTWTLTYLLSKNSSSLKACNEVDRVLQGRSBSYEDIKLKLTRC 397

CmCHXE ---MRLYPHPVPLIRRAQVADLPGNYKVNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVNPESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 96
CsCHXE ILESMLRYPHPVPLIRRAQVADLPGNYKVNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVNPESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 460
VvCHXE INESMLRYPHPVPLIRRAQVADLPGNYKVNAGQDIMISVYNIHRSQVWERAEHSPERFDLEGPVNPESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 495
FvCHXE IMESTRLYPHPVPLIRRAQVADLPGNYKVNAGQDIMISVYNIHRSQVWERAEHSPERFDLEGPVNPESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 494
DcCHXE INESMLRYPHPVPLIRRAQVADLPGNYKVNAGQDIMISVYNIHRSQVWERAEHSPERFDLEGPVNPESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 497

CmCHXE LAIFLQHLNFELVPCNTICMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR 148
CsCHXE LAIFLQHLNFELVPCNTICMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR 512
VvCHXE LAIFVQHLNFELVPCNTISMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR-- 546
FvCHXE LAIFVQHLNFELVPCNTISMTTGATIHTTNGLYMKLSQRCAKSVFASSII-- 544
DcCHXE LAIFLQHLNFELVPCNTINMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR-- 548

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Figure S4. Multiple alignments of the amino acid sequences of CmCHXE with other CHXEs. Identical residues are indicated by a black background, and similar residues are shaded with a gray background. CsCHXE, *Cucumis sativus* (XM_004156280); VvCHXE, *Vitis vinifera* (XM_002264979); FvCHXE, *Fragaria vesca* (XM_004306122); DcCHXE, *Daucus carota* (DQ192196).

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CmZEP MALTRFHNPFNLSSSLSRTCFPVPAFREYLVEISPCQRIGCNFEGGKSACGRKKVYQVKAAVAEPAPAEAGAEISRSLSLPTKNVRILVAGGGIGGLVFA 100
CsZEP MALTRFHNPFNLSSSLSRTCFPVPAFREYLVEISPCQRIGCNFEGGKSACGRKKVYQVKAAVAEPAPAEAGAEISRSLSLPTKNVRILVAGGGIGGLVFA 100
ClZEP MALTRFHNPFNLSSSLSRTCFPVPAFREYLVEISPCQRIGCNFEGGKSACGRKKVYQVKAAVAEPAPAEAGAEISRSLSLPTKNVRILVAGGGIGGLVFA 100
CmoZEP NVLTRFHNPFNLSSSLSRTCFPVPAFREYLVEISPCQRIGCNFEGGKSACGRKKVYQVKAAVAEPAPAEAGAEISRSLSLPTKNVRILVAGGGIGGLVFA 100
PaZEP MASLTFVNSNLSAAVFSRTEFFLHINKDFPLEFESPCVHTDYLHRSRSTRSGQKFCITVRAIVASPTTEVPSAP----ASTQPKLRILVAGGGIGGLVFA 96

CmZEP LAARRKGFDDVVVFEKDISAIRGEGQYRGPVQIQSNALAALEAIDLVAEEVMRVGCGITGDRINGLVDGVSGNWIYKFDFTTTPAERGLPVTRVISRMLQ 200
CsZEP LAARRKGFDDVVVFEKDISAIRGEGQYRGPVQIQSNALAALEAIDLVAEEVMRVGCGITGDRINGLVDGVSGNWIYKFDFTTTPAERGLPVTRVISRMLQ 200
ClZEP LAARRKGFDDVVVFEKDISAIRGEGQYRGPVQIQSNALAALEAIDLVAEEVMRVGCGITGDRINGLVDGVSGNWIYKFDFTTTPAERGLPVTRVISRMLQ 200
CmoZEP LAARRKGFDDVVVFEKDISAIRGEGQYRGPVQIQSNALAALEAIDLVAEEVMRVGCGITGDRINGLVDGVSGNWIYKFDFTTTPAERGLPVTRVISRMLQ 200
PaZEP LAARRKGFDDVVVFEKDISAIRGEGQYRGPVQIQSNALAALEAIDLVAEEVMRVGCGITGDRINGLVDGVSGNWIYKFDFTTTPAERGLPVTRVISRMLQ 196

CmZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLLENGCQHEGDLVLDGDIWISKVRKKNLFGHSEAVVSGYTCYTGIADFIPADIEVGYRVFLGHKQYFVSS 300
CsZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLLENGCQHEGDLVLDGDIWISKVRKKNLFGHSEAVVSGYTCYTGIADFIPADIEVGYRVFLGHKQYFVSS 300
ClZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLLENGCQHEGDLVLDGDIWISKVRKKNLFGHSEAVVSGYTCYTGIADFIPADIEVGYRVFLGHKQYFVSS 300
CmoZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLLENGCQHEGDLVLDGDIWISKVRKKNLFGHSEAVVSGYTCYTGIADFIPADIEVGYRVFLGHKQYFVSS 300
PaZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLLENGCQHEGDLVLDGDIWISKVRKKNLFGHSEAVVSGYTCYTGIADFIPADIEVGYRVFLGHKQYFVSS 296

CmZEP DVGAGKMCQWYAFHKEPPGGTADAPNGKKERLFKIFEGWCDNVIDLLEATDEDSVLRDDIYDRTPIFTWGKGRVTLTLLGDSVHAMQPNMGQGGCMAIEDGYQL 400
CsZEP DVGAGKMCQWYAFHKEPPGGTADAPNGKKERLFKIFEGWCDNVIDLLEATDEDSVLRDDIYDRTPIFTWGKGRVTLTLLGDSVHAMQPNMGQGGCMAIEDGYQL 400
ClZEP DVGAGKMCQWYAFHKEPPGGTADAPNGKKERLFKIFEGWCDNVIDLLEATDEDSVLRDDIYDRTPIFTWGKGRVTLTLLGDSVHAMQPNMGQGGCMAIEDGYQL 400
CmoZEP DVGAGKMCQWYAFHKEPPGGTADAPNGKKERLFKIFEGWCDNVIDLLEATDEDSVLRDDIYDRTPIFTWGKGRVTLTLLGDSVHAMQPNMGQGGCMAIEDGYQL 400
PaZEP DVGAGKMCQWYAFHKEPPGGTADAPNGKKERLFKIFEGWCDNVIDLLEATDEDSVLRDDIYDRTPIFTWGKGRVTLTLLGDSVHAMQPNMGQGGCMAIEDGYQL 396

CmZEP ALELDKAWNESVRSVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVGLGPLSFLTQFRIPHPGTGGRFFIDLAMPLMLNWLGGNSS 500
CsZEP ALELDKAWNESVRSVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVGLGPLSFLTQFRIPHPGTGGRFFIDLAMPLMLNWLGGNSS 500
ClZEP ALELDKAWNESVRSVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVGLGPLSFLTQFRIPHPGTGGRFFIDLAMPLMLNWLGGNSS 500
CmoZEP ALELDKAWNESVRSVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVGLGPLSFLTQFRIPHPGTGGRFFIDLAMPLMLNWLGGNSS 500
PaZEP ALELDKAWNESVRSVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVGLGPLSFLTQFRIPHPGTGGRFFIDLAMPLMLNWLGGNSS 496

CmZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVCEVDSGLSIAIPLPQVSEKHARIVYKDGAFFL 600
CsZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVCEVDSGLSIAIPLPQVSEKHARIVYKDGAFFL 600
ClZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVCEVDSGLSIAIPLPQVSEKHARIVYKDGAFFL 600
CmoZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVCEVDSGLSIAIPLPQVSEKHARIVYKDGAFFL 600
PaZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVCEVDSGLSIAIPLPQVSEKHARIVYKDGAFFL 596

CmZEP TDLRSEHGTWLSDEHGRRYRVPNFPVRFHQSDLIEFGSDKKAIFRVKVISSVE--NDREKVMNS 665
CsZEP TDLRSEHGTWLSDEHGRRYRVPNFPVRFHQSDLIEFGSDKKAIFRVKVISSVE--NDREKVMNS 665
ClZEP TDLRSEHGTWLSDEHGRRYRVPNFPVRFHQSDLIEFGSDKKAIFRVKVISSVE--YDREKVMNS 665
CmoZEP TDLRSEHGTWLSDEHGRRYRVPNFPVRFHQSDLIEFGSDKKAIFRVKVISSVE--NDREKVMNS 665
PaZEP TDLRSEHGTWLSDEHGRRYRVPNFPVRFHQSDLIEFGSDKKAIFRVKVISSVE--NDREKVMNS 661

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Figure S5. Multiple alignments of the amino acid sequences of CmZEP with other ZEPs. Identical residues are indicated by a black background, and similar residues are shaded with a gray background. The solid underlines indicate the short motifs typical of the lipocalin family of proteins, and the dotted underline indicates the FHA domain. CsZEP, *Cucumis sativus* (XM_004163228); ClZEP, *Citrullus lanatus* (HM107775); CmoZEP, *Cucurbita moschata* (JN581943); PaZEP, *Prunus armeniaca* (AF159948).