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CmZDS MASGILSFV--SFSGKH--NCHDFRLPARH--SVVLKGCQFLVSSLLRDVSDMSVNAKGLFPPEPERYRGPKLKVAIIAGLAGMSTAVELLDDQGEV 97
CsZDS MASGILSFV--SFSGKH--NCHDFRLPARH--SVVLKGCQFLVSSLLRDVSDMSVNAKGLFPPEPERYRGPKLKVAIIAGLAGMSTAVELLDDQGEV 97
CmoZDS MASGILSFV--SFSGKH--NCHDFRLPARH--SVVLKGCQFLVSSLLRDVSDMSVNAKGLFPPEPERYRGPKLKVAIIAGLAGMSTAVELLDDQGEV 94
VvZDS1 MESSILFEAAGSRAGFXGTVGLFLSGGRRPMPSCLLKGQRLVSRSSLLSDVSDMSVNAKGLFPPEPERYRGPKLKVAIIAGLAGMSTAVELLDDQGEV 100
CuZDS MESSILFEA--SILG-----VSWSR--VQPRCFRFGVRSLLANVSDMSVNAKGLFPPEPERYRGPKLKVAIIAGLAGMSTAVELLDDQGEV 86

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

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

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

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

CmZDS EAPGKDPPRPDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRQASAYICDAGEELMMLREKICDESS---ETAKSS--DELSLV 576
CsZDS EAPGKDPPRPDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRQASAYICDAGEELMMLREKICDESS---ETAKSS--DELSLV 576
CmoZDS EAPGKDPPRPDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRQASAYICDAGEELMMLREKICDESS---ETAKSS--DELSLV 573
VvZDS1 EAPGKDPPRPDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRQASAYICDAGEELMMLREKICDESS---ETAKSS--DELSLV 583
CuZDS EAPGKDPPRPDQRTPIKNFFLAGSYTKQDYIDSMEGATLSGRQASAYICDAGEELMMLREKICDESS---ETAKSS--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  MEQCGLAARNFAAMASNTSNTASTGTRRLQILCRTESRFRLRRPSVLAM-----ASAGSESCIAVEEGFADIEDYIKGGSELLFVQMCKNTMEMQS 95
CsLCYE  MEQCGLTARNFAAMASNTSNTASTGTRRLQILCRTESLQFRLRRPSVFM-----ASAGSESCIAVEEGFADIEDYIKGGSELLFVQMCKNTMEMQS 95
CsaLCYE MEQCG--ARNFAAMAVS--TCPIWRYRKRRQNTLTRVIHHSSYTSSTLRVRS-----SAGSESCVAFEEGFADEEDYIKAGGSELLFVQMCKNTMEMQS 93
GmLCYE  MECVA--ARNLAAMAFV--VSPISRLRIRRRKIRRRRTASSSSCGGRGVRLKVEAFAGSESCVATTEDEFADEEDYIKAGGSELLFVQMCKNTMEMQS 97
VvLCYE  MECIC--AFNFAAMAVS--TSAPWRERRRRRMPENACFNHSDCYLPSVRVR-----ASAGSESCVVEEGFADEEDYIKAGGSELLFVQMCKNTMEMQS 92

CmLCYE  KLADLPPISIGNGLDLVVIGCGPAGLALAAESAPLGLKVGLIGPDLPTNNYGVWEDEFKDLGLEGCIEHVMDTIVYLDKDK--PVLIG--RAYGRVSR 193
CsLCYE  KLADLPPISVGNGLDLVVIGCGPAGLALAAESAPLGLKVGLIGPDLPTNNYGVWEDEFKDLGLEGCIEHVMDTIVYLDKDK--PVLIG--RAYGRVSR 193
CsaLCYE KLADKLPPISVGNGLDLVVIGCGPAGLALAAESAKLGLSVGLIGPDLPTNNYGVWEDEFKDLGLEGCIEHVMDTIVYLDKDK--PVLIG--RAYGRVSR 193
GmLCYE  KLADKLPPISVGNGLDLVVIGCGPAGLALAAESAKLGLSVGLIGPDLPTNNYGVWEDEFKDLGLEGCIEHVMDTIVYLDKDK--PVLIG--RAYGRVSR 193
VvLCYE  KLADKLPPISVGNGLDLVVIGCGPAGLALAAESAKLGLSVGLIGPDLPTNNYGVWEDEFKDLGLEGCIEHVMDTIVYLDKDK--PVLIG--RAYGRVSR 190

CmLCYE  HLLHEELLKRCIKSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEENNPYDPSLMVFM DYRD 292
CsLCYE  HLLHEELLKRCIKSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEENNPYDPSLMVFM DYRD 292
CsaLCYE HLLHEELLKRCVSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEENNPYDPSLMVFM DYRD 292
GmLCYE  HLLHEELLKRCVSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEENNPYDPSLMVFM DYRD 292
VvLCYE  HLLHEELLKRCVSGVSYLNSRVNSIVETTSNGHSLVCEEDIVPCRLATVASGAASGKLLQYEVGGPK--VSVQTAYGVEVEENNPYDPSLMVFM DYRD 290

CmLCYE  YARHENSLEAQYPTFLYAMPMSPTKVFFETCLASKEAMPFDLLKKKLSRLRTMGIRIRVKTYYYEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
CsLCYE  YARHENSLEAQYPTFLYAMPMSPTKVFFETCLASKEAMPFDLLKKKLSRLRTMGIRIRVKTYYYEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
CsaLCYE YARHENSLEAQYPTFLYAMPMSPTKVFFETCLASKEAMPFDLLKKKLSRLRTMGIRIRVKTYYYEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
GmLCYE  YARHENSLEAQYPTFLYAMPMSPTKVFFETCLASKEAMPFDLLKKKLSRLRTMGIRIRVKTYYYEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 392
VvLCYE  YARHENSLEAQYPTFLYAMPMSPTKVFFETCLASKEAMPFDLLKKKLSRLRTMGIRIRVKTYYYEWSYIPVGGSLPNTQKNLAFGAAASMVHPATGY 390

CmLCYE  SVVRSLSAPKYASVIAKILKQGHSEKLSRSTENISMCAWNTLWPQERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQGLGSTLSSAD 492
CsLCYE  SVVRSLSAPKYASVIAKILKQGHSEKLSRSTENISMCAWNTLWPQERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQGLGSTLSSAD 492
CsaLCYE SVVRSLSAPKYASVIAKILKQGHSEKLSRSTENISMCAWNTLWPQERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQGLGSTLSSAD 492
GmLCYE  SVVRSLSAPKYASVIAKILKQGHSEKLSRSTENISMCAWNTLWPQERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQGLGSTLSSAD 492
VvLCYE  SVVRSLSAPKYASVIAKILKQGHSEKLSRSTENISMCAWNTLWPQERKRQRAFFLFGALILQLDIEGIRTFRTFFCLPDWMWQGLGSTLSSAD 490

CmLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTIA 533
CsLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTIA 533
CsaLCYE LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTIA 532
GmLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTIA 532
VvLCYE  LALFAFYMFVIAPNLRMCLVKHLLSDPTGATMIRTYLTIA 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).

CmCHXB	MAAPLSAALLPKP----FHIFLSSSLSPKPPFELFPSPVFNSRFQWKMRRKTLLTVCVLVEDQ--SSGFWHSLDDESEFIIVPQIPSPHVSERLARK	95
CsCHXB	MAAGLSAATLPK----FHIFLSSSLSPKPPFELFPSPVFNSRFQWKMRRKTLLTVCVLVEDQ--SSGFWHSLDDESEFIIVPQIPSPHVSERLARK	95
CmoCHXB	MAASLSAVLGPKP----FHIFLSSSLSPKPPFELFPSPVFNSRFQWKMRRKTLLTVCVLVEDQ--SSSEVENLADKLLIIVPQIPSPHVAEKLARK	95
VvCHXB2	MAVENSVATSSRSPLGRNEFLGPKPTSEFTPT-SLEIPSTRHEN-IFRCRKTRLTVCVVEEKLSTEWENRSEB---TLASQISARVAEKLARK	95
InCHXB	MAVGLSIAASSRTVYSCQFSLVRPATHSAPPS-ILFSLSPFRSSVLSRRKPSLTVCVFIIEDEKLESGGVEIRAEIERALEKQISASRTAEKLARK	99
	HXXXH HXXHH	
CmCHXB	KSERFTYLVAAMSSFGITSMAMVAVYYRFWQMEGGEIPFSEMFGTFSLVGAAVGMFWARWAHRLWHSLSLWHMHESHHPREGPFELNDVFAITNA	195
CsCHXB	KSERFTYLVAAMVMSFGITSMAMVAVYYRFWQMEGGEIPFSEMFGTFSLVGAAVGMFWARWAHRLWHSLSLWHMHESHHPREGPFELNDVFAITNA	195
CmoCHXB	KSERFTYLVAAMSSFGITSMAMVAVYYRFWQMEGGEIPFSEMFGTFALVGAAVGMFWARWAHRLWHSLSLWHMHESHHPREGPFELNDVFAITNA	195
VvCHXB2	KSERFTYLVAAMSSFGITSMAMVAVYYRFWQMEGGEIPFSEMFGTFALVGAAVGMFWARWAHRLWHSLSLWHMHESHHPREGPFELNDVFAITNA	195
InCHXB	KSERFTYLVAAMSSLGITSMAMVAVYYRFWQMEGGEIPFSEMFGTFALVGAAVGMFWARWAHRLWHSLSLWHMHESHHPREGPFELNDVFAITNA	199
	HXXXH HXXHH	
CmCHXB	VPAIALLSYGFFHKGLVPGLCFAGLGITVFGMAYMFVHDGLVHKRFPVGPPIANVPYFRKVAHAHQHSDKFNGVPYGLFLGPKELEEVGGLLEELEKEI	295
CsCHXB	VPAIALLSYGFFHKGLVPGLCFAGLGITVFGMAYMFVHDGLVHKRFPVGPPIANVPYFRKVAHAHQHSDKFNGVPYGLFLGPKELEEVGGLLEELEKEI	295
CmoCHXB	VPAIALLSYGFFHKGLVPGLCFAGLGITVFGMAYMFVHDGLVHKRFPVGPPIANVPYFRKVAHAHQHSDKFNGVPYGLFLGPKELEEVGGLLEELEKEI	295
VvCHXB2	VPAIALLSYGFFHKGLVPGLCFAGLGITVFGMAYMFVHDGLVHKRFPVGPPIANVPYFRKVAHAHQHSDKFNGVPYGLFLGPKELEEVGGLLEELEKEI	295
InCHXB	VPAIALLSYGFFHKGLVPGLCFAGLGITVFGMAYMFVHDGLVHKRFPVGPPIANVPYFRKVAHAHQHSDKFNGVPYGLFLGPKELEEVGGINLEVEI	299
CmCHXB	NRRIKWTARKSNYGS	310
CsCHXB	NRRIKWTARKSIIGS	310
CmoCHXB	NRRIKWTARKPINGS	310
VvCHXB2	NRRAISNGPR----	306
InCHXB	NRRIKMSSTGR----	310

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 -MPSLMSLSFALLTETFTFNFKPTTLFNPSPFY---LSITCSSDNNPKPTRSSSWVSPDWLTSLSRSLTMCQ-DDSGIPNATAKLDVSELLGGALFLP 95
FvCHXE MLCSLHSFSSLTLLPSESS---PKPTTFHFSFSI---RSTNKDPENNSKPTSTSWVSPDWLTSLSRSLTTSKNDSDGIPNATAKLDVSELLGGALFLP 94
DcCHXE --MPYHSISLSLPLPEIRQNLSKHHPEFHQPPHSLPLSIKSSLDIKPPKSNQGSWVSPDWLTSLSRSLTTSK--DDSNIPNATAKLDVSELLGGALFLP 97

CmCHXE ----- 1
CsCHXE LFKWMNMYGPIYRLAAGPRNFVVSDPAIAKHVLRNYGYAKGLVSEVSEFLFGSGFAIAEGPLWTRRRRAVVPSLHKKYL SVIVDRVFCKCAMLVEKL 160
VvCHXE LFKWMNMYGPIYRLAAGPRNFVVSDPAIAKHVLRNYGYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVPSLHKKYL SVIVDRVFCKCAMLVEKL 195
FvCHXE LFKWMNMYGPIYRLAAGPRNFVVSDPAIAKHVLRNYGYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVPSLHKKYL SVIVDRVFCKCAMLVEKL 194
DcCHXE LFKWMNMYGPIYRLAAGPRNFVVSDPAIAKHVLRNYGYAKGLVAEVSEFLFGSGFAIAEGPLWTRRRRAVVPSLHKKYL SVIVDRVFCKCAMLVEKL 197

CmCHXE ----- 1
CsCHXE RKDALNNSVNMEEFSQLTLDVIGLSVFNYFDSLSLTDSPVIDAVYTALKEAEARSTDILPYWKIALCKIIPRQIKAEAVTVIRKTVVEELIAKCKEI 260
VvCHXE RTDALNGSAVNMEEFSQLTLDVIGLSVFNYNFDLSLTADSPVIDAVYTALKEAEARSTDILPYWKIALCKIIPRQIKAEAVTVIRKTVVEELIAKCKEI 295
FvCHXE QADALNGSAVNMEEFSQLTLDVIGLSVFNYNFDLSLTADSPVIDAVYTALKEAEARSTDILPYWKIALCKIIPRQIKAEAVTVIRKTVVEELIAKCKEI 294
DcCHXE RISALNGSAVNMEEFSQLTLDVIGLSVFNYNFDLSLTADSPVIDAVYTALKEAEARSTDILPYWKIALCKIIPRQIKAEAVTVIRKTVVEELIAKCKEI 297

CmCHXE ----- 1
CsCHXE VEREGERISEEYVNEADPSILRFLASREEVSSQLRDDLLSMLVAGHETTGSGVLTWTLYLLSKHSSSLKACAEVDRVLQGRFPSYEDIKELKELTRC 360
VvCHXE VEREGERISEEYVNEADPSILRFLASREEVSSQLRDDLLSMLVAGHETTGSGVLTWTLYLLSKHSSSLKACAEVDRVLQGRFPSYEDIKELKELTRC 395
FvCHXE VEREGERISEEYVNEADPSILRFLASREEVSSQLRDDLLSMLVAGHETTGSGVLTWTLYLLSKHSSSLKACAEVDRVLQGRFPSYEDIKELKELTRC 394
DcCHXE VEREGERISEEYVNEADPSILRFLASREEVSSQLRDDLLSMLVAGHETTGSGVLTWTLYLLSKHSSSLKACAEVDRVLQGRFPSYEDIKELKELTRC 397

CmCHXE ---MRLYPHPVLIIRRAQVADLPGNKYKNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVPNESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 96
CsCHXE ILESMLRYPHPVLIIRRAQVADLPGNKYKNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVPNESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 460
VvCHXE INESMLRYPHPVLIIRRAQVADLPGNKYKNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVPNESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 495
FvCHXE IMESTRLYPHPVLIIRRAQVADLPGNKYKNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVPNESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 494
DcCHXE INESMLRYPHPVLIIRRAQVADLPGNKYKNAGQDIMISVYNIHRSQVWECAEEFIPERFDLEGPVPNESNTDFRFIPFSGGPRKCVGDQFALLEAIVA 497

CmCHXE LAIFLQHLNFELVPDNIEMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR 148
CsCHXE LAIFLQHLNFELVPDNIEMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR 512
VvCHXE LAIFLQHLNFELVPDNIEMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR-- 546
FvCHXE LAIFLQHLNFELVPDNIEMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR-- 544
DcCHXE LAIFLQHLNFELVPDNIEMTTGATIHTTNGLYMKLSQRKLTPELVSSATSR-- 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).

CmZEP MALTRFHNPNLSSSLSRTCFPVPAPFREYLVEISPCQRIGCNFEGGKSACGRKKVTVQKAAVAEAPPAEGAAGEISRSPLTKNVRILVAGGGIGGLVFA 100
 CsZEP MALTRFHNPNLSSSLSRTCFPVPAPFREYLVEISPCQRIGCNFEGGKSACGRKKVTVQKAAVAEAPPAEGAAGEISRSPLTKNVRILVAGGGIGGLVFA 100
 ClZEP MALTRFHNPNLSSSLSRTCFPVPAPFREYLVEISPCQRIGCNFEGGKSACGRKKVTVQKAAVAEAPPAEGAAGEISRSPLTKNVRILVAGGGIGGLVFA 100
 CmoZEP NVNTRFHNPNLSSSLSRTCFPVPAPFREYLVEISPCQRIGCNFEGGKSACGRKKVTVQKAAVAEAPPAEGAAGEISRSPLTKNVRILVAGGGIGGLVFA 100
 PaZEP MASLTFNNSNLAAVFSSTFFETINKDEFLEISPSQTHTDYHLRSATRSGQKFCITFVRAIVASPTFVPSAP----ASTQPKILRILVAGGGIGGLVFA 96

CmZEP LAARKRGFDVVVFEDISAIRGEGQYRGPIQIQSNALAALAEIDLVAEEVMRVGCITGDRINGLVDGVSGNWIYKFDFTTPAERGLPVTRVISRMALQ 200
 CsZEP LAARKRGFDVVVFEDISAIRGEGQYRGPIQIQSNALAALAEIDLVAEEVMRVGCITGDRINGLVDGVSGNWIYKFDFTTPAERGLPVTRVISRMALQ 200
 ClZEP LAARKRGFDVVVFEDISAIRGEGQYRGPIQIQSNALAALAEIDLVAEEVMRVGCITGDRINGLVDGVSGNWIYKFDFTTPAERGLPVTRVISRMALQ 200
 CmoZEP LAARKRGFDVVVFEDISAIRGEGQYRGPIQIQSNALAALAEIDLVAEEVMRVGCITGDRINGLVDGVSGNWIYKFDFTTPAERGLPVTRVISRMALQ 200
 PaZEP LAARKRGFDVVVFEDISAIRGEGQYRGPIQIQSNALAALAEIDLVAEEVMRVGCITGDRINGLVDGVSGNWIYKFDFTTPAERGLPVTRVISRMALQ 196

CmZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLENGQCQHEGDLVAGDIWSKVRKNLFGHSEAVYSGYTCYTGIADFIPADIE TVGYRVFLGHKQYFVSS 300
 CsZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLENGQCQHEGDLVAGDIWSKVRKNLFGHSEAVYSGYTCYTGIADFIPADIE TVGYRVFLGHKQYFVSS 300
 ClZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLENGQCQHEGDLVAGDIWSKVRKNLFGHSEAVYSGYTCYTGIADFIPADIE TVGYRVFLGHKQYFVSS 300
 CmoZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLENGQCQHEGDLVAGDIWSKVRKNLFGHSEAVYSGYTCYTGIADFIPADIE TVGYRVFLGHKQYFVSS 300
 PaZEP QILARAVGDDVVIINDSNVDFEDNGEKVKVTLENGQCQHEGDLVAGDIWSKVRKNLFGHSEAVYSGYTCYTGIADFIPADIE TVGYRVFLGHKQYFVSS 296

CmZEP DVGAGKMCQWYAFHKEPPGGTDAPNGKKERLFKIFEGWCDNVLDLQATDEDSVLRDIYDRTPIFTWKGKRVTLTGDSVHAMQPNMGQGGCMAIEDGYQL 400
 CsZEP DVGAGKMCQWYAFHKEPPGGTDAPNGKKERLFKIFEGWCDNVLDLQATDEDSVLRDIYDRTPIFTWKGKRVTLTGDSVHAMQPNMGQGGCMAIEDGYQL 400
 ClZEP DVGAGKMCQWYAFHKEPPGGTDAPNGKKERLFKIFEGWCDNVLDLQATDEDSVLRDIYDRTPIFTWKGKRVTLTGDSVHAMQPNMGQGGCMAIEDGYQL 400
 CmoZEP DVGAGKMCQWYAFHKEPPGGTDAPNGKKERLFKIFEGWCDNVLDLQATDEDSVLRDIYDRTPIFTWKGKRVTLTGDSVHAMQPNMGQGGCMAIEDGYQL 400
 PaZEP DVGAGKMCQWYAFHKEPPGGTDAPNGKKERLFKIFEGWCDNVLDLQATDEDSVLRDIYDRTPIFTWKGKRVTLTGDSVHAMQPNMGQGGCMAIEDGYQL 396

CmZEP ALELDKAWNESVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVLGPLSFLTQFRIPHPGTFGGREFIDLAMPLMLNWLGNSS 500
 CsZEP ALELDKAWNESVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVLGPLSFLTQFRIPHPGTFGGREFIDLAMPLMLNWLGNSS 500
 ClZEP ALELDKAWNESVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVLGPLSFLTQFRIPHPGTFGGREFIDLAMPLMLNWLGNSS 500
 CmoZEP ALELDKAWNESVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVLGPLSFLTQFRIPHPGTFGGREFIDLAMPLMLNWLGNSS 500
 PaZEP ALELDKAWNESVSGSPIDIVSSLKSYESSRRIRVAVIHGMARMAALMASTYKAYLGVLGPLSFLTQFRIPHPGTFGGREFIDLAMPLMLNWLGNSS 496

CmZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVBCEVDSGLSIAIPLPQVSEKHARISYKDGAFFL 600
 CsZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVBCEVDSGLSIAIPLPQVSEKHARISYKDGAFFL 600
 ClZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVBCEVDSGLSIAIPLPQVSEKHARISYKDGAFFL 600
 CmoZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVBCEVDSGLSIAIPLPQVSEKHARISYKDGAFFL 600
 PaZEP KLEGRPPACRLSDKANDQLRKWFEDDDALERAINGDWFLLPQGGEASVSQPICLRDENQPCPLIGSVBCEVDSGLSIAIPLPQVSEKHARISYKDGAFFL 596

CmZEP TDLRSEHGTLSDHEGRRYRVPNFPVRFHQSDLIEFGSDKKAFRVKVRSSVE--NDREKVMNS 665
 CsZEP TDLRSEHGTLSDHEGRRYRVPNFPVRFHQSDLIEFGSDKKAFRVKVRSSVE--NDREKVMNS 665
 ClZEP TDLRSEHGTLSDHEGRRYRVPNFPVRFHQSDLIEFGSDKKAFRVKVRSSVE--NDREKVMNS 665
 CmoZEP TDLRSEHGTLSDHEGRRYRVPNFPVRFHQSDLIEFGSDKKAFRVKVRSSVE--NDREKVMNS 665
 PaZEP TDLRSEHGTLSDHEGRRYRVPNFPVRFHQSDLIEFGSDKKAFRVKVRSSVE--NDREKVMNS 661

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).