```
CvPEPC2_CAM_type      FHGRGGTVGRGGGPSHLAILSQPPDTIHGLLRVTVQGEVIEQSFGEEHLCFRTLQRFTAA 60
CsPEPC2_CAM_type      FHGRGGTVGRGGGPSHLAILSQPPDTIHGLLRVTVQGEVIEQSFGEEHLCFRTLQRFTAA 60
CrPEPC2_CAM_type      FHGRGGTVGRGGGPSHLAILSQPPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAA 60
ChPEPC2_CAM_type      FHGRGGTVGRGGGPSHLAILSQPPDTIRGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAA 60
CsPEPC3_CAM_type      FHGRGGTVGRGGGPSHLAILSQPPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAA 60
CaPEPC_CAM_type       FHGRGGTVGRGGGPSHLAILSQPPDTIHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAA 60
McPEPC1_CAM_type      FHGRGGTVGRGGGPTHLAILAQPAETIGGSLRVTIQGEVIEQSFGEQHLCFRTLQRYTAA 60
KbPEPC1_CAM_type      FHGRGGTVGRGGGPTHLAILSQPADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAA 60
KbPEPC2_CAM_type      FHGRGGTVGRGGGPTHLAILSQPADTIQGSLRVTIQGEVIERSFGEAQLCFKTLQRYTAA 60
Sa_Contig08207        FHGRGGTVGRGGGPTHLAILSQPPDTVQGSLRVTVQGEVIERSFGESQLCFRTLQRFTAA 60
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CvPEPC2_CAM_type      TLEHGMHPPVSPKPEWRA-LLDEMAVIATEEYRSIVFKEPQFVEYFRLATPELEYGRMNI 119
CsPEPC2_CAM_type      TLEHGMHPPVSPKPEWRA-LLDEMAVIATEEYRSIVFKEPQFVEYFRLATPELEYGRMNI 119
CrPEPC2_CAM_type      TLEHGMHPPVSPKPEWRA-LLDEMAVIATEEYRSIVFKEPKFVEYFRLATPELEYGRMNI 119
ChPEPC2_CAM_type      TLEHGMHPPVSPKPEWRA-LLDEMAVIATEEYRSIVFKEPQFVEYFRLATPELEYGRMNI 119
CsPEPC3_CAM_type      TLEHGMHPPVSPKPEWRA-LLDEMAVVATEEYRSIVFKEPQFVEYFRLATPELEYGRMNI 119
CaPEPC_CAM_type       TLEHGMHPPVSPKPEWRA-LLDEMAVVATEEYRSIVFKEPQFVEYFRLATPELEYGRMNI 119
McPEPC1_CAM_type      TLEHGMNPPKSPKPEWRA-LLDQMAVVATEEYRSIVFKEPRFVEYFRLATPETEYGRMNI 119
KbPEPC1_CAM_type      TLEHGMIPPSSPKQECRACLMDEMAVVTTERYRSIVFREPRFVEYFRLATPELEYGRMNI 120
KbPEPC2_CAM_type      TLEHGMIPPSSPKQEWRACLMDEMAVVTTERYRSIVFREPRFVEYFRLATPELEYGRMNI 120
Sa_Contig08207        TLEHGMNPPLAPKQEWRD-LMDEMAVVATEHYRSIVFEEPRFVEYFRLATPEMEYGRMNI 119
                      ****** ** :** * *  *:*:***::**.******.**:********** *******

CvPEPC2_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNLYVLQEMY 179
CsPEPC2_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNLHVLQEMY 179
CrPEPC2_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNLHVLQEMY 179
ChPEPC2_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNLHVLQEMH 179
CsPEPC3_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNLHVLQEMY 179
CaPEPC_CAM_type       GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIIKKDIRNLHVLQEMY 179
McPEPC1_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGVGGALKHVLEKDIRNHNMLRDMY 179
KbPEPC1_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNLLMLQQMY 180
KbPEPC2_CAM_type      GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHVIDKDNKNLLMLQQMY 180
Sa_Contig08207        GSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGEAFRHIIDKDNKNLLMLQQMY 179
                      ************************************.* *::*::.** :*  :*::*:

CvPEPC2_CAM_type      NAWPFFRVTIDMLEMVFAKGNPGIAALYDKLLVSEDLWTFGEKLRTNYEETKKLLLQIAG 239
CsPEPC2_CAM_type      NAWPFFRVTIDMLEMVFAKGDPGIAALYDKLLVSEDLWTFGEELRTNYEETKKLLLQIAG 239
CrPEPC2_CAM_type      NAWPFFRVTIDMLEMVFAKGDPGIAALYDKLLVSEELWTFGEKLRTNYEETKKLLLQIAG 239
ChPEPC2_CAM_type      NAWPFFRVTIDLLEMVFAKGDPGIAALYDKLLVSEDLWTFGEKLRTNYEETKTFLLQIAG 239
CsPEPC3_CAM_type      NAWPFFRVTIDMLEMVFAKGNPEIAALYDKLLVSEDLWTFGEKLRTNYEETKKLLLQIAG 239
CaPEPC_CAM_type       NAWPFFRVTIDMLEMVFAKGNPEIAALYDKLLVSEDLWTFGEKLRTNYEETKRLLLQIAG 239
McPEPC1_CAM_type      NNFPFFRVTIDLLEMVFAKGDPEIAALYDKLLVSEELQSFGERLRANYEDTKRRLLEVAG 239
KbPEPC1_CAM_type      NEWPFFRVTIDLVEMVFAKGDPGIAALYDKLLS-EELWPLGEQLRTAYNDTKSYLLKITG 239
KbPEPC2_CAM_type      NEWPFFRATIDLVEMVFAKGDPGIAALYDKLLS-EELWPLGEQLRTAYNDTKSYLLKITG 239
Sa_Contig08207        NEWPFFRVTIDLVEMVFAKGNPGIAALYDKLLVSEDLLALGERLRTAYNDTQGFLLKITG 239
                      * :****.***::********:* *********  *:* .:**.**: *::*:  **:::*
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Figure S4 Partial protein sequence alignment of CAM-type PEPCs. Accession numbers are listed in Table S5. Identical amino acids are marked with stars (*) under the lines, colons and dots indicate different amino acids with strong and weak similarity, respectively.