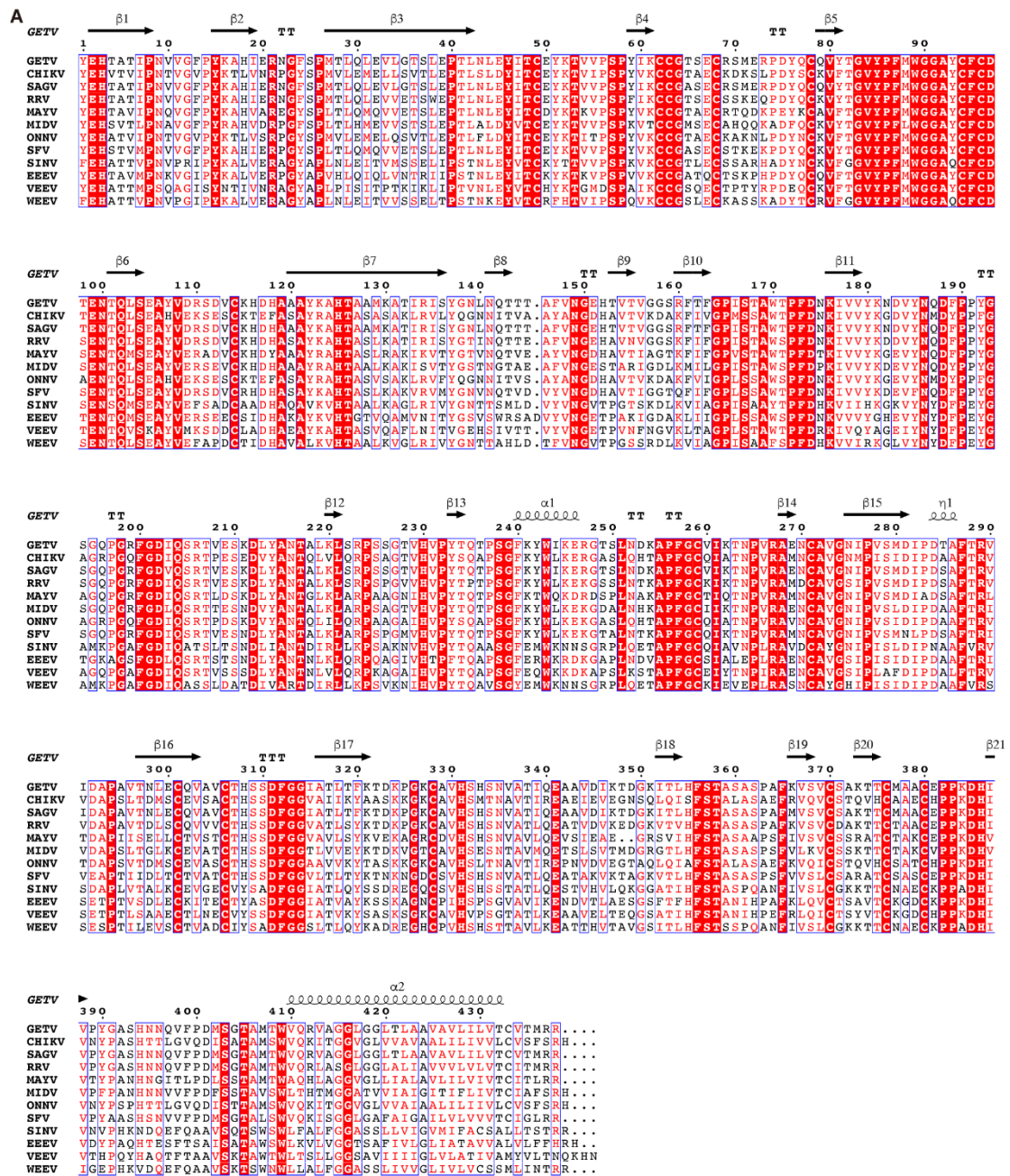


Figure S1. Cryo-EM reconstruction of GETV virions. (A) Cryo-EM micrographs of purified GETV virions. (B) Two-dimensional classification scheme of GETV virions. (C) Location of the three blocks (B1-3) selected for conducting the Block-based reconstruction. B1, B2, and B3 are indicated by a red, black, and yellow dashed circle, respectively. (D) Fourier Shell Correlation (FSC 0.143) profile of GETV Cryo-EM density map. The primary resolution curve is colored grey, and the final resolution curves of three blocks and CP are colored red, black, yellow, and blue, respectively. (E) Local resolution of the three blocks B1 (left), B2 (middle), and B3 (right).



B

GETV

1 10 20 30 40 50 60 70 80 90

GETV S VTEH FNNVYKATKPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HEHNKIRYTAGHDMKFAANDRSLOVHTSGVCAIR
CHIKV SIKDHFNNVYKATKPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HEHNKIRYTAGHDMKFAANDRSLOVHTSGVCAIR
SAGV S VTEH FNNVYKATKPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HAHTKIRYTAGHDMKFAANDRSLOVHTSGVCAIR
RRV S VTEH FNNVYKATKPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HEHNKIRYTAGHDMKFAANDRSLOVHTSGVCAIR
MAYV S TANHFNNAVKLITRPYVAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HDHTRIRYAGHDMKFAANDRSLOVHTSGVCAIR
MIDV GLATEDFYAKYLITPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HSWTKIRYAGHDMKFAANDRSLOVHTSGVCAIR
ONNV NLRNFNNVYKATKPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HDWTKIRYAGHDMKFAANDRSLOVHTSGVCAIR
SPV S VSOHFNNAVYKATKPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...HDYTKIRYAGHDMKFAANDRSLOVHTSGVCAIR
SIN V F.....LTLSPTLYAGTGSYCHHTPEQSVKPIEAVWDEADDTIRIQSAQFVQDSGASVNYKIRISLKDQDHTEIEGSDMAIKISTSGPCRRVH
EEV DLDTHFYQYKLITPYLAYCADCDGDFG CYSVPAIEKIRHDEASDCMIRKIQAAGIGIKNGGTT...VDLAYMSFNMNGTKQKSIKIDNLHVRTSPGLV
VEEV STEELFKYKLTIRPYMARIRCAVSGS...OSPFIATIEAVKSDGHGDYVRLQSSQYGLDSSGN...LKGRTMYDMHGHTIKBIPLHGVSLRTSRPCHIV
WEEV S...IADDFTLTSYLGFPYGRHSAPEPSILKIEVWDESDGSLIRIQVSAQFGTQNAAGTADVTCKFRYMSFDHDLIKEDSDMDKLAISTSGPCRRV

GETV

100 110 120 130 140 150 160 170 180 190

GETV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
CHIKV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
SAGV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
RRV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
MAYV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
MIDV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
ONNV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
SPV GTMGHFIVAVCPPEDELVKVFQDAESHTQACVQVTRHAPAVVGRKFTVVRPHFGIIEVPCITQLTATPTEEEIDMHPFPDIPITILLSSQSGNVKIT
SINV NHKGYFLIAACPPGDSVTYSISAG.DNSATSLARLKKVFPFVGRKGYDLPPVHGKKIPGIRDRLKTSAGYITIRHPGPHAYATVLEBSSQGVYAK
EEV SHHGYFLIAACPPGDSVTYSISAG.DNSATSLARLKKVFPFVGRKGYDLPPVHGKKIPGIRDRLKTSAGYITIRHPGPHAYATVLEBSSQGVYAK
VEEV DGHGYFLIAACPPGDSVTYSISAG.DNSATSLARLKKVFPFVGRKGYDLPPVHGKKIPGIRDRLKTSAGYITIRHPGPHAYATVLEBSSQGVYAK
WEEV GHKGYFLIAACPPGDSVTYSISAG.DNSATSLARLKKVFPFVGRKGYDLPPVHGKKIPGIRDRLKTSAGYITIRHPGPHAYATVLEBSSQGVYAK

GETV

200 210 220 230 240 250 260 270 280 290

GETV A.GGKIRTYRNCITCG..SGNVGTTSDDKTINSCIAQCHAAVTNHHKQYNSVLPV..ADOLSRKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
CHIKV A.NSGITVRYKNCITCG..DSSEGLTDTKVINNSCKVQCHAAVTNHHKQYNSVLPV..NAEFGDRKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
SAGV A.GGKIRTYRNCITCG..SGNVGTTSDDKTINSCIAQCHAAVTNHHKQYNSVLPV..ADOLSRKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
RRV A.GGKIRTYRNCITCG..RDNVGTTSDDKTINSCIAQCHAAVTNHHKQYNSVLPV..ADOTARRKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
MAYV V.NGRTVRYKNCITCG..SKPSGVTTSDDKTINSCITDCAQVYTSHTDKQWQNSFPVVP..AQOARRKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
MIDV P.KGKSTRYKNCITCG..SKESGVTQDKQDFDNCEVQCHTAVTADHDKQWQNSFPVVP..AGSGKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
ONNV V.DGRTVRYKNCITCG..GSNEGILTDTKVINNSCKVQCHTAVTADHDKQWQNSFPVVP..PRNSEQGRKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
SPV V.GGKKVYKNCITCG..TGNVGTTSDDMTINCLIEQCHVSVTHDKKQWQNSFPVVP..ADEPARKGVVHPPLPNSICRVPKRAFPVTVGKRELTV
SINV PPSGKNIT.....YKSDGKTVFNSPDLIR.HADHTAOGKMMPPKIVPSICLVPLAPVQVHGFKPHISL
EEV VPSGKQVYKNCITCG..DREKVTINNKQVQCHTAVTADHDKQWQNSFPVVP..GGEDKLP..AAGATLKGKGVVHPPLADGKCVPLAPEPMITGFSVSL
VEEV PPSGKNIT.....YKSDGKTVFNSPDLIR.HADHTAOGKMMPPKIVPSICLVPLAPVQVHGFKPHISL
WEEV PPSGKNIT.....YKSDGKTVFNSPDLIR.HADHTAOGKMMPPKIVPSICLVPLAPVQVHGFKPHISL

GETV

300 310 320 330 340 350 360 370 380

GETV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
CHIKV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
SAGV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
RRV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
MAYV S.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
MIDV O.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
ONNV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
SPV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
SINV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
EEV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
VEEV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL
WEEV K.HYDPHPLFLSYRSLGADPRPYEEDWIDRVYERTIPVTEGGEYRWGNPVRVWALTLTEGKPHGWPHIEILYGYLPPAATAAVVASAGLAVLISL

GETV

390 400 410 420

GETV L.ASCYMFATARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
CHIKV G.AVAGCMCAARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
SAGV L.ASCYMFATARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
RRV AATCCMCAARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
MAYV AASVYMCVARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
MIDV AASCCCLCAARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
ONNV SLSGLCMCAARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
SPV AASVYMCVARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
SINV S.AVAGCMCAARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA
EEV VTSVWLLCRTANLCTTPYALTPGCAVPVPTLGLVLCAPRABA
VEEV AASTVFLCRSRAVCTTPYALTPGCAVPVPTLGLVLCAPRABA
WEEV ASSAACIAKARRKCTTPYALTPGCAVPVPTLGLVLCAPRABA

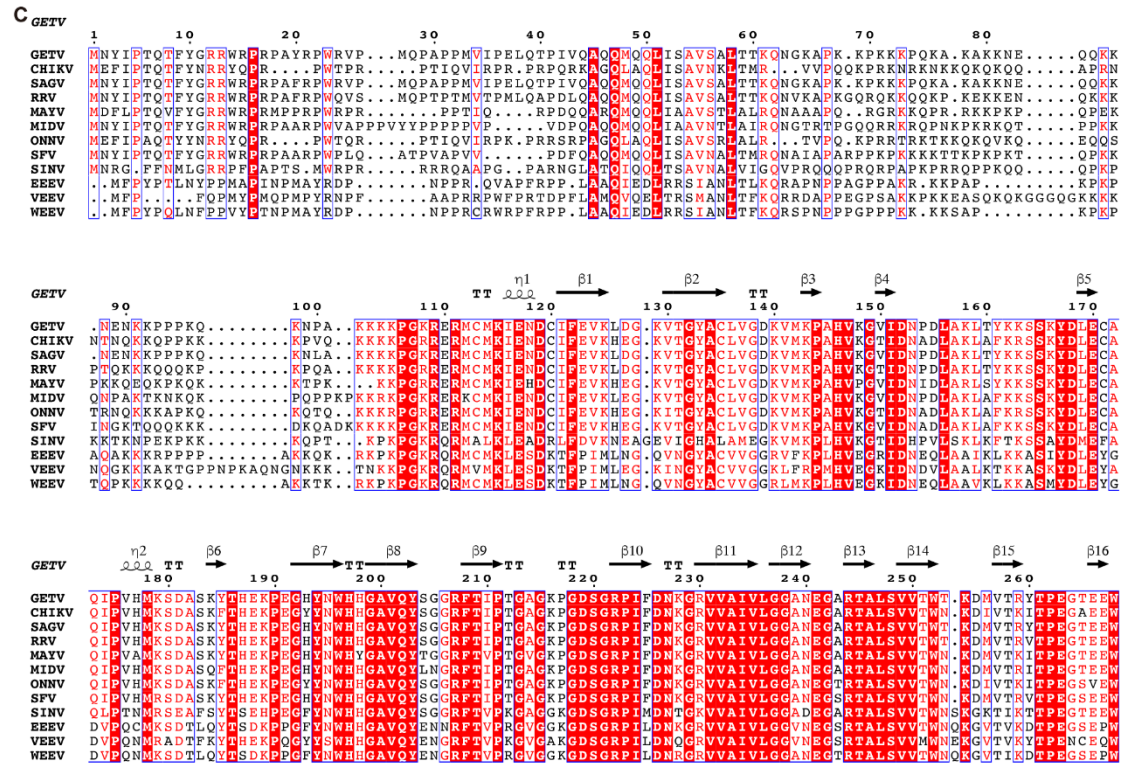


Figure S2. Multiple sequence alignment of the structural proteins from 12 alphaviruses. The alignment was done using the ClustalW and displayed with ESPrift. The red background highlights the strictly conserved residues. The secondary structure determined by the Cryo-EM atomic structure model of the GETV is shown with linear diagram. (A) Alignment of E1. (B) Alignment of E2. (C) Alignment of CP.