

# Capsid

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	Msn-xxKk <sup>■</sup> ggr <sup>■</sup> rxvNMLKRgrnRVSxIxGL-KRrfsxgLLxGxGPxRIVLAFIAFxFRFAI---pPTaGILkRWgsvkKsxAiKxLtgFKKEigxMLnIiN
ILHV	MSKKPGKSAAKRTVNMLKRL-ASVSPLKGA-KKLFGE <sup>■</sup> LLSGGGAIRLILALMAFFRFAAI---KPTLGLK <sup>■</sup> KRWRSVNKTVAVKHLTNFKKELTTMLDSVN
ROCV	MSKKPGGPAGRRVVNMLKRP-ASVSP <sup>■</sup> IKGI-KRLIGNLTDGRGPLRVVLAFAIAFFRFAAI---MPTQGLLRRWRVMNKS <sup>■</sup> EALKHLTSFKKEISNMLNIIN
WNV	MSKKPGGGPKSRVNMLKRGMPRVL <sup>■</sup> SLIGL-KRAMLSLIDGKGP <sup>■</sup> IRFVLALLAFFRFTAIGL---APTRAVLDRWRGVN <sup>■</sup> KQTAMKHL <sup>■</sup> LSFKKELGTLTSAIN
JEV	MTKKPGGGPKNRAINMLKRGLPRVFP <sup>■</sup> LVGV-KRVVMSLLDGRGPVRFVLA <sup>■</sup> LITFFKFTAL---APT <sup>■</sup> KALLGRWKA <sup>■</sup> VEKSVAMKHL <sup>■</sup> TSFKRELGLT <sup>■</sup> LIDAVN
DENV1	MNN-QRKKTG <sup>■</sup> RPSFNMLKRARNRVSTVSQLAKRFSKGLLSGQGGPMKLVMAFIAFLRFLAIGL---PPTAGILARWGSF <sup>■</sup> KKNGA <sup>■</sup> IKVLRGF <sup>■</sup> FKKEISNMLNIMN
DENV2	MNN-QRKKARNT <sup>■</sup> PFNMLKRE <sup>■</sup> RNRVSTVQQLTKRFS <sup>■</sup> SLGMLQGRGPLKLFMALVAFLRFLTIGL---PPTAGIL <sup>■</sup> KRWGT <sup>■</sup> IKKSKA <sup>■</sup> INVL <sup>■</sup> RGFR <sup>■</sup> KEIGRMLN <sup>■</sup> ILN
DENV3	MNN-QRKKTGKPSINMLKRV <sup>■</sup> RNRVSTGSQLAKRFS <sup>■</sup> RLNGQGGPMKLVMAFIAFLRFLAIGL---PPTAGV <sup>■</sup> LARWGT <sup>■</sup> FKKSGA <sup>■</sup> IKVLRGF <sup>■</sup> FKKEISNMLSIIN
DENV4	-MN-QRKKVVR <sup>■</sup> PPFNMLKRE <sup>■</sup> RNRVSTPQGLVKRFS <sup>■</sup> TGLFSGKGPLRMVLA <sup>■</sup> FITFLRVL <sup>■</sup> SI---PPTAGIL <sup>■</sup> KRWGQL <sup>■</sup> KKNKA <sup>■</sup> IKILTGF <sup>■</sup> RKEIGRMLN <sup>■</sup> ILN
ZIKV	MKNPKK <sup>■</sup> KS <sup>■</sup> GGFRIVNMLKRGVARVNPLGGL-KRLPAGLL <sup>■</sup> LGHGPI <sup>■</sup> RMVLA <sup>■</sup> ILAF <sup>■</sup> LRFTAIGL---KPSLGLINRWG <sup>■</sup> SVG <sup>■</sup> KK <sup>■</sup> EAME <sup>■</sup> IIKKF <sup>■</sup> KKDLAAMLRIIN
YFV	MSG-RKAQ <sup>■</sup> GKTLGVNMVRRGVRSL <sup>■</sup> SNKI---KQKT <sup>■</sup> KQIGNRPGPS <sup>■</sup> RGVQGF <sup>■</sup> IFFFLFNIL <sup>■</sup> TGKK <sup>■</sup> ITAH <sup>■</sup> LKRLW <sup>■</sup> KMLD <sup>■</sup> PRQGLAVL <sup>■</sup> RKV <sup>■</sup> KRVVAS <sup>■</sup> LMRGLS

Ruler 1	110 120 130
Consensus	rRKrkx-----lxxixLlptvMA---
ILHV	KR <sup>■</sup> KE <sup>■</sup> KK <sup>■</sup> ---K <sup>■</sup> S <sup>■</sup> F <sup>■</sup> STALLWI <sup>■</sup> TMITAVAG---
ROCV	RR <sup>■</sup> KA <sup>■</sup> KR <sup>■</sup> ---G <sup>■</sup> NGSVLLWIALVTGSMA---
WNV	RR <sup>■</sup> SS <sup>■</sup> KQ <sup>■</sup> KKRGGK <sup>■</sup> TGIAVMIGLIA <sup>■</sup> SVG---A
JEV	KR <sup>■</sup> GR <sup>■</sup> KQ <sup>■</sup> NKRGGNE <sup>■</sup> GSIMWLASLAVI <sup>■</sup> IACAGA
DENV1	RR <sup>■</sup> KRS <sup>■</sup> V-----T <sup>■</sup> MLLMLLPTALA---
DENV2	RR <sup>■</sup> RTA <sup>■</sup> -----G <sup>■</sup> MIML <sup>■</sup> IPTVMA---
DENV3	KR <sup>■</sup> KK <sup>■</sup> TS <sup>■</sup> -----L <sup>■</sup> CLMMMLPATLA---
DENV4	G <sup>■</sup> RKR <sup>■</sup> ST <sup>■</sup> -----M <sup>■</sup> TLLCLIPTVMA---
ZIKV	AR <sup>■</sup> KE <sup>■</sup> R <sup>■</sup> KRR <sup>■</sup> ---G <sup>■</sup> ADTS <sup>■</sup> IGI <sup>■</sup> IGLLLTTAMA---
YFV	SR <sup>■</sup> KRR <sup>■</sup> SH <sup>■</sup> DV <sup>■</sup> --L <sup>■</sup> TVQ <sup>■</sup> FLILGMLLMTGG---

**Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses.** Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

# prM

Ruler 1	1	10	20	30	40	50	60	70	80	90	
Consensus	f h L x t r q G e p I M i V n k t D x G k s i l f x T x k G v N m C T x r A M D I G y M C e D T i T Y E C P x L t e g n E P E D I D C W C n l - t s x w V t Y G t C t q t g - e x R R s R R S V a L p p										
ILHV	L K I S S H R D R P L L M V N K T D V S D A I P V P S V K G T N M C T I R A L D V G Y T C A Y D T T Y E C P H L E V T M D P E D I D C W C T L - E S V Y V N Y G L C K Q N H - H V R R G R R A I N I P H										
ROCV	L R L G T Y Q G K V L M S I N K T D V A E I I P I P T T K G D N L C T V R A M D V G Y M C Q K D I T Y E C P R L E P G M D P E D I D C W C D R - E A I Y V H Y G L C T K N H - R E R R G R R S V N I P S										
WNV	V T L S N F Q G K V M M T V N A T D V T D V I T I P T A A G K N L C I V R A M D V G Y M C Q D T I T Y E C P V L S A G N D P E D I D C W C T K - S A V Y V R Y G R C T K T R - H S R R S R R S L T V Q T										
JEV	M K L S N F Q G K L L M T V N N T D I A D V I V I P T S K G E N R C W V R A I D V G Y M C E D T I T Y E C P K L T M G N D P E D V D C W C D N - Q E Y V V Y G R C T R T R - H S K R S R R S V S V Q T										
DENV1	F H L T T R G G E P H M I V S K Q E R G K S L L F K T S A G V N M C T L I A M D L G E L C E D T M T Y K C P R I T E - T E P D D V D C W C N A - T E T W V T Y G T C S Q T G - E H R R D K R S V A L A P										
DENV2	F H L T T R N G E P H M I V S R Q E K G K S L L F K T X D G V N M C T L M A M D L G E L C E D T I T Y K C P X L R Q - N E P E D I D C W C N S - T S T W V T Y G T C T T T G - E H R R E K R S V A L V P										
DENV3	F H L T S R D G E P R M I V G K N E R G K S L L F K T A S G I N M C T L I A M D L G E M C D D T V T Y K C P H I T E - V E P E D I D C W C N L - T S T W V T Y G T C N Q A G - E H R R D K R S V A L A P										
DENV4	F H L S T R D G E P L M I V A K H E R G R P L L F K T T E G I N K C T L I A M D L G E M C E D T V T Y E C P L L V N - T E P E D I D C W C N L - T S A W V M Y G T C T Q S G - E R R R E K R S V A L T P										
ZIKV	A E I T R R G S A Y Y M Y L D R S D A G K A I S F A T T L G V N K C H V Q I M D L G H M C D A T M S Y E C P M L D E G V E P D D V D C W C N T - T S T W V V Y G T C H H K K G E A R R S R R A V T L P S										
YFV	V T L V R K N R W L L L N V T S E D L G K T F - - - - S V G T G N C T T N I L E A K Y W C P D S M E Y N C P N L S P R E E P D D I D C W C Y G V E N V R V A Y G K C D S A G - R S R R S R R A I D L P T										

Ruler 1	110	120	130	140	150	160
Consensus	H g x s g L e T R t e t W M x S e x A t K y L q K V E n W i I R N P G F A I v A I x I A w m I G S n t t Q R V V f f I L L I L V A P A Y S					
ILHV	H G E S H L E N R A T P W M D T T K T T K Y L T K V E N W V I R N P G Y A L V A L A T A W M L G S N T P Q R V V F M I M M M L I A P A Y S					
ROCV	H G E S Q L E N R G T P W L D T A K T T K Y L T K V E N W M I R N P G Y A I V A V A A A W M L G S N T S Q K V I F T I M L L L I A P A Y S					
WNV	H G E S T L A N K K G A W M D S T K A T R Y L V K T E S W I L R N P G Y A L V A A V I G W M L G S N T M Q R V V F V V L L L L V A P A Y S					
JEV	H G E S S L V N K K E A W L D S T K A T R Y L M K T E N W I V R N P G Y A F L A A I L G W M L G S N N G Q R V V F T I L L L L V A P A Y S					
DENV1	H V G L G L E T R T E T W M S S E G A W K Q I Q K V E T W A L R H P G F T V I A L F L A H A I G T S I T Q K G I I F I L L M L V T P S M A					
DENV2	H V G M G L E T R T E T W M S S E G A W K H A Q R I E T W I L R H P G F T I M A A I L A Y T I G T T H F Q R A L I F I L L T A V A P S M T					
DENV3	H V G M G L D T R T Q T W M S A E G A W R Q V E K V E T W A L R H P G F T I L A L F L A H Y I G T S L T Q K V V I F I L L M L V T P S M T					
DENV4	H S G M G L E T R A E T W M S S E G A W K H A Q R V E S W I L R N P G F A L L A G F M A Y M I G Q T G I Q R T V F F V L M M L V A P S Y G					
ZIKV	H S T R K L Q T R S Q T W L E S R E Y T K H L I K V E N W I F R N P G F A L V A V A I A W L L G S S T S Q K V I Y L V M I L L I A P A Y S					
YFV	H E N H G L K T R Q E K W M T G R M G E R Q L Q K I E R W L V R N P F F A V T A L T I A Y L V G S N M T Q R V V I A L L V L A V G P A Y S					

**Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses.** Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.



# NS1

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	DtGCAIdwxxrkELKCGSGGFIhNDVeTWxqxYKYqPesPxrLAKaIqkAheEGVGIRSVtRLExxMWKqlaxELNAlLeENgVDLxVVVgdykGiyrG
ILHV	DTGCAIDMARRELKCGSGGFIHNDVETWRNNYKYHPLTPRGFAKVIQMSKDKGVCGRISVGRLEHEMWEAIAPELNAIFEDNGVDLSVVVKGQTGIYKRA
ROCV	DTGCAIDITRRELKCGSGGFIHNDVETWRDNYKYHPSTPKNFAKIIHKAYKEGICGVRASARLEHEMWEAIAPELNAILEDNEVDLSVVVEEHKGIYKKA
WNV	DTGCAIDISRQELKCGSGGFIHNDVEAWMDRYKYYPETPQGLAKIIQKAHKEGVCGLRSVSRLEHQMWEAIVKDELNTLLKENGVDLSVVVEKQEGMYKSA
JEV	DTGCAIDVTRKEMRKGSGGIFVHNDVEAWVDRYKYLPEPRSLAKIVHKAHKEGVCGRSVTRLEHQMWEAIVRDELNLVLLKENAVDLSVVVKNKPVGRYSAS
DENV1	DSGCIVNWKGRELKCGSGGIFVTVNEVHTWTEQYKQFQADSPKRLSAAIQKAWEEGVCGRISATRLLENIMWKQISNELNHILLENDMKFTVVVGDVSGILAQQ
DENV2	DSGCIVVSWKNKELKCGSGGIFITDENVHTWTEQYKQFQESPCKLASAIQKAHEEGICGRISVTRLENLWKQITPELNHILSENNIVKLTIMTGDIKGIMQAG
DENV3	DMGCVINWKGKELKCGSGGIFVTVNEVHTWTEQYKQFQADSPKRLATAIAGAWENGVCGRISVTRRMENLWKQIENLNYLWENNIVKLTIVVVDGITGVLEQQ
DENV4	DTGCAVSWSGKELKCGSGGIFVINDVHTWTEQYKQFQESPARLASAILNAHKDGVCGRISVTRLENIMWKQITNELNYVLWEGGHDLTVVAGDVKGVLSKKG
ZIKV	DVGCSDVDFSKKETRCGTGVFIYNDVEAWRDYKYHPDSPRRLAAAVKQAWEEGICGRISVSRMENIMWKSVEGELNAILEENGVQLTVVVGSVKNPMWRG
YFV	DQGCALINFGKRELKCGDGGIFIFRDSDDLNLKYSYYPEDPVKLASIVKASFEEGKGLNSVDSLEHEMWRSRADENAILEENEVDISVVVQDPKNVYQRG

Ruler 1	110 120 130 140 150 160 170 180 190
Consensus	pKRLtptpdELlkyGWkTWGKskI fSpExnSfTx xDGPtKECPtenRAWNSIEVEDfGFGxftTniwLkVRExyTxxCdsxImGxAVKgnxAVHsDlGy
ILHV	PKRLTETKDEMSFGWKNWGSKSFIFSTETANSTFIVDGPESKECP TSDRAWNSLELEDfGFGIISTKIFLKVNEQRGNSCSAVIGTAVKGNIAVHSDLGy
ROCV	PLRLENTSDEMHFGWKNWGSFLFKTQMANSTFVVDGPEtKECP TERRAWNSLEIEDfGFGIMSTKVFLKVNQDKTEVCDSMVMGTAIKGNRAVHSDLGy
WNV	PKRLTATTEKLEIGWKAWGKSLFAPELANNTFVVDGPEtKECP TQRRAWNSLEVEDfGFGLTSTRMFLKRESNITTECDKSIIGTAVKNNLAIHSDLSy
JEV	PKRLSMTQEKFEEMGWKAWGKSLFAPELANSTFVVDGPEtKECP DEHRAWNSMQIEDfGFGITSTRVWLKIREESTDECDGAIIGTAVKGHVAVHSDLSy
DENV1	KKMIRPQPMHKKYSWKSWGKAKIIGADVQNTTFIIDGPNTPeCPDNQRAWNSIWEVEDYGFGITTTNIWLKLRDYSYTVQCDHRLMSAAIKDSKAVHADMGy
DENV2	KRSLXPQPTELKYSWKTWGAKMLSTESHNTQFLIDGPEtAeCPNTNRRAWNSLEVEDYGFGVFTTNIWLKLRKQDFVCDSKLMSAAIKDNRRAVHADMGy
DENV3	KRTLTPQPMELKYSWKTWGAKIVTAETQNSSFIIDGPEtPteCPASRAWNVWEVEDYGFGVFTTNIWLKLRVYTTQCDHRLMSAAVKDERAVHADMGy
DENV4	KRALAPPVNDLKYSWKTWGAKIIFTPEAKNSTFLIDGPDtSECPNERRAWNFLEVEDYGFGMFTTNIWMLKFRGSSVECDHRLMSAAIKDQKAVHADMGy
ZIKV	PQRLPVPVLELPHGSKAWGKSYFVRAAKTNSFVVDGDLtKECPLEHRAWNSFLVEDYHGFGVFTSVWLKVRDYSLECDPAVIGTAVKGREAAHSDLGy
YFV	THPFSRI RDGLQYGWKTWGNLlVfSPGRKNGSFIIDGKSRKECPFSNRVWNSFQIEEFGTGVFTTRVYMDAVFEYtIDCDGSLGAAVNGKKSAAHGSPtF

Ruler 1	210 220 230 240 250 260 270 280 290
Consensus	WIEsx-KNdTWkLERAxLiEVKsCtWPkSHTLWxxGVxESdxIIPktIAGPxsqHNyRPGYkTQTxGPWHxg-kLEIdFdeCPGTTvtieExCsnRGPSI
ILHV	WIEsk-KNEswqlERAVLGEVKSCTWPEsHTLWGDGYEsdLIIPtLAGPKSHHMRPGYKTQTGKPWHEETPLVIEFAECpgttvtqeescggRgPSI
ROCV	WIEsg-KNTswrlERAVLGEVRSCtWPEsHTLWNEgVEDSDLIIPtLGGPrTHhNkREGYKtQLKGPWNEEGPIIEFGCEpgtkvtqeescRNRAASA
WNV	WIEsr-LNDtwkLERAVLGEVKSCTWPEtHTLWGDGILEsdLIIPVtLAGPrSNhNRrPGYKtQNqGPWDEG-RVEIDFDYcpgttvtlseechrgPAT
JEV	WIEsr-YNDtwkLERAVFGEVKSCTWPEtHTLWGDGYEseLIIPhtIAGPKShhNRREGYKtQNqGPWDEG-GIVLDFDYcpgtkvtITEDcGRGSPV
DENV1	WIESE-KNETWKLARASfIEVKTClWPkSHTLWSNGVLESEMIIPKIYGGPIsqHNyRPGYHTQTAGPWHLG-KLELDFNCEgTTVVVDEHcGNRGPsl
DENV2	WIEsa-LNDtwkIEKASfIEVKSCHWPkSHTLWSNGVLESEMIIPKNFAGPVsqHNyRPGYHTQTAGPWHLG-KLEMDFDfCEgTTVVVTEdCnRGPSl
DENV3	WIEsq-KNGswkLEKASLIEVKTCTWPkSHTLWSNGVLESDMIIPKSLAGPIsqHNhRPGYHTQTAGPWHLG-KLELDFNCEgTTVVVIESEncGRGPSl
DENV4	WIESS-KNQTWQIEKASLIEVKTCLWPkHTLWSNGVLEsqMLIPKAYAGPFSqHNyRqGYATQTGVPWHLG-KLEIDFGNCEgTTVTIQEDcHRGPSl
ZIKV	WIESE-KNDtwRLKRAHLIEMKTEWPkSHTLWTDGYEsdLIIPKSLAGPLSHhNtREGYRTQVKGpWHS-ELEIRFEeCpgtkvYVEETcGTRGPSl
YFV	WMGSHEVNGTWMIHtLEALDYKEcEWPLHTI-GTSVESEMFMPRSIGGPVSShNHIPGYKvQTNGPwMQV-PLEVKEReAcpgTSITIDGNCdGRGKSt

Ruler 1	310 320 330 340 350
Consensus	RTTtASGKIItEWcRSCtLPPLRfRgeDGCWYGMERpXkEkEeNLVksqVxA
ILHV	RTTtASGRtIRDWcKNCtLPPLRfMAGENcWYGMERpKRENEETLIKSKVSA
ROCV	RTTtASGKvIRDWcKNCtMPPLRfTTKNGcWYGMERpKHESEETLIKSKVTA
WNV	RTTtESGKLITDWCRCSCtLPPLRyQTDSGCWYGMERpQRHDEKTLVQSQVNA
JEV	RTTtDSGKLITDWCRCSCSLPPLRfRfTEngcWYGMERpVRHDEtTLVRSQVDA
DENV1	RTTtVtGKtIHEWcRSCtLPPLRfKGDGCWYGMERpVKEKEEeNLVKS MVSA
DENV2	RTTtASGKLITEWcRSCtLPPLRyRGEDGCWYGMERpLKEKEEeNLVNSLVTA
DENV3	RTTtVSGKLIEHEWcRSCtLPPLRyMGEDGCWYGMERpINEKEEeNMVKSLSA
DENV4	RTTtASGKLVTQWCRCSCtMPPLRfLGDGCWYGMERpLSEKEEeNMVKSQVSA
ZIKV	RSTtASGRVIEEWcRSCtMPPLSFRAKDGcWYGMERpRKEPEeNLVRS MVTA
YFV	RSTtDSGKLIEPEWCRCSCtMPPLVfHGSdGCWYPMERpRKEESHlVRSWVTA

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# NS2A

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	- g g g x i D p F x L G L L x m f l f t x E V L R k R w T a K x x i p x v l x l L x v l i i G g x T y x D L x R y v l l V G A a F a E - N s G G D V t H L A L i A a F K i q P a f i V g f f L R k - W T
ILHV	G N G Q T I E P F Q L G I L M A F V F T Q E V L R R R W T A N L A L P T S A L L M A C F I F G G F T Y L D L F R Y F I L V G A A F A E A N S G G D V V H L A M I A A F N I Q P V A L V T T F F R K N W T
ROCV	G T G N D I C R F Q L G L L M A F V F T Q E V L R K R W T A R L A L P T A A L L L A C F V L G A F T Y S D M I R Y F V L V G C A F A E S N S G G D V I H L A L I A V F N I Q P A A L V S T F F R N R W T
WNV	Y N A D M I D P F Q L G L L V V F L A T Q E V L R K R W T A K I S M P A I L I A L L V L V F G G I T Y T D V L R Y V I L V G A A F A E S N S G G D V V H L A L M A T F K I Q P V F M V A S F L K A R W T
JEV	F N G E M V D P F Q L G L L V M F L A T Q E V L R K R W T A R L T I P A V L G A L L V L M L G G I T Y T D L A R Y V V L V A A F A E A N S G G D V L H L A L I A V F K I Q P A F L V M N M L S T R W T
DENV1	- G S G E V D S F S L G L L C I S I M I E E V M R S R W S R K M L M T G T L A V F L L T M G Q L T W N D L I R L C I M V G A N A S D - K M G M G T T Y L A L M A T F R M R P M F A V G L L F R R - L T
DENV2	- G H G Q I D N F S L G V L G M A L F L E E M L R T R V G T K H A I L L V A V S F V T I T G N M S F R D L G R V M V M V G A T M T D - D I G M G V T Y L A L A A F K V R P T F A A G L L L R K - L T
DENV3	- G S G K V D N F T M G V L C L A I L F E E Y M R G K F G K K H M I A G V L F T F V L L S G Q I T W R D M A H T L I M I G S N A S D - R M G M G V T Y L A L I A T F K I Q P F L A L G F F L R K - L T
DENV4	- G Q G T S E T F S M G L L C L T L F V E E C L R R R V T R K H M I L V V V T T L C A I I L G G L T W M D L L R A L I M L G D T M S G - R M G - G Q I H L A I M A V F K M S P G Y V L G I F L R K - L T
ZIKV	G S T D H M D H F S L G V L V I L L M V Q E G L K K R M T T K I M S T S M A V L V M I L G G F S M S D L A K L V I L M G A T F A E M N T G G D V A H L A L V A A F K V R P A L L V S F I F R A N W T
YFV	- - - G E I H A V P F G L V S M M I A M E V V L R K R Q G P K Q M L V G G V V L L G A M L V G Q V T L D L L K L T V A V G L H F H E M N N G G D A M Y M A L I A A F S I R P G L L I G F G L R T L W S

Ruler 1	110 120 130 140 150 160 170 180 190
Consensus	x R E n I L L x x G a A m x q m A - s d l p - - - i x l m e l l n x i A L a w M i L K a v T f f t t s q l a m P l A L L t P p x r x l l l - - d a w R x l l l i l G v v s l i p x x s s s a k k k
ILHV	N R E N M I L I A A A C T Q M A C M E L K - - - I E L F H V M N S L S L A W M I L K A L T T G T T S T L A M P F L A A L S P P M N W L G L - - D V V R C L L I M A G V A A L I S E R R E S L A K K K
ROCV	N R E N L L V I A A A M A Q M A W S D V G - - - I E I M P I M N A M A L A W M I L K A V S I G T V S T I A M P I L S G L A P P M E W F G L - - D V L R C L L I V G V A A L I K E R K E N L A K K K
WNV	N Q E N I L L M L A A V F F Q M A Y H D A R Q I L L W E I P D V L N S L A V A W M I L R A I T F T T T S N V V V P L L A L L T P G L R C L N L - - D V Y R I L L M V G I G S L I R E K R S A A A K K K
JEV	N Q E N V V L V L G A A F F Q L A S V D L Q - - - I G V H G I L N A A A I A W M I V R A I T F P T T S V T M P V L A L L T P G M R A L Y L - - D T Y R I L L V I G I C S L L Q E R K K T M A K K K
DENV1	S R E V L L L T V G L S L V A S - - V E L P - - - N S L E E L G D G L A M G I M M L K L L D F Q S H Q L W A T L L S L T F V K T T F S L H - - Y A W K T M A M I L S I V S L F P L C L S T T S Q K -
DENV2	S K E L M M T T I G I V L L S Q - - S T I P - - - E T I E L T D A L A L G M M V L K M V R K M E K Y Q L A V T I M A I L C P N A V I L Q - - N A W K V S C T I L A V V S V S P L F T T S S Q Q K -
DENV3	S R E N L L G V G L A M A A T - - L R L P - - - E D I E Q M A N G I A L G M A L K L I T Q F E Y Q L W T A L V S L T C S N T I F T L P - - V A W R T A L I L A G I S L L P V C Q S S M R K -
DENV4	S R E T A L M V I G M A M T T V - - L S I P - - - H D L M E F I D G I S L G L I L L K M V T H F D N T Q V G T L A L S L T F I R S T M P L V - - M A W R T I M A V L F V V T L I P L C R T S C L Q K Q
ZIKV	P R E S M L L A L A S C L L Q T A I S A L E - - - G D L M V L I N G F A L A W L A I R A M A V P R T D N I A L P I L A A L T P L A R G T L L - - V A W R A G L A T C G G I M L L S L K G K G S V K K N
YFV	P R E R L V L T L G A A M V E I A L G G M M - - - G G L W K Y L N A V S L C I L T I N A V A S R K A S N T I L P L M A L L T P V T M A E V R L A T M L F C T V V I I G - - V L H Q N S K D T S M Q K T

Ruler 1	210 220 230
Consensus	g a w L p x l a l a - t G x f s P l - l x x l l x l t r x n k K R
ILHV	G A L L I S A A L A L T G A F S P L V L Q G A L M F T Q S L G K R
ROCV	G A L L I S A G L A L T G A F S P L V L Q G A L M L S E C A T K R
WNV	G A S L L C L A L A S T G L F N P M I L A A G L I A C D P N R K R
JEV	G A V L L G L A L T S T G W F S P T T I A A G L M V C N P N K K R
DENV1	T T W L P V L L G S - L G C - K P L - T M F L I T E N K I W G R K
DENV2	A D W I P L A L T I - K G L - N P T - A I F L T T L S R T N K K R
DENV3	T D W L P M T V A A - M G V - P P L - P L F I F S L K D T L K R R
DENV4	S H W V E I T A L I - L G A - Q A L - P V Y L M T L M K G A S K R
ZIKV	L P F V M A L G L T A V R V D P I N V V G L L L L T R S G K R -
YFV	I P L V A L T L T S Y L G L T Q P F L G L C A F L A T R I F G R R

**Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses.** Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green. Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

# NS2B

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	SWPxnEvIxAVGLVsaLAGsLAKxDip-MAGPIaagGLLixYVxSGkSxDxwLEERAADVSWEEAEITGSSpRLDVeLDdDGDfKxxxdegvPmltwll
ILHV	GWPASEVLTAVGMTFALAGSVARLDGGTMAIPLATMAILAVAYVLSGKSTDMWLERCADISWINEAEITGTSPrLDVVELDdSNGDFKMINDPGVPMWMTCT
ROCV	GWPASEVLTAVGMTIALAGSVARLDsGTMAIPLATTSILFVSYVLSGKSTDMWIERCADVTWEEAEITGTSPrLDVVELDDNGDFKMINDPGVPMWMTCT
WNV	GWPATEVMTAVGLMFAIVGGLAELIDSMAPMTIAGLMFAAFVISGKSTDMWIERADISWESDAEITGSSERVDYRLDDDDGNFQLMNDPGAPWKIWMML
JEV	GWPATEFLSAVGLMFAIVGGLAELIDESMSPFMLAGLMAVSYYVSGKATDMWLERAADISWEMDAAITGSSRRLDVKLDDDDGDFHLIDDPGVPWKVWVVL
DENV1	SWPLNEGIMAVGIVSILLSSLLKNDVP-LAGPLIAGGMLIACYVISGSSADLSLEKAAEVSWEEAEHSGASHNILEVEVQDDGTMKIKDEERDDTLTILL
DENV2	SWPLNEAIMAVGMVSIASSLLKNDIP-MTGPLVAGGLLTVCYVLTGRSADLELERAADVKWEDQAEISGSSPILSITISEDGSMSIKNEEEEQILTILL
DENV3	SWPLNEGVMVAVGLVSIASSLLRNDVP-MAGPLVAGGLIACYVITGTSADLTVEKAADVTEEEAEQTGVSHNLMITVDDDDGTMRIKDEETENILTIVLL
DENV4	SWPLNEGIMAVGLVSLLSALLKNDVP-LAGPMVAGGLLLAAYVMSGSSADLSLEKAAENVQWDEMADITGSSPIIEVKQDEDGFSIRDIEETNMITLLV
ZIKV	SWPPSEVLTAVGLICALAGGFAKADIE-MAGPMAAVGLLIVSYVVSgKsvDMYIERAGDITWEKDAEVTGNSPrLDVALDESGDFSLVEEDGPPMREIILL
YFV	SIPVNEALAAAGLVGVLG-LAFQEMENFLGPIAVGGILMMLVSVAGRVDGLELKKLGEVSWEEAEISGSSARYDVALSEQGEFKLLSEEKVPWDQVVM

Ruler 1	110 120 130
Consensus	rmgLaiaisxxnPvalPvtxagWxmxKktkR
ILHV	RMGLMAMAAYNPVLIPVSMAGYWMTVKIHKR
ROCV	RMGLMCMAAYNPVLIPVSVAGYWMTRKIHKR
WNV	RMVCLAISAYTPWAILPSVVGFWITLQYTKR
JEV	RMSCIGLAALTPWAVPAAFGYWLTLKTTKR
DENV1	KATLLAISGVYPMSIPATLFFVYFWQKKKQR
DENV2	RTGLLVISGLFPVSIPIATAAWYLWEVKKQR
DENV3	KTALLIVSGIFPYSIPATLLVWHTWQKQTQR
DENV4	KLALITVSGLYPLAIPVTMTLWYMWQVKTQR
ZIKV	KVVLMAICGMNPIAIPFAAGAWYVYVKTGKR
YFV	TSLALVGAAIHPFALLLVLAGWLFHVRGARR

**Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses.** Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

# NS3

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	-gGVLDWVrPSPKevgKa-eLtdGVYRIMqrGxLGsyQvGVGVmQEGVFHTMWHVTRGAALmXgeGRLePsWxSVKxDLI SYGGGwKLSaKwXgGEEVQvI
ILHV	-GGVMDVVPAPKQFGKT-ELKPGVYRVMTMGLGRVYQSGVGVMDVGFHTMWHVTRGAALRNNGEGRLLNPTWGSVRDDLISYGGKWLKLSATWNGSEEVQMI
ROCV	-GGVLDLPAKQMGRS-DMKPGVYRVMTSGVLGSYQSGVGVMDVGFHTMWHVTRGAALRNNGEGRLLNPTWGSVRDDLITYGGKWLKLSATWNGTEEVQLI
WNV	-GGVLDWTPSPKEYKKG-DTTTGVYRIMTRGLLGSYQAGAGVMVEGVFHTLWHTTKGAALMSGEGRLDPYWGVSVKEDRLCYGGPWKLQHKWNGQDEVQMI
JEV	-GGVFDWTPSPKPCSKG-DTTTGVYRIMARGILGTQAGVGVMYENVFHTLWHTTRGAALMSGEGKLTYPYWGVSVKEDRIAYGGWPFRDRKWNNGTDDVQVI
DENV1	-SGVLDWTPSPPEVERA-VLDDGIYRILQRGLLGRSQVGVGVFQEGVFHTMWHVTRGAALMYPQGRLEPSWASVKKDLISYGGGWRFQGSWNAGEEVQVI
DENV2	-AGVLDWVPSPPVPGKA-ELEDGAYRIKQKGLIGYSQIAGVYKEGTFHTMWHVTRGAVLMHKKRIEPSWADVKKDLISYGGGWKLEGEWKEGEDEVQVL
DENV3	-SGVLDWVPSPPETQKA-LEEEGVYRIKQGGIFGKTQVGVGVQKEGVFHTMWHVTRGAVLTHNGKRLKRNPAWVKKDLISYGGGWRLSAQWQKGEDEVQVI
DENV4	-SGALWDVPSAAAQKA-ELTEGVYRIMQRGLFGKTQVGVGIMEGVFHTMWHVTRGSVICHETGRLEPSWADVRNDMISYGGGWRLGDKWKEDEVQVL
ZIKV	-SGALWDVVPAPKEVKKG-ETTDGVYRVMTRRLLGSTQVGVGVMEGVFHTMWHVTRKGAALRSSEGRLLDPYWGVSVKQDLVSYGGPWKLDAWDGLSEVQLL
YFV	SGDVLWDIPTPKIIEECEHLEDGIYGFQSTFLGASQRGVGVAQGGVFHTMWHVTRGAFLVRNGKLLPSWASVKKEDLVAYGGSWKLEGRWDGEEEVQLI

Ruler 1	110 120 130 140 150 160 170 180 190
Consensus	AVEPGKNpKNvQTKPGvFKTp-aEIGAVxLDFPpGTSGSPIxNknGkVIGLYGNVtksGsYVSAIxQgErQeEgpppe-fePeMLRKRqLTIIDLHP
ILHV	AVEPGKAAKNYQTKPGVFKTP-AGEIGAITLDFPKGTSGSPIINKAGEIIGLYGNGLVLSAGAYVSAITQGERQEEETPEA-FTPDMLKRRRLTIIDLHP
ROCV	AAEPGKPVKNFQTRPGVFKTP-AGEVGAITLDFPKGTSGSPIVKNAGAVIGLYGNGLVLSAGAYVSAISQGERQEEEAPEA-FTPEMLRKRRLTIIDLHP
WNV	VVEPGKNVKNVQTKPGVFKTP-EGEIGAVTLDFPTGTSGSPIVDKNGDVIIGLYGNVIMPNGSYISAIVQGERMDEPIIAG-FEPEMLRKKQITVLDLHP
JEV	VVEPGKAAVNIQTKPGVFRTP-FGEVGAIVSLDYPRTGTSGSPIILDNGDIIGLYGNGLVLDGGSYVSAIVQGRQEEPPVEA-YTPNMLRKRQMTVLDLHP
DENV1	AVEPGKNPKNVQTPAGTFKTP-EGEVGAIALDFPKGTSGSPIVNRGKIVGLYGNVVTSGTYVSAIAQAKASQEGPLPE-IEDEVFRKRRLTIMDLHP
DENV2	ALVEPGKNRAVQTKPGFLKTN-AGTIGAVSLDFSPGTSGSPIIDKKGKVVGLYGNVVTSGAYVSAIAQTEKSEI-DNPE-IEDDIFRKRRLTIMDLHP
DENV3	AVEPGKPNKFMPTGFIQTT-TGEIGAIALDFPKGTSGSPIINREGKVVGLYGNVVTSGAYVSAIAQTNAPEDGPTPE-LEEEFMKRRLTIMDLHP
DENV4	AIEPGKNPKHVQTKPGFLKTL-TGEIGAVTLDFPKGTSGSPIINRKGKVIIGLYGNVVTSGDYVSAITQAERTGE-PDVE-VDEDFRKRRLTIMDLHP
ZIKV	AVPPGERARNIQTLPGIFKTK-DGDIGAVALDYPAGTSGSPIIDKGRVIGLYGNVVTSGDYVSAITQGRKEETPVEC-FEPEMLRKKQITVLDLHP
YFV	AAVPGKNVNVQTKPSLFLKVRNGGEIGAVALDYPSTSGSPIVNRNGEIGLYGNGLVGDNSVSAISQTEVKEEGEELQEIPTMLKKGMTIILDFHP

Ruler 1	210 220 230 240 250 260 270 280 290
Consensus	GAGKTRRxLPqIVREAIRKRLRTIILAPTRVVAEMAeALRGLPIRYQTSaVkaEHxGrEIVDIMCHATxTmRLLSpVrVPNYNLixMDEAHFTDPASIA
ILHV	GAGKTRRVIPQIVRECVKARLRTVILAPTRVVAEMAeALRGLPIRYQTSaVkaEHxGrEIVDIMCHATLTLQRLTPAKVPNYNVFVMDAEAHFTDPASIA
ROCV	GAGKTRRVIPQIVREAVKQRLRTVILAPTRVVAEIAEALRGLPVRFQTSaVkaEHxGrEIVDMCHATLTLQRLMTPMRVPNYNVFVMDAEAHFTDPASIA
WNV	GAGKTRRILPQIKKAIINRRLRTAVLAPTRVVAEMAeALRGLPIRYQTSaVPREHNGNEIVDMCHATLTHRLMSPHRVPNYNLFVMDAEAHFTDPASIA
JEV	GSGKTRKILPQIKDAIQQLRTAVLAPTRVVAEMAeALRGLPVRYQTSaVQREHQNGNEIVDMCHATLTHRLMSPNRPVNYNLFVMDAEAHFTDPASIA
DENV1	GSGKTRRYLPAIVREAIRRVNRTLVLAPTRVVAEMAeALRGLPIRYQTTAVKSEHTGREIVDLMCHATFTMRLLSPVVVPNYNMIIMDEAHFTDPASIA
DENV2	GAGKTKRYLPAIVREAIRKRLRTLILAPTRVVAEMAeALRGLPIRYQTPAIRAHTGREIVDLMCHATFTMRLLSPVVVPNYNLIIMDEAHFTDPASIA
DENV3	GSGKTRKYLPAIVREAIRKRLRTLILAPTRVVAEMAeALRGLPIRYQTTAVKSEHTGREIVDLMCHATFTMRLLSPVVVPNYNLIIMDEAHFTDPASIA
DENV4	GAGKTKRILPQIVREALKRLRTLILAPTRVVAEMAeALRGLPIRYQTPAVKSEHTGREIVDLMCHATFTMRLLSSTRVPNYNLIIMDEAHFTDPSSIA
ZIKV	GAGKTRRILPQIVREALKRLRTLILAPTRVVAEMAeALRGLPIRYMTTAVNVTHSGREIVDLMCHATFTSRLQPIVVPNYNLIIMDEAHFTDPSSIA
YFV	GAGKTRRFLPQILAEARRRLRTLVLAPTRVVLSEMKFAFHGLDVKFHTQAFSAHSGREVIDAMCHATLTYRMLPEPTRVNVWEVIMDEAHFLDPASIA

Ruler 1	310 320 330 340 350 360 370 380 390
Consensus	ARGYISTRVEmGEAAAFMTATPPGTtDPPFPxSNaPIxDDeErEIPeRaWNSGfEWITDyTGKTVWFVPSxKaGNeIAxCLrKAGKKVlQLxRKTfDEYq
ILHV	ARGYISTKVELGEAAAFMTATPPGTtDPPFDSNAPIIDQEAEIPDRAWNSGFEWITDYTGKTVWFVPSVVRMGNEIAMCLTKAGKKVlQLNRKSYDSEYQ
ROCV	ARGYISTKVELGEAAAFMTATPPGTtDPPFDSNSPIIIDQEAEIPDRAWNSGFEWITDYTGKTVWFVPSVRSNGNEIAMCLTKAGKKVlQLNRKSYETEYQ
WNV	ARGYISTKVELGEAAAFMTATPPGTSDPPFESNSPIISDLQTEIPDRAWNSGFEWITEYTGKTVWFVPSVKMGNEIALCLQRAGKKVlQLNRKSYETEYP
JEV	ARGYIATKVELGEAAAFMTATPPGTtDPPFDSNAPIHDLQDEIPDRAWNSGFEWITEYAGKTVWFVPSVVKMGNEIAMCLQRAGKKVlQLNRKSYETEYP
DENV1	ARGYISTRVGMGEAAAFMTATPPGSVEAFPQSNAPIQDEERDIPERSWNSGFEWITDFPGKTVWFVPSIKSGNDIANCLRKNKGRVlQLSRKTFDEYQ
DENV2	ARGYISTRVEMGEAAAFMTATPPGSRDPPFQSNAPIIMDEEREIPERSWSGHEWITDFKGTWVFPVPSIKAGNDIAACLKRNKGGVlQLSRKTFDSEYQ
DENV3	ARGYISTRVGMGEAAAFMTATPPGTADAFPQSNAPIQDEERDIPERSWNSGFEWITDFYKGTWVFPVPSIKAGNDIANCLRKNKGGVlQLSRKTFDEYQ
DENV4	ARGYISTRVEMGEAAAFMTATPPGATDPPFQSNAPIQDEEREIPERSWNTGFDWITDYQKGTWVFPVPSIKAGNDIANCLRKNKGGVlQLSRKTFDEYQ
ZIKV	ARGYISTRVEMGEAAAFMTATPPGTRDAFPDSNSPIIMDTEVEVPERAWSGFDWITDHSKGTWVFPVPSVVRNGNEIAMCLTKAGKRVlQLSRKTFETEYQ
YFV	ARGWAAHRRANESATILMTATPPGTSDFEPHSNGEIEDVQTDIPSEPWNTGHDWILADKRPTAWFLPSIRANVMAASLRKAGKSVVVLNRKTFEREYQ

Ruler 1	410 420 430 440 450 460 470 480 490
Consensus	KtKnnDWDfVvTTDISEMGANFkAdRVIdXRrCxKPVILtdGeeRVILaGpMvPTaASAAQRGRIGRNPNqEGDeYiYgGpxIeDDeDHAWtEAKMLL
ILHV	KCKGNDWDFVvTTDISEMGANFGAHRVIDSRCKVKPVIL-DGDDRVLMNGPAPITPASAAQRGRIGRDPTQSGDEYFYGGPttDDTGHAHWIEAKILL
ROCV	KCKGNDWDFVvTTDISEMGANFGAHRVIDSRCKVKPVIINDGGERVQLNGPLITASAAQRGRVGRDPTQSGDEYFYGGPITNDTGHAHWIEAKMLL
WNV	KCKNDWDFVvTTDISEMGANFKASRVIDSRSVKPTIIEGEGRVILGEPVAVTASAAQRGRIGRNPSQSGDEYCYGGHTNEDDSNFAHWIEAKIML
JEV	KCKGNDWDFVvTTDISEMGANFGASRVIDCRKSVKPTIIEEGEGRVILGNPSPITSASAAQRGRVGRNPNQVGDDEYHYGGATSEDDSNLAHWIEAKIML
DENV1	KTKNNDWDFVvTTDISEMGANFRADRIDPRRCLKPVILKDGPERVILAGPMPVTVASAAQRGRIGRNQKEDGQYIYMGQPLNDEDAHWT EAKMLL
DENV2	KTRTNDWDFVvTTDISEMGANFKASRVIDPRRCMKPVILTDEGERVILAGPMPVTVASAAQRGRIGRNPNKNDQYIYMGQPLENDEDAHWT EAKMLL
DENV3	KTKLNDWDFVvTTDISEMGANFKADRVIDPRRCLKPVILTNGPERVILAGPMPVTVASAAQRGRVGRNPNQKENDQYIFMGQPLNDEDAHWT EAKMLL
DENV4	KTKLNDWDFVvTTDISEMGANFRAGRVIDPRRCLKPVILTNGPERVILAGPMPVTVASAAQRGRIGRNPAQEDDQYVFGDPLKNDEDAHWT EAKMLL
ZIKV	KTKNQEDWDFVvTTDISEMGANFKADRVIDSRRCLKPVILD--GERVILAGPMPVTVASAAQRGRIGRNPNKPGDEYMGYGGCAETDEDAHWT EAKMLL
YFV	TIKQKPPDFILATDIAEMGANLCEVRLDCRTAFKPVLVDEG-RKVAIKGPLRISASSAAQRGRIGRNPNRDGDSYVYSEPTSEDNAHHVCWLEASMLL

Ruler 1	510 520 530 540 550 560 570 580 590
Consensus	DNIntPxGIIAqLYgPEREKvAaIDGEYRLRGEqRktFVELMRrGDLpVWLxYKVAAsAGIxYtDRRWCfDgPrNNxILEDNmEV-EIWTkeGExKkLRPR
ILHV	DNILQLNGLVAQLYGPREDKVFtTDDGEYRLRGEQKKNFVFLRTGDLpVWLxYKVAEAGYAYTDRRWCfDgPANNtILEDNNEV-EIWTQRQGEKRILRPR
ROCV	DNILQLNGLVAQLYGPREDKVFtTDDGEYRLRGEQKKNFVFLRTGDLpVWLxYKVAEAGYAYTDRRWCfDgPHNNtILEDNTEV-EIWTQRQGERKVLPR
WNV	DNINMPNGLIAQFYQPEREKVYtMDGEYRLRGEERKNFLELLRTADLPVWLAYKVAAGVSYHDDRWCfDgPRTNTILEDNNEV-EVITKLGERRKILRPR
JEV	DNINMPNGLVAQLYGPREDKALtMDGEYRLRGEERKNFLELLRTADLPVWLAYKVASGQYTDKWCfDgPRTNAILEDNTEV-EIVTRMGERKILRPR
DENV1	DNINTPEGIIPALFPEREKSAaIDGEYRLRGEARKTfVELMRGDLPVWLAYKVASAGIEGfYSDRRWCfDGERNNQVLEENMDV-EIWTKEGERKCLRPR
DENV2	DNINTPEGIIPSMFPEREKVDAIDGEYRLRGEARKTfVdLMRRGDLPVWLAYRVAEEGfNYADRRWCfDGIKNNQILEENVEV-EIWTKEGERKCLRPR
DENV3	DNINTPEGIIPALFPEREKSAaIDGEYRLRGEARKTfVELMRGDLPVWLAYKVASAGIEGfYTDKWCfDGERNNQILEENMDV-EIWTKEGERKCLRPR
DENV4	DNITYTPEGIIPALFPEREKSAaIDGEFRLRGEARKTfVELMRGDLPVWLAYKVASAGIEGfYKDRWCfDGERNNQILEENMDV-EIWTREGEKCLRPR
ZIKV	DNILYLDGLIASLYRPEADKVAaIEGfKLRTEQRKtFVELMRGDLPVWLAYQVAsAGIYtDRRWCfDGTNTNTIMEDSVPA-EVWTKYGERKCLRPR
YFV	DNMEVRGGMVAPLYGVEGtKTPVSPGEMRLRDDQRKVFRELVRNCDLPVWLxSWQVAKAGLKTNDKWCfEGPEEHEILNDSGETVCKRPPGAKKPLRPR

Ruler 1	610 620
Consensus	WIDARVYSDpqaLKeFKEFAAGxR
ILHV	WSDARVYCDNQALRSFKEFAAGKR
ROCV	WSDARVYSDNQALRAFKEFAAGKR
WNV	WIDARVYSDHQALKAFKDFASGR
JEV	WLDARVYADHQALKWFKDFAAAGKR
DENV1	WLDARTYSDPLALREFKEFAAGRR
DENV2	WLDARVYSDPLALKEFKEFAAGRK
DENV3	WLDARTYSDPLALKEFKDFAAAGRK
DENV4	WLDARVYADPMALKDFKEFAAGRK
ZIKV	WMDARVYSDHAALKSFKEFAAGKR
YFV	WCDERVYSDQSALSEFIKFAEGR

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# NS4A and 2K

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	-sAlxliEVIgRIPdhtxKtrxALDNLyVLxTAEkGGRAYRhALEELPxTLETxxLiAlIgvxTgGxFIFIMxxKGIGKxgIGxIvIxaaxxLLWmAeV
ILHV	-SAGSVMEVMGRMPDYFWTKTLNAADNLVYVLTANKGGRRAHQAALEELPDVTETILLMTMMCVASLGMFALMVHRRGLGKTGLGTLVLATVTVLLWISDV
ROCV	-SAGSMMDVMA RMPDYFWTKTMNAADNLVYVLTATEKGGRAHRAALEELPDLTETVLLIAMMSLASCGMLALMMQRKGIKGTGMGTAVLTAVTILLWMAADV
WNV	-SQIGLIEVLGKMPHFHMGKTWEALDTMYVVAATAEKGGRAHRMALEELPDALQTIALLSVMTMGVFFLLMQRKGIKIGLGGAVLGVATFFCWMAEV
JEV	-SAVSFIEVLGRMPEHFHMGKTRREALDTMYLVATAEKGGKAHRMALEELPDALETITLIVAIVTMTGGFFLLMMQRKGIKMGGLGALVLTATFFLWAAEV
DENV1	SVSGDLILEIGKLPQHLTQRAQNALDNLVMLHNSEQGGKAYRHAMEELPDITETLMLLALIAVLTGGVTLFFLSGRGLGKTSIGLLCVIASSALLWMAASV
DENV2	SLTLNLIITEMGRLPFTMQKARDALDNLAVLHTAEAGGRAYNHALSELPETLETLLLLTLLATVTGGIFLFLMSGRGIGKMTLGMCCIITASILLWYAQI
DENV3	SIALDLVTEIGRVPSHLAHRTRNALDNLVMLHTSEHGGRAYRHAVEELPEMTETLMLLLGLMILLTGGAMLFLISGKGIGKTSIGLICVIASSGMLWMAADV
DENV4	SITLDILTEIASLPTYLSSRAKALDNLVMLHTTERGGRAYQHANELPESELETMLLVALLGAMTAGIFLFFMQGKIGIKLSMGLIAIAVASGLLWVAEI
ZIKV	GAALGVMEALGTLPGHMTERFQEAIDNLAVLMRAETGSRPYKAAAQLEPETLETIMLLGLLGTVSLGIFVFLMRNKGIGKMGFGMVTLGASAWLMWLSEI
YFV	-GAAEVLVVLSELPDFLAKKGGAEAMDTISVFLHSEEGSRAYRNALSMMPPEAMTIVMLFILAAGLLTSGMVIFFMSPKGISRMSMAMGMTMAGCGYLMFLGGV

Ruler 1	110 120 130 140
Consensus	pptxIAGxIIIeFILMVVLIPEPEKQRSpQDNQLAyxIlicITLvgA VAA
ILHV	PAPKIAGVLLIAFLLMIVL IPEPEKQRSQTDNHLAIFLVCVLLLIGAVSA
ROCV	PAPKIAGVLLISFLLMIVL IPEPEKQRSQTDNHLAVFLICALLLVSAVSA
WNV	PGTKIAGMLLLSLLLMIVL IPEPEKQRSQTDNQLAVFLICVMTLVSAVAA
JEV	PGTKIAGTLLIAALLMMVVL IPEPEKQRSQTDNQLAVFLICVLTVVGMVAA
DENV1	EPHWIAASIIIEFFLMVLL IPEPDQRTPQDNQLAYVVIGLLFMILTAA
DENV2	QPHWIAASIIIEFFLIVLL IPEPEKQRTPQDNQLTYVVIAILTVVAATMA
DENV3	PLQWIAASIVLEFFMMVLL IPEPEKQRTPQDNQLAYVVIGILTAAIVAA
DENV4	QPQWIAASIIIEFFLMVLL IPEPEKQRTPQDNQLIYVILTITLTIIGLIAA
ZIKV	EPARIACVLI VVFLLLVVL IPEPEKQRSQDNQMAIIMVAVGLLGLITA
YFV	KPTHISYIMLIFVLMVVV IPEPGQQRSIQDNQVAYLIIIGILTLVSVVAA

**Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses.** Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

# NS4B

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	NEMGWLExTKkDLGxIfggr-e-----we-sxIDIDL RPA sAWtLYAvATTvLTPmLRHIIIt nsYxNxSLtAIA nQAsvL fGLxKGwPFx kmDLgVpLL
ILHV	NEMGWLETTKKDIGKLF R SSGD TQEQSTWQSW--APEVRAATAWAGYAGLVFTLPLFRHLITTTQYVFSFLTAITAQASALFGLSAGYPFVGI DLAVGFL
ROCV	NEMGWLDTTKRDLGKLFSGPSAV-TTSRWEPLKLALALKPATAWAGYAGMTMLTLPFRHLITTTQYIFSFLTAITSQASALFGLNSGYPFVVDLSVVFLL
WNV	NEMGWLDKTKSDISSLFGQRIEYKENFSM--GEFLDLRPA TAWSLYAVTTAVLTPLL KHLITSDYINTSLTSINVQASALFTLARGFPFVDVGV SALLL
JEV	NEYGMLEXTKADLKSFMFGGKTQASGLTGL--PSMALDLRPA TAWALYGGSTVVLTPLL KHLITSEYVTTSLASINSQAGSLFVLPGRGYPFTDLDLTVGLV
DENV1	NEMGLLETTKKDLGIGHAA-ENH---HHAAMLVDLHPASAWTLYAVATTIITPMMRHTIENTTANISLTAIANQAAILMGLDKGWPI SKMDIGVPLL
DENV2	NEMGFLEKTKKDLGLGSIIT-Q-Q---PESNILDLRPA SAWTLYAVATTFVTPMLRHSIENS SVNSLTAIANQATVLMGLGKGWPLSKMDIGVPLL
DENV3	NEMGLLETTKRDLGMSKEPG-V-V---SSTSYLDVLDHPASAWTLYAVATTVITPMLRHTIENS TANVSLAAIANQAVVLMGLDKGWPI SKMDLGVPLL
DENV4	NEMGLIEKTKTDFGFYQVK-----TETTLVDL RPA SAWTLYAVATTIITPMLRHTIENSANLSLAAIANQAAVLMGLGKGWPLHRMDLGVPLL
ZIKV	NELGWLERTKNDIAHLMRREEGA---TMGFSMDILRPA SAWA IYAAL TLTIPAVQHAVTTSYNNYS LMAMATQAGVLF GMGKGMPFYAWDLGVPLL
YFV	NELGMLEKTKEDLFGKKNLIPS--SASPW--SWPDLDLKPGA AVTVYVGI V TMLSPMLHHWIKVEYGNLSLSGIAQSASVLSFMDKGI PFMKMNISVIL

Ruler 1	110 120 130 140 150 160 170 180 190
Consensus	aIGCYsQvNpXTLxAAixLLvaHYaxigPGIQAxA tRxAQKRTAAGIMKNPVVDGIVa tDxxevx-ydPkfEKKLGQVMLLVLCaaqxLImRTwa l cEa
ILHV	LLGCGYQYNLPTAVATGLLLLAHYGYMIPGWQA EAMRAAQKRTAAGVMKNAVVDGIVATDIPEDVTATPI TEKLLGQILLILL CGASLLVKFDTMVLVEA
ROCV	LVGCGYQYNLPTTMTATIGLLVGHYAFMIPGWQA EAMRAAQRRTAAGVMKNAVVDGIVATDIPEDMTATPI VEKMMGQVMLLISALAILLNDPTMTVVEG
WNV	AAGCGWQVTLT VVTAA TLLFCHYAYMVPGWQA EAMRS AQRRTAAGIMKNAVVDGIVATDVPELERTTPI MQKKGQIMLLILVSLAAVVVNP SVKTVREA
JEV	FLGCGWQITLTTVL TAMVLA TLHYGYMLPGWQA EALRAAQRRTAAGIMKNAVVDGMVATDVPELERTTPLMQKKGQVLLIGV SVAFLVNPVNTTVREA
DENV1	ALGCGSQVNP LTLAAVFLVAHYAIIGPGLQAKATRE AQKRTAAGIMKNPTVDGIVAILDLPVV-YDAKFEKQLGQIMLLILCTSQILLMRTT WALCEA
DENV2	AIGCGSQVNPITLTAALXLLVAHYAIIGPGLQAKATRE AQKRAAGIMKNPTVDGITVIDLDPPI-YDPKFEKQLGQVMLLVLCVTVLMMRTT WALCEA
DENV3	ALGCGSQVNP LTLAAVLLVTHYAIIGPGLQAKATRE AQKRTAAGIMKNPTVDGIMTVIDLDPVI-YDSKFEKQLGQVMLLVLCAGVQLLMRTS WALCEV
DENV4	AMGCGSQVNP TLLIASLVMLLVHYAIIGPGLQAKATRE AQKRTAAGIMKNPTVDGITVIDLEPIS-YDPKFEKQLGQVMLLVLCAGQQLLMRTT WAFCEV
ZIKV	MMGCGSQLTPTLLIVAILLVVAHYMYLIPGLQAAAAAAQKRTAAGIMKNPVVDGIVVTDIDTMT-IDPQVEKMMGQVLLIAYASVAVLLRTAWGWGEA
YFV	LVS G WNSITVMPLLCIGCAMLHWSLILPGIKAQQS KLAQR RVHGVAKNPVVDGNPTVDIEEAPEMPALY EKLLALVLLLALS LASVAMCRTPFSLAEG

Ruler 1	210 220 230 240 250
Consensus	gxLaTaAixTLWEGnpgkxWNxTiAVSmcnIxRGSYLAGaxIax tliiKNxxpxr--
ILHV	GVLTTSAMATLIEGNANTVWNS TVAVGVCHLMRGAWLAGPSIGWTIVRNLENP K LKR
ROCV	GVLITAAALATLIEGNANTVWNS TVAVGVCHLMRGGWAAGPSIGWTIVRNLEAPKVKR
WNV	GILITAAAVTLWENGASVWNATTAIGLCHIMRGGWLSCLSIWTWLIK NMEK PGLKR
JEV	GVLVTAATLLWDNGASAVWNS TTATGLCHVMRGSYLAGGSAIWTLIK NADKPSLKR
DENV1	ITLATGPTTLWEGSPGKFWNTTIAVSMANIFRGSYLAGAGLAFSLMKSLGGRR--
DENV2	LLLATGPISTLWEGNPGRFWNTTIAVSMANIFRGSYLAGAGLLFSIMKNTTNTRR--
DENV3	LLLATGPISTLWEGSPGKFWNTTIAVSMANIFRGSYLAGAGLAFSLMKSVGTGR--
DENV4	LLLATGPPVTLWEGNPGRFWNTTIAVSTANIFRGSYLAGAGLAFSLIKNAQTFR--
ZIKV	GALITAAATSLWEGSPKNYWNSTATSLCNIFRGSYLAGASLIYVTVTRNAGLVKRR--
YFV	IVLASAALGPIEGNTSLWNGPMAVSMTGVMRGNYYAFVGVMYNLWKMKTGR--

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# NS5

Ruler 1	1 10 20 30 40 50 60 70 80 90
Consensus	-GGaxGeTLGekWkRrLNQLsrEEFxxYKxsGiiEVDRTeAxAiKeGxxtgGHAVSRGxAKLRWxVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
ILHV	-GGGSAPTIGEiWKAQLNQLTREEFMAYRRDGiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
ROCV	-GGIAAPTIGEiWKSRLNQLTREQFMEYRKDGiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
WNV	-GGAGKRTIGEiWkERLNQMTKEEFTRYRKEAiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
JEV	-GRPGGRTIGEiWkEKLNAMSRKEEFKYRREAiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
DENV1	GTGAQGGTEIGEiWkKRQLNQLSKSEFNTRYKRSGiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
DENV2	GTGNIGETIGEiWkKRNALGKSEFQIYKKSQiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
DENV3	GTGSGGETIGEiWkKRNALGKSEFQIYKKSQiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
DENV4	GTGTTGETIGEiWkKRQLNQLSRKEEFKYRREAiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
ZIKV	-GGGTGETIGEiWkKARLNQMSALEFYSYKKSQiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe
YFV	-GSANGKTLIGEiWkKRELNQLDQKQFELyKRTDiLEVDRTAARRARQSGiTTGGHPVSRGTAkLRWlVVERGFvKPeGKVxDLGCGRGGWYYcATLkKvQe

Ruler 1	110 120 130 140 150 160 170 180 190
Consensus	VRGYTKGGPGHEEPmxMQSYGWNiVxLKSgVDVfYkPpEkCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-gpnqFCIKVLCpYMPkviEkleRLQ
ILHV	VRGYTKGGPGHEEPVMMQSYGWNiVxLKSgVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-AANSFCIKVLCpYMPkviEkleRLQ
ROCV	VRGYTKGGPGHEEPMLMQSYGWNiVxLKSgVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-TANQYCVKLCpYMPkviEkleRLQ
WNV	VRGYTKGGPGHEEPQLVQSYGWNiVxLKSgVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-CVKKLCpYMPkviEkleRLQ
JEV	VRGYTKGGAGHEEPMLMQSYGWNiVxLKSgVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-CIKVLCpYMPkviEkleRLQ
DENV1	VKGYTKGGPGHEEPiPMATYGNWLVKLYSGVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-G-NQFCIKVLCpYMPkviEkleRLQ
DENV2	VKGLTKGGPGHEEPiPMSTYGNWLVKLYSGVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-NNTQFCIKVLCpYMPkviEkleRLQ
DENV3	VRGYTKGGPGHEEPVPMSTYGNWLVKLYSGVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-N-NQFCIKVLCpYMPkviEkleRLQ
DENV4	VKGYTKGGPGHEEPiPMATYGNWLVKLYSGVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-SKPEFCIKVLCpYMPkviEkleRLQ
ZIKV	VRGYTKGGPGHEEPMLVQSYGWNiVxLKSgVDVfYkPpECCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-CIKVLCpYMPkviEkleRLQ
YFV	VKGFLLGRDGHKPMNVQSLGWNiITFKDKTDIHRLEPVKCDTLLEDIGESSxSPtVEEgRTLRLVxMVEpWlR-CVKKLCpYMPkviEkleRLQ

Ruler 1	210 220 230 240 250 260 270 280 290
Consensus	RkxGGgLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
ILHV	RAYGGGLVrVPLSRNSTHEMYVWSGASSNiINAVTvtSqiLVQRmNKGCRHGRPYEEDVCLGSGTRAVATQASPSDHTKIKHRLERLRKEFSATWHDLE
ROCV	RKYGGGLVrVPLSRNSTHEMYVWSGASSNiINAVNATsqVLLQRLEKDRKGRPYEEDVCLGSGTRAVATQASPSDHTKIKHRLERLRKEFSATWHDLE
WNV	RRYGGGLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
JEV	RRFGGGLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
DENV1	RKHGGMLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
DENV2	RKHGGMLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
DENV3	RKHGGMLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
DENV4	RKHGGMLVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
ZIKV	RRHGGGLVrVPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde
YFV	RRFGGTVrNPLSRNSTHEMYVWSGASniVsvNmTsqxLLnRmtxrh-rxPtyEeDvDLGSGTRaVatexepmxIxgRIERxKeEhstTWHYDde

Ruler 1	310 320 330 340 350 360 370 380 390
Consensus	HPYRTWaYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
ILHV	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
ROCV	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
WNV	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
JEV	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
DENV1	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
DENV2	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
DENV3	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
DENV4	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
ZIKV	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE
YFV	HPYRTWHYHGSEYKpTGSASSMVNGVvLxKpWdVipmVtXmAMTDTPFGQQRVfKEKVDTRaPePxxGtXvMniTxnWlWafLgReKrPrXCTRE

Ruler 1	410 420 430 440 450 460 470 480 490
Consensus	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
ILHV	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
ROCV	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
WNV	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
JEV	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
DENV1	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
DENV2	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
DENV3	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
DENV4	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
ZIKV	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW
YFV	EFiXKvRSNAALGAVFEEQNWQSTARAEVDPFVWNLVDEERKAHLGRCECTIYNMMGKREKKEGFGKAGSRAIWMWLGARFLFEALGFLNEDHW

Ruler 1	510 520 530 540 550 560 570 580 590
Consensus	FSRENSGGVGEGLQKLGlyILRDiSkppGgkMyADDTAGWDTRITeDLeNEAKITnqMxPehRkLlAxAlixLtyqNkVvKvRPApGgkTVMdIISrX
ILHV	MSRENSGGVGEGLQKLGlyILRDiShLEGGNMFADDTAGWDTRITRADLENEAKVMNMMDGHEKQLAKAIIElTYRHkVvKvMPrARGGkTVMdIISrX
ROCV	MSRENSGGVGEGLQKLGlyILRDiSrKEGGHMFADDTAGWDTRITRADLENEAKITRWMEPEHRKLAEMAIElTYKkVvKvRPGEGkTVMdIISrX
WNV	LGRKNSGGVGEGLQKLGlyILRDiREYVTRPGGKIYADDTAGWDTRITRADLENEAKVLELDGHRRLARAIElTYRHkVvKvMPrAADGkTVMdIISrX
JEV	LSRENSGGVGEGLQKLGlyILRDiAGKGGKMYADDTAGWDTRITRADLENEAKVLELDGHRRLARAIElTYRHkVvKvMPrAAGkTVMdIISrX
DENV1	FSRENSGGVGEGLQKLGlyILRDiSkIPGGNMFADDTAGWDTRITEDDLNEAKITnqMxPehRkLlAxAlixLtyqNkVvKvRPApGgkTVMdIISrX
DENV2	FSRENSGGVGEGLQKLGlyILRDiSkKEGGAMyADDTAGWDTRITLEDLkNEEMVtNHMEGHEKkLAEAlfKlTYQkVvKvRQRPtPrg-TVMdIISrX
DENV3	FSRENSGGVGEGLQKLGlyILRDiSkIPGGAMyADDTAGWDTRITEDDLNEAKITnqMxPehRkLlAxAlixLtyqNkVvKvRQRPtPrg-TVMdIISrX
DENV4	FSRENSGGVGEGLQKLGlyILRDiSkIDKDDGLYADDTAGWDTRITEDDLNEAKITnqMxPehRkLlAxAlixLtyqNkVvKvRQRPtPrg-TVMdIISrX
ZIKV	MGRENSGGVGEGLQKLGlyILRDiEEMNRPAGGKMYADDTAGWDTRITSKFDLENEAlTnqMxPehRkLlAxAlixLtyqNkVvKvRPApGgkTVMdIISrX
YFV	ASRENSGGVGEGLQKLGlyILRDiLAAMDGGGfYADDTAGWDTRITEDDLNEAKITnqMxPehRkLlAxAlixLtyqNkVvKvRPApGgkTVMdIISrX

Ruler 1	610 620 630 640 650 660 670 680 690
Consensus	DQRGSQVVTYALNTFTNiXVQLIRqMEgEGVxxpadiexl-kxkkaevrXWlxenGxERLkRMAxSGDDCVVkpIDDRFATAlHFLNDMgKVRKDIQEW
ILHV	DQRGSQVVTYALNTFTNLAQLVRCMEGELLTESDyHGLSPKkKQAVRNWLIQNGRERLSMAVSGDDCVVkpIDDRFASALHFLNGMAKIRKDTQEW
ROCV	DQRGSQVVTYALNTFTNLAQLVRCMEGELLTEETMRISDAGRRAQWLDNtGTERLSMAVSGDDCVVkpIDDRFATAlHFLNGMSKVRKDIQEW
WNV	DQRGSQVVTYALNTFTNLAQLVRCMEGELLTEETMRISDAGRRAQWLDNtGTERLSMAVSGDDCVVkpIDDRFATAlHFLNGMSKVRKDIQEW
JEV	DQRGSQVVTYALNTFTNLAQLVRCMEGELLTEETMRISDAGRRAQWLDNtGTERLSMAVSGDDCVVkpIDDRFATAlHFLNGMSKVRKDIQEW
DENV1	DQRGSQVVTYALNTFTNiAVQLVRLMEAGVIGPQHLQELPRKNIkAVRTWLFENGEERYTRMAISGDDCVVkpIDDRFATAlHFLNAMS KVRKDIQEW
DENV2	DQRGSQVGTyGLNTFTNMEaQLIRQMESEGIspSELETP-NL-AERVLdWlKKGHTERLKRMAISGDDCVVkpIDDRFATAlHFLNDMGKVRKDIQEW
DENV3	DQRGSQVGTyGLNTFTNMEaQLIRQMESEGIspSELETP-NL-AERVLdWlKKGHTERLKRMAISGDDCVVkpIDDRFATAlHFLNDMGKVRKDIQEW
DENV4	DQRGSQVGTyGLNTFTNMEaQLIRQMESEGIspSELETP-NL-AERVLdWlKKGHTERLKRMAISGDDCVVkpIDDRFATAlHFLNDMGKVRKDIQEW
ZIKV	DQRGSQVVTYALNTFTNLAQLVRCMEAGVILEEMQDLWLLRk--PEKvYRWLQSGWDRlKRMAVSGDDCVVkpIDDRFATAlHFLNDMGKVRKDIQEW
YFV	DQRGSQVVTYALNTFTNLAQLVRCMEAGVILEEMQDLWLLRk--PEKvYRWLQSGWDRlKRMAVSGDDCVVkpIDDRFATAlHFLNDMGKVRKDIQEW

Ruler 1	710 720 730 740 750 760 770 780 790
Consensus	kPskGwNDWQqVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
ILHV	KPsvGWSNWQEVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
ROCV	KPSTGWTNWQEVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
WNV	KPSTGWTNWQEVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
JEV	KPshGWDWQVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
DENV1	EPskGWNWQVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
DENV2	EPskGWNWQVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
DENV3	EPskGWNWQVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
DENV4	EPskGWNWQVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
ZIKV	KPSTGWSNWQEVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYAQMWLLMYFHRRDLRLmANaICSAVpVdWVPTGRTT
YFV	QPSKGNWDEWVpFCSHHFhELiMkDGRiVvPCRnQDELIGRARxSPGAGWSLRETAclGkAYANMWSLMYFHRRDLRLmANaICSAVpVdWVPTGRTT

Ruler 1	810 820 830 840 850 860 870 880 890
Consensus	WSiHAKGEMWTTEDMLxVWNRVWiiEENpMwMEDKTPtSwxVpYlGKREDqWCGSLIGIRsRATWAEiNixtAInQVRnLIGD-EkyvDYmpSmkRxeDee
ILHV	WSiHAKGEMWTTEDMLxVWNRVWiiEDNEHMEKTPiTSWTDiPyiGKREDQWCGSLIGTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
ROCV	WSiHAKGEMWTTEDMLxVWNRVWiiEENEHMEKTPiTSWTDiPyiGKREDQWCGSLIGTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
WNV	WSiHAGGEMWTTEDMLxVWNRVWiiEENEHMEKTPiTSWTDiPyiGKREDQWCGSLIGTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
JEV	WSiHAKGEMWTTEDMLxVWNRVWiiEENEHMEKTPiTSWTDiPyiGKREDQWCGSLIGTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
DENV1	WSiHAKHQMWTEDMLxVWNRVWiiEENPMWEDKTHVSWEDiPyiGKREDQWCGSLIGLTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
DENV2	WSiHAKHQMWTEDMLxVWNRVWiiEENPMWEDKTHVSWEDiPyiGKREDQWCGSLIGLTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
DENV3	WSiHAKHQMWTEDMLxVWNRVWiiEENPMWEDKTHVSWEDiPyiGKREDQWCGSLIGLTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
DENV4	WSiHAKHQMWTEDMLxVWNRVWiiEENPMWEDKTHVSWEDiPyiGKREDQWCGSLIGLTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
ZIKV	WSiHAKGEMWTTEDMLxVWNRVWiiEENHMEKTPiTSWTDiPyiGKREDQWCGSLIGTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee
YFV	WSiHAKGEMWTTEDMLxVWNRVWiiEENHMEKTPiTSWTDiPyiGKREDQWCGSLIGTRATWAEiNixtAInQVRnLIGD-EKYVDYMPsmkRxeDee

Ruler 1	Consensus
ILHV	PVLFtGAI-
ROCV	ELQ-GGVl-
WNV	LVED-TVL-
JEV	IQED-RVI-
DENV1	DPE--GALW
DENV2	EAA--GVLW
DENV3	ESE--GAiW
DENV4	ESE--GVL-
ZIKV	GSTP-GVL-
YFV	DLQPELI-

**Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses.** Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green. Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.