

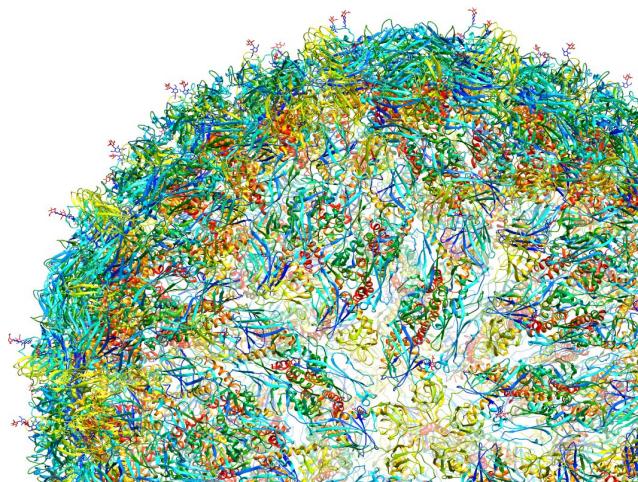
Structure of *Zika virus* (*Flavivirus*)

Campos M, Canales A,
Díaz J, Llerena M.

Structural Biology
Human Biology, UPF
2018-2019

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FLAVIVIRIDAE FAMILY

- Includes a huge number of virus
- **Genuses:** *Flavivirus*, *Pestivirus*, *Hepacivirus*

Mosquito-borne viruses

Zika virus (ZIKV)

Dengue virus (DENV)

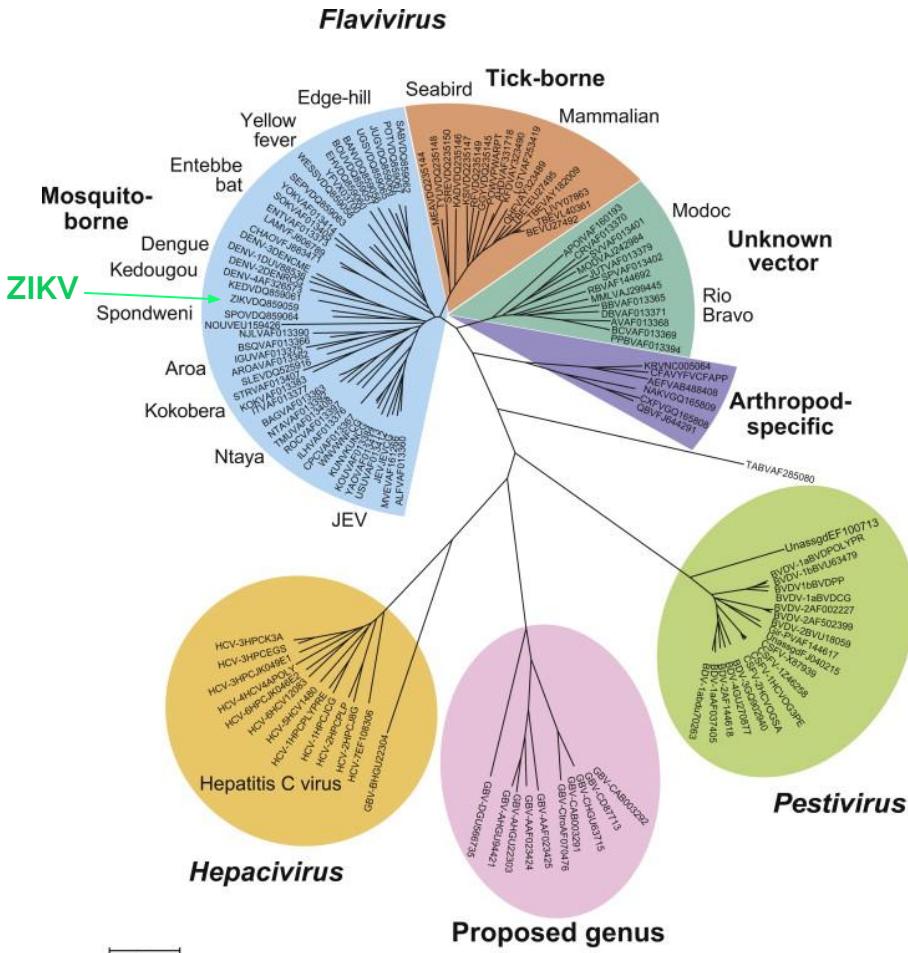
West Nile virus (WNV)

Japanese encephalitis virus (JEV)

10

Flaviviridae phylogeny.

Source: International Committee on Taxonomy of Viruses (2012)



Zika virus (ZIKV)



PUBLIC HEALTH CONCERN

FEBRUARY 2, 2016

Zika Virus: Global Public Health Emergency

ALERTA SANITARIA

Primera muerte de un bebé en EEUU por zika

09/08/2016 - 20:04 CEST

Zika: one in seven babies with mothers exposed to virus developed health issues

New study is first to examine health of children beyond birth after mothers were exposed to mosquito-borne disease

Catalunya afronta un risc moderat-alt de Zika, dengue i Chikungunya, segons l'Organització Mundial de la Salut

El número de diagnosticados por zika en España se eleva ya a 247

29/08/2016 - 16:09 CEST

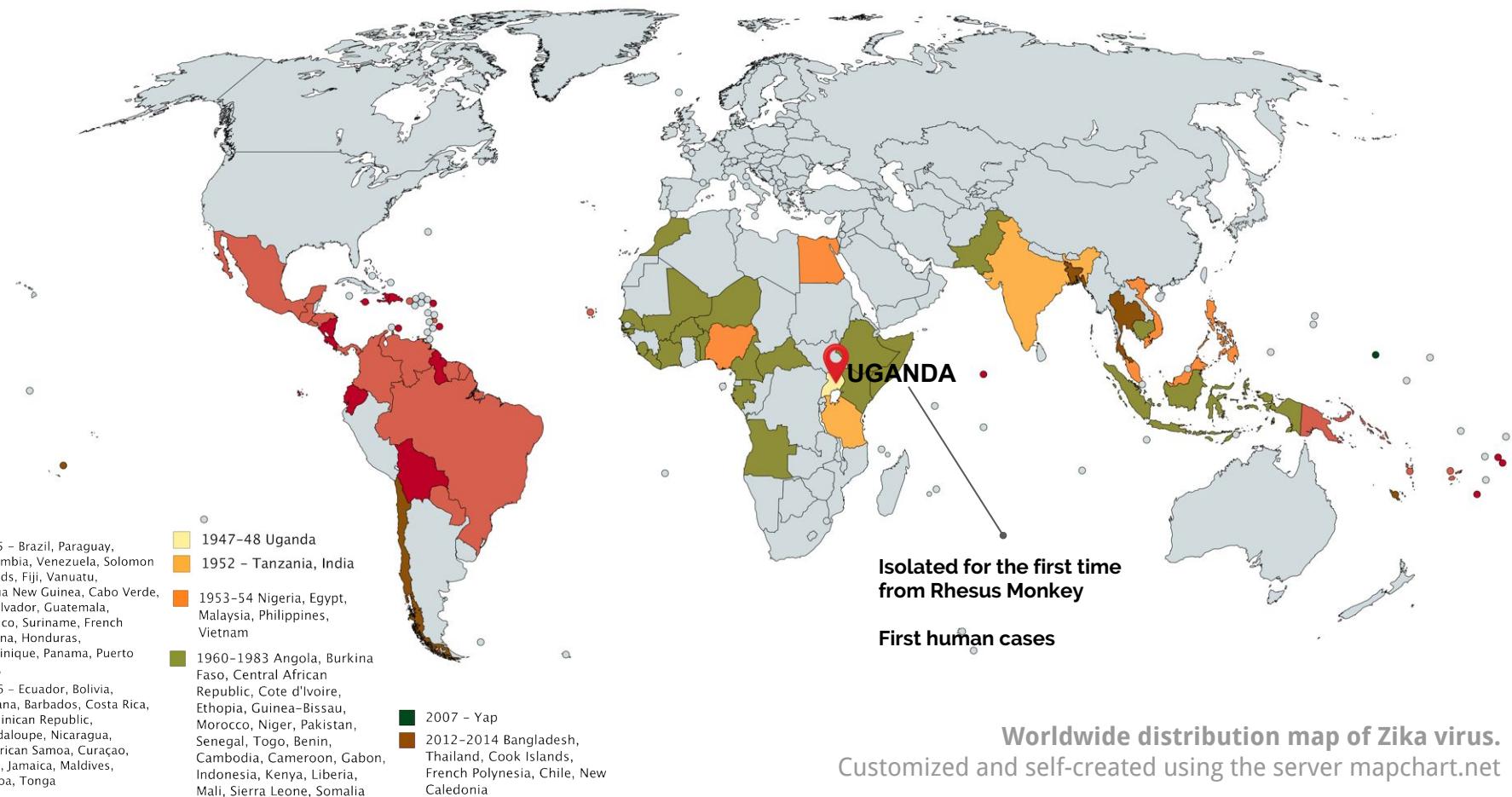
Entre los afectados hay 39 embarazadas, una más que en el anterior recuento

Detecten quatre nous casos de Zika a Catalunya, entre els quals una embarassada

Amb aquests, el nombre d'infectats a casa nostra s'eleva fins a 45, 19 homes i 26 dones

Acn | Barcelona | 17.05.2016 | 12:33

WORLDWIDE DISTRIBUTION OF ZIKA VIRUS



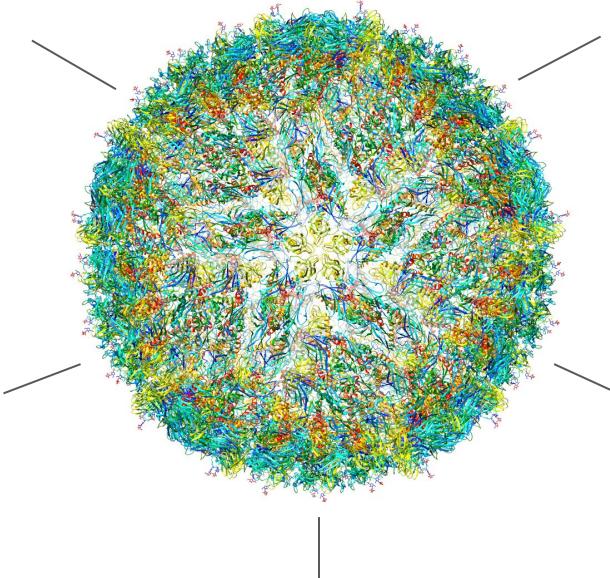
MAIN FEATURES OF ZIKA VIRUS

Characteristics:

Flavivirus genus

With icosahedral envelope

Positive stranded RNA virus



Symptoms:

Mild disease, lasting around 2-7 days

(rash, headache, diarrhea, fever, joint and muscle pain, conjuntivitis)



- Low death risk
- Increased **risk of microcephaly** in fetus

Transmission:

Mosquito bite

(*Aedes aegypti*, *Aedes albopictus*)

Sexual

Intrauterine

Blood transfusion



Hosts:

Rodents

Pigs

Birds

Primates

Humans



NO treatment or vaccine is available



ZIKV STRUCTURE

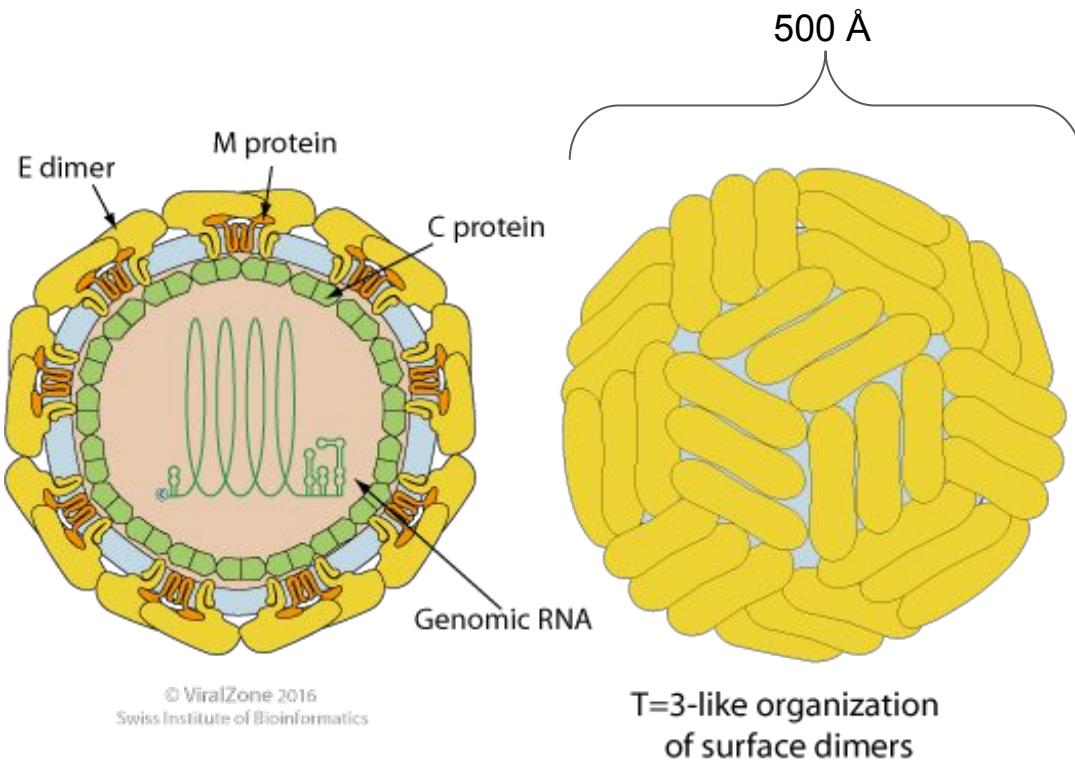
Capsid protein (C)

Envelope protein (E)

Membrane protein (M)

Immature:

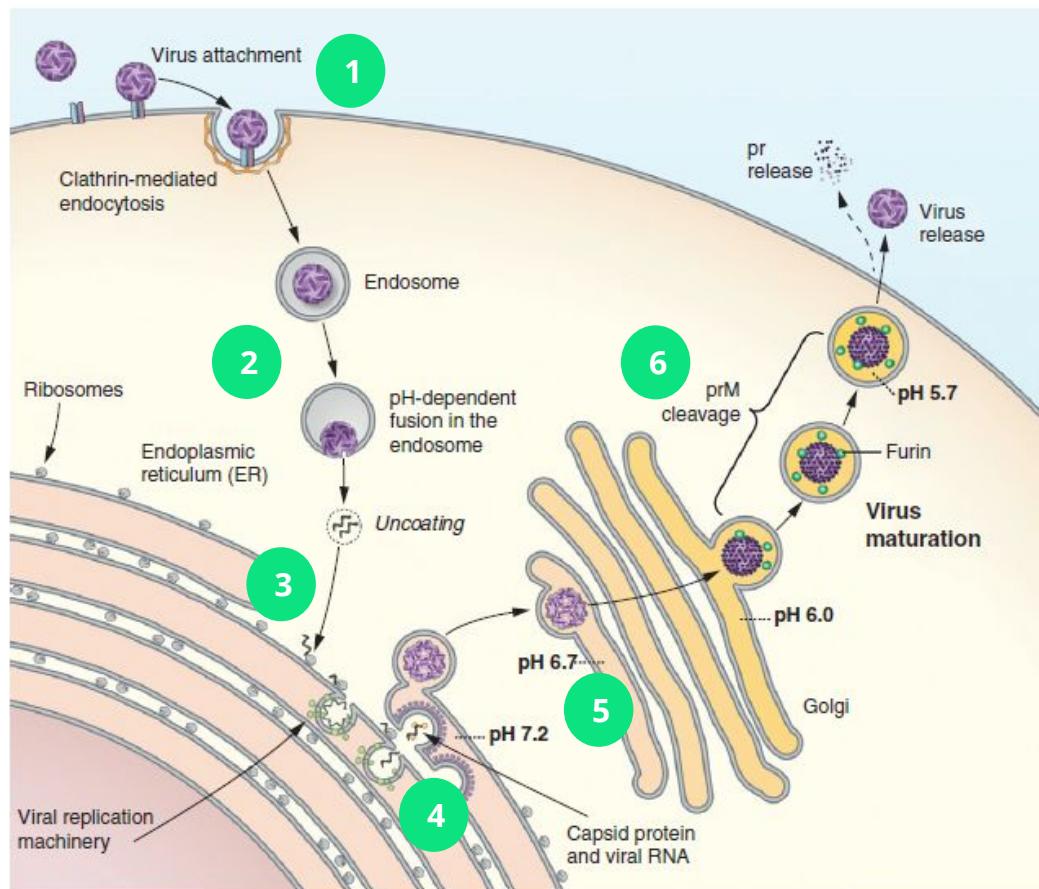
Premembrane protein (prM)



T=3-like organization
of surface dimers

INFECTION CYCLE

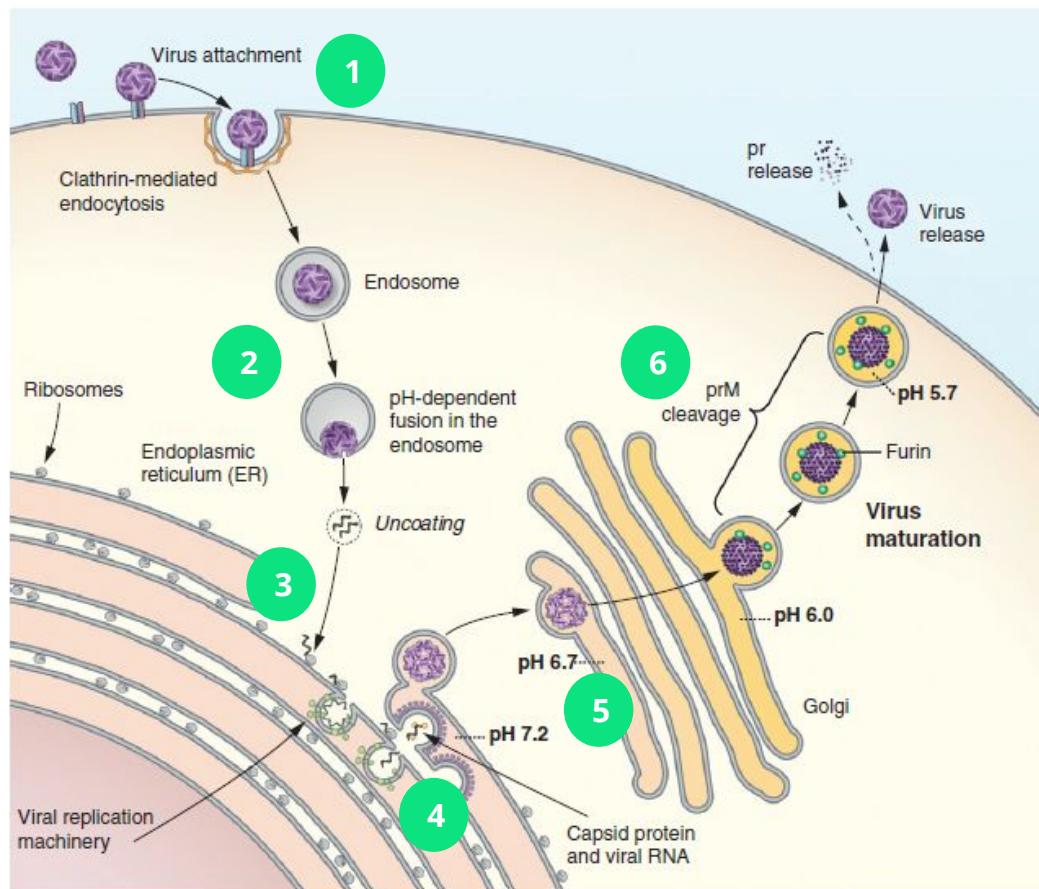
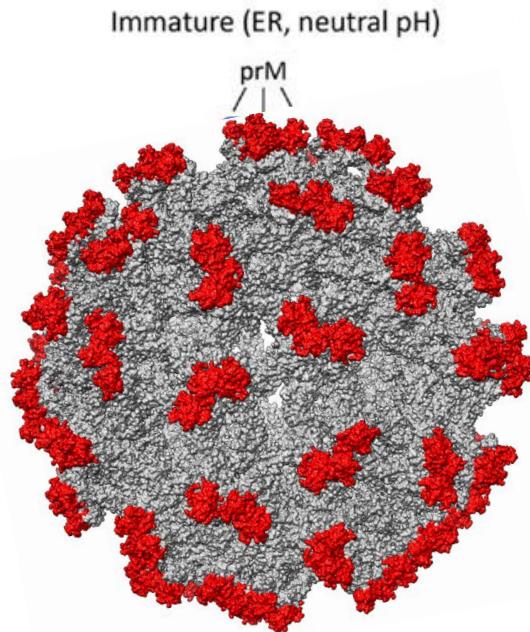
- 1 Attachment + Endocytosis
- 2 pH-dependent fusion
- 3 Releasement of RNA to the cytoplasm and entry to Endoplasmic Reticulum (ER)
- 4 Synthesis of viral proteins
- 5 Assembly of virions particles
- 6 Rearrangement - furin cleavage



Flavivirus infection cycle. Source: Pierson TC et al. (2012)

Current Opinion in Virology

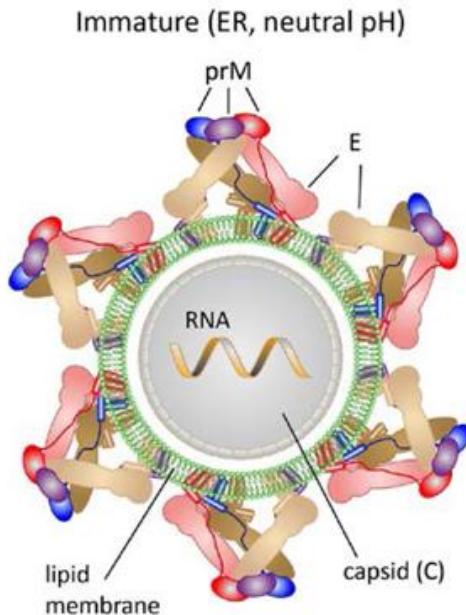
INFECTION CYCLE



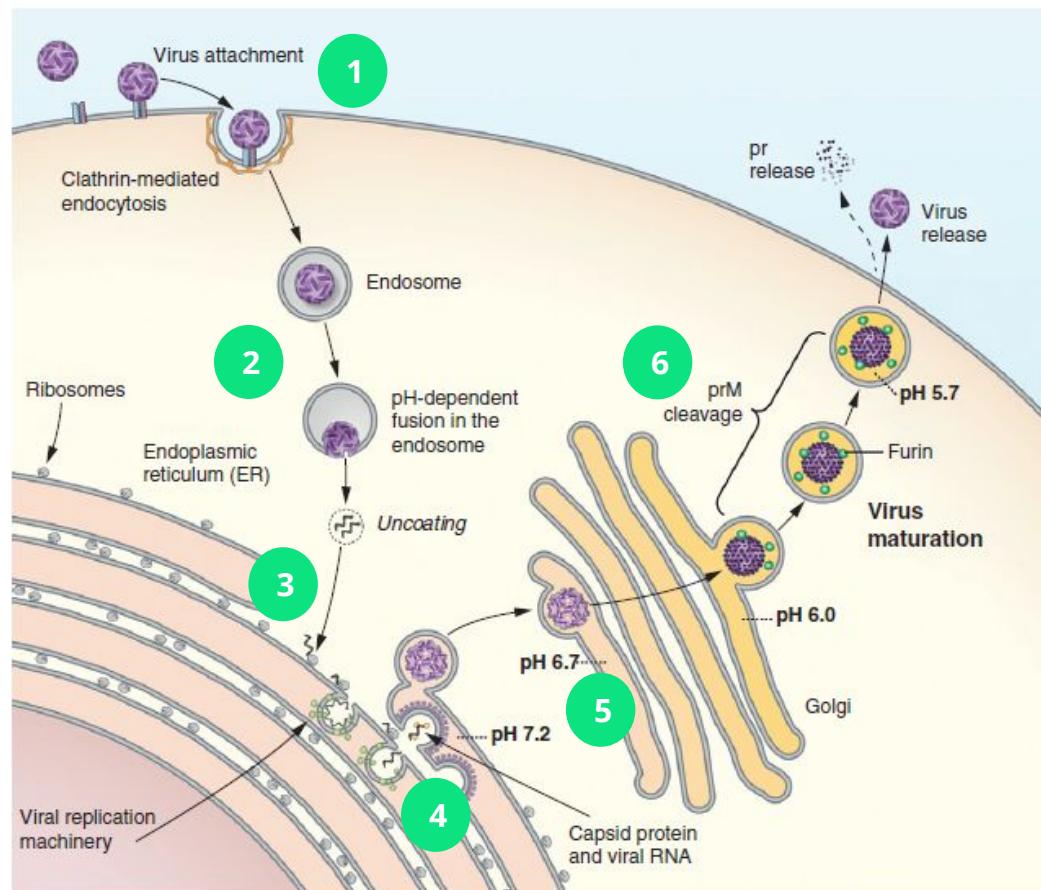
Flavivirus infection cycle. Source: Pierson TC et al. (2012)

Current Opinion in Virology

INFECTION CYCLE



Modified from Rey F et al. (2017)

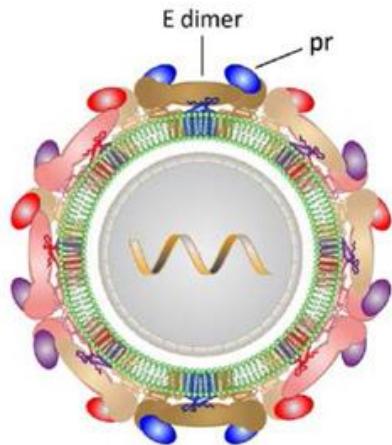


Flavivirus infection cycle. Source: Pierson TC et al. (2012)

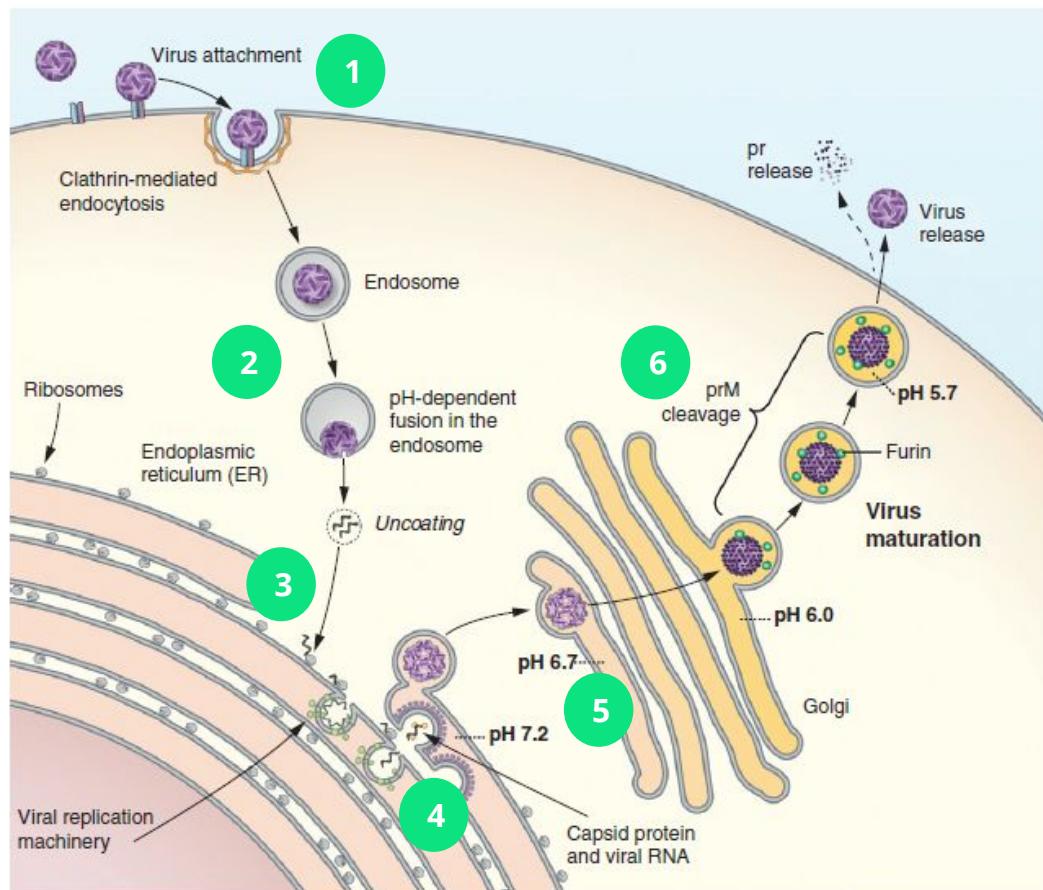
Current Opinion in Virology

INFECTION CYCLE

Immature (TGN, acidic pH)



Modified from Rey F et al. (2017)

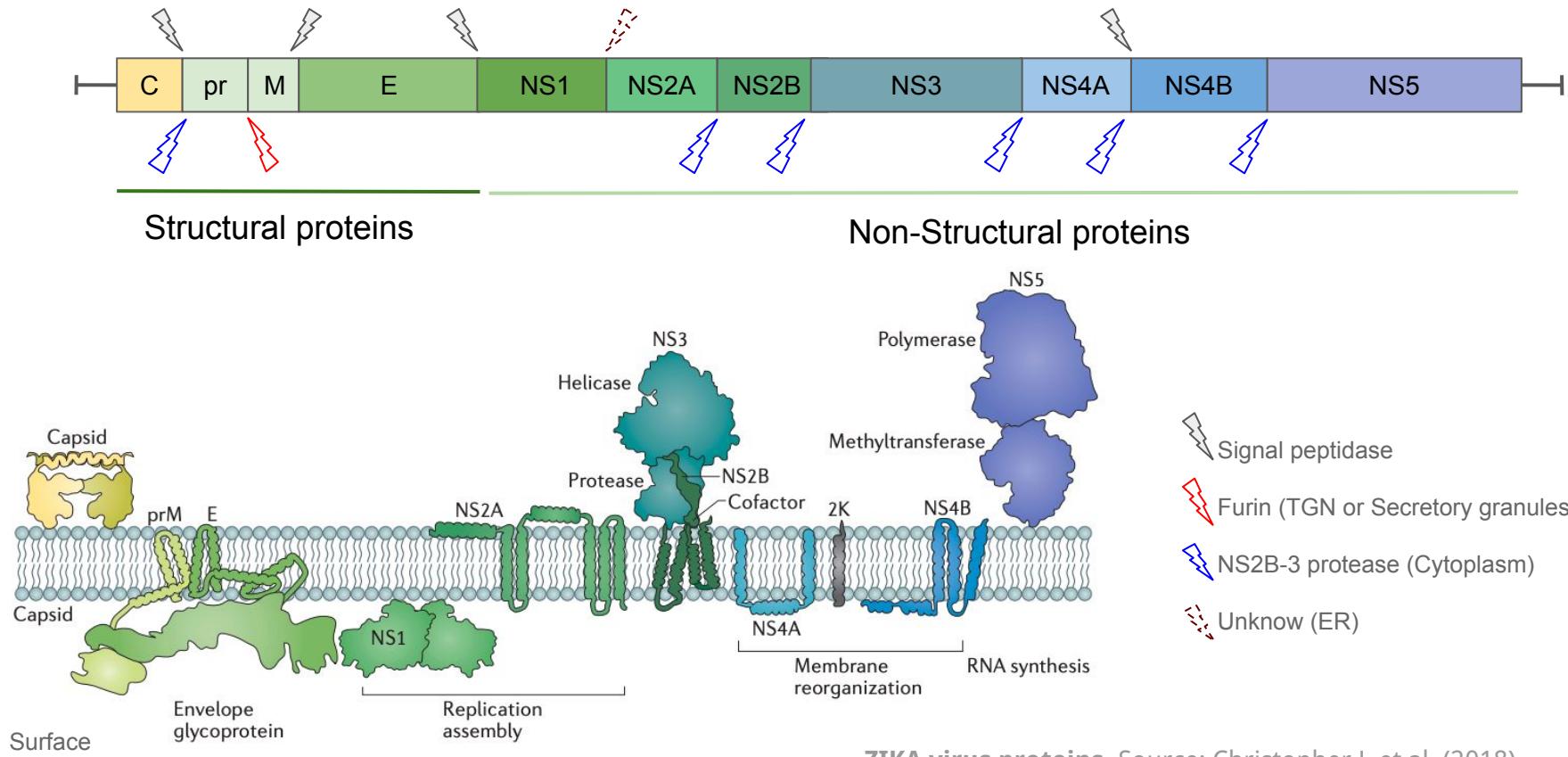


Flavivirus infection cycle. Source: Pierson TC et al. (2012)

Current Opinion in Virology

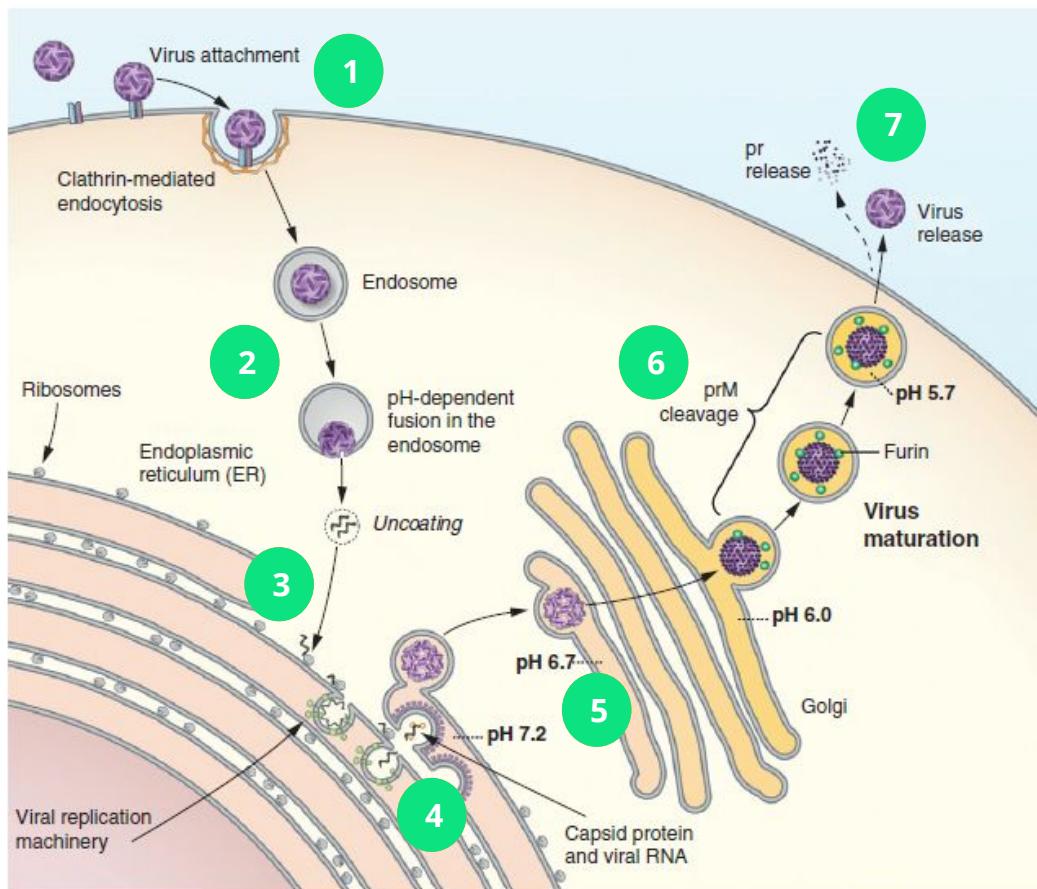
INFECTION CYCLE

PROTEIN PROCESSING



INFECTION CYCLE

- 1 Attachment + Endocytosis
- 2 pH-dependent fusion
- 3 Releasement of RNA to the cytoplasm and entry to Endoplasmic Reticulum (ER)
- 4 Synthesis of viral proteins
- 5 Assembly of virions particles
- 6 Rearrangement - furin cleavage
- 7 Pr domain releasement

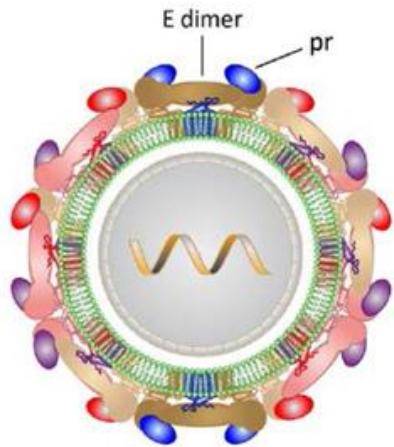


Flavivirus infection cycle. Source: Pierson TC et al. (2012)

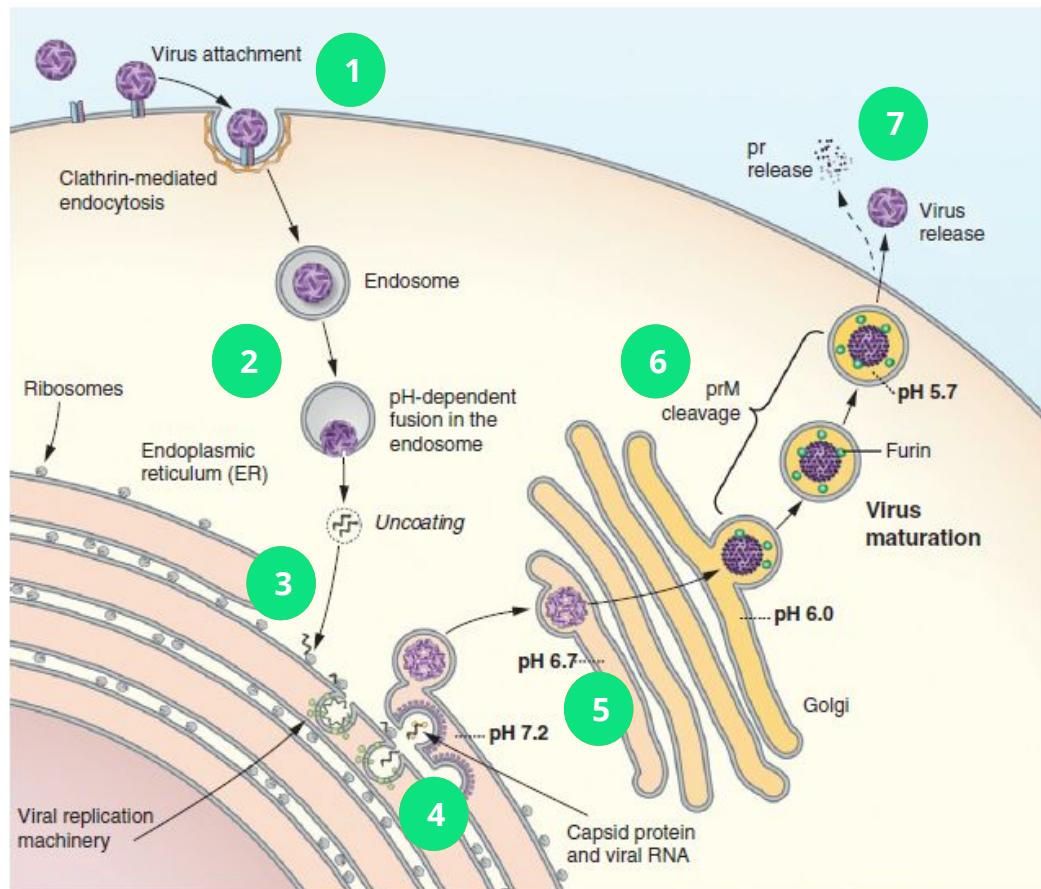
Current Opinion in Virology

INFECTION CYCLE

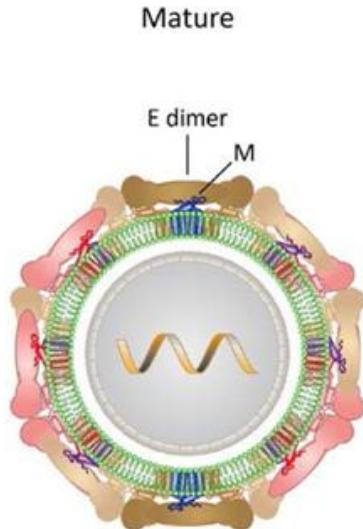
Immature (TGN, acidic pH)



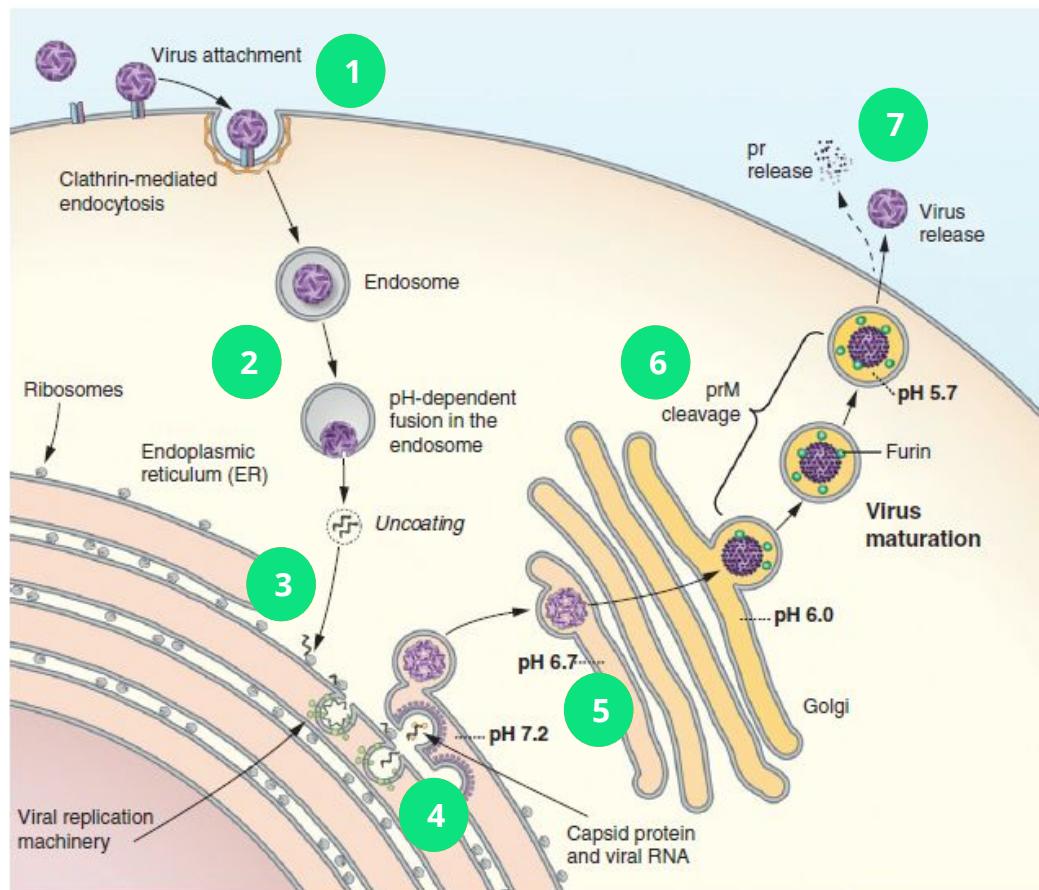
Modified from Rey F et al. (2017)



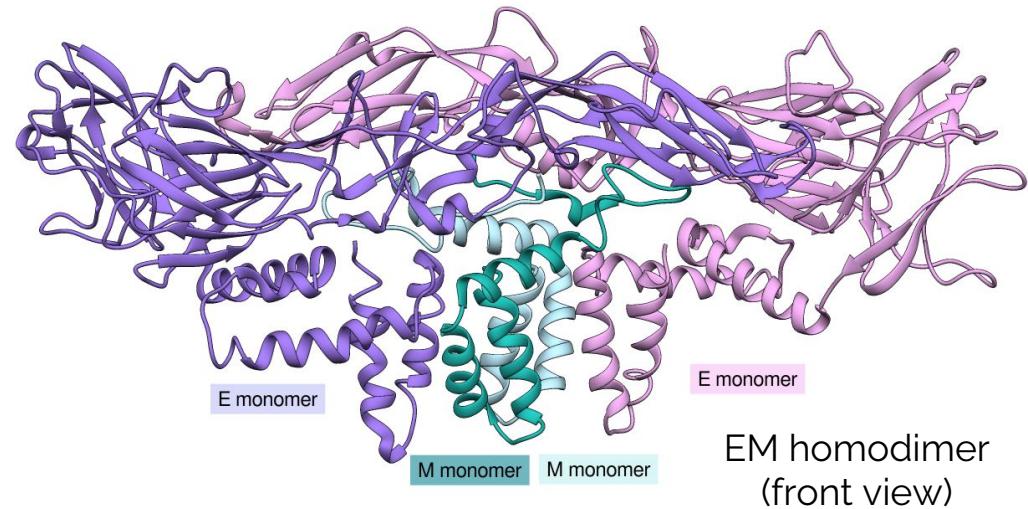
INFECTION CYCLE



Modified from Rey F et al. (2017)

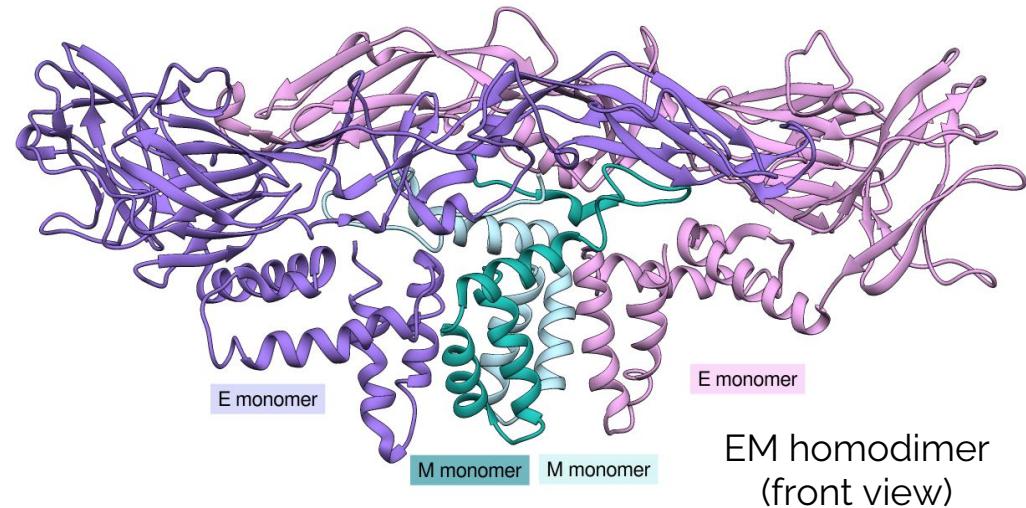


Envelope elements



Envelope elements

E protein



E PROTEIN: MAIN FEATURES

Important role in

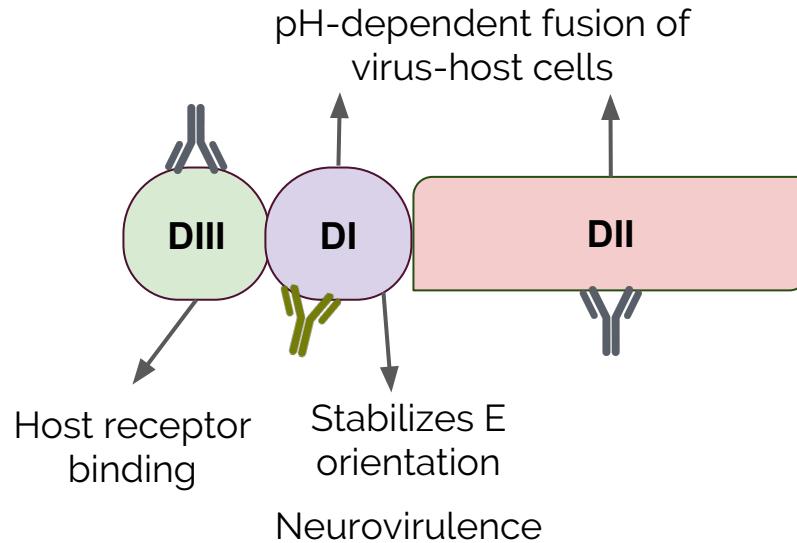
Cell attachment

Membrane fusion

Cell tropism

Assembly and maturation

Antigenicity



Main target of antibodies

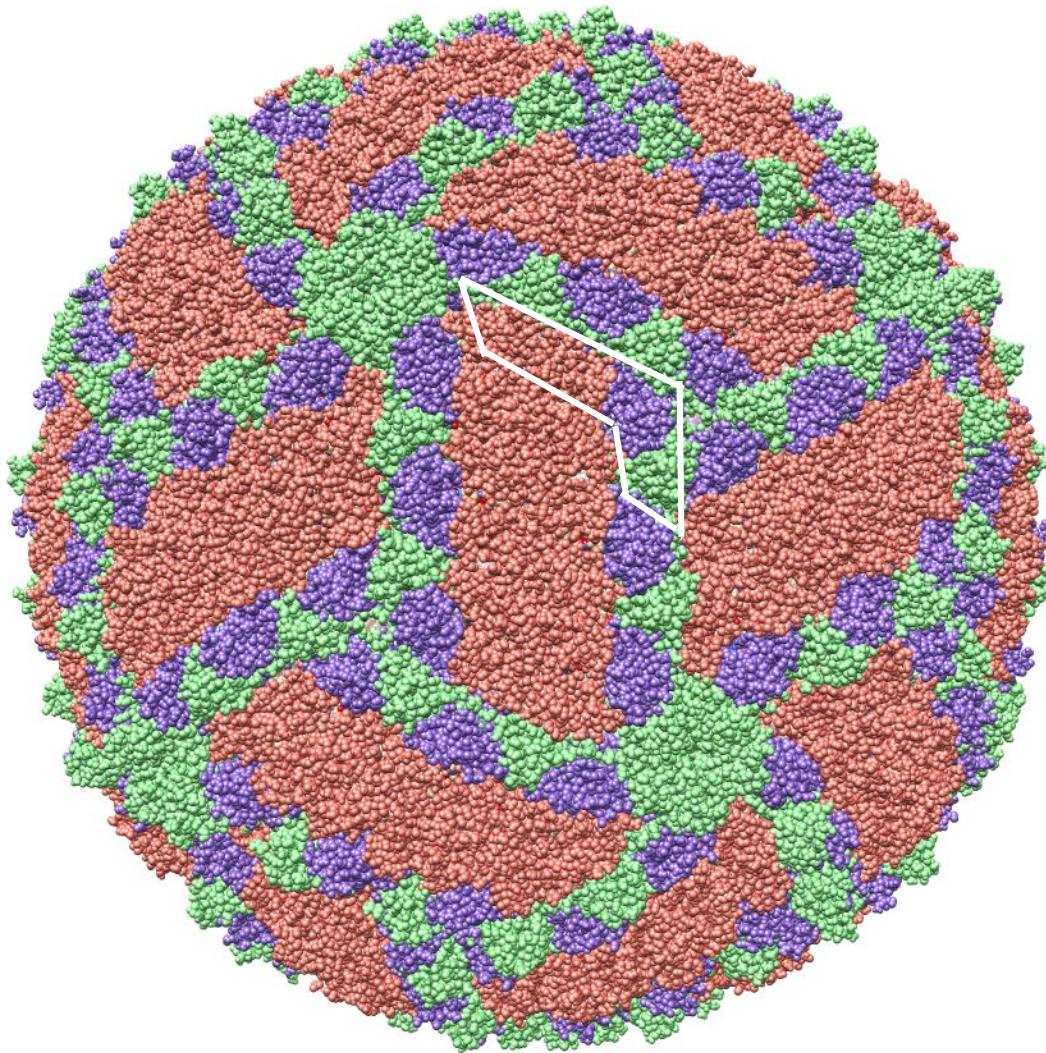


Neutralizing epitopes



Non-neutralizing epitopes

E PROTEIN

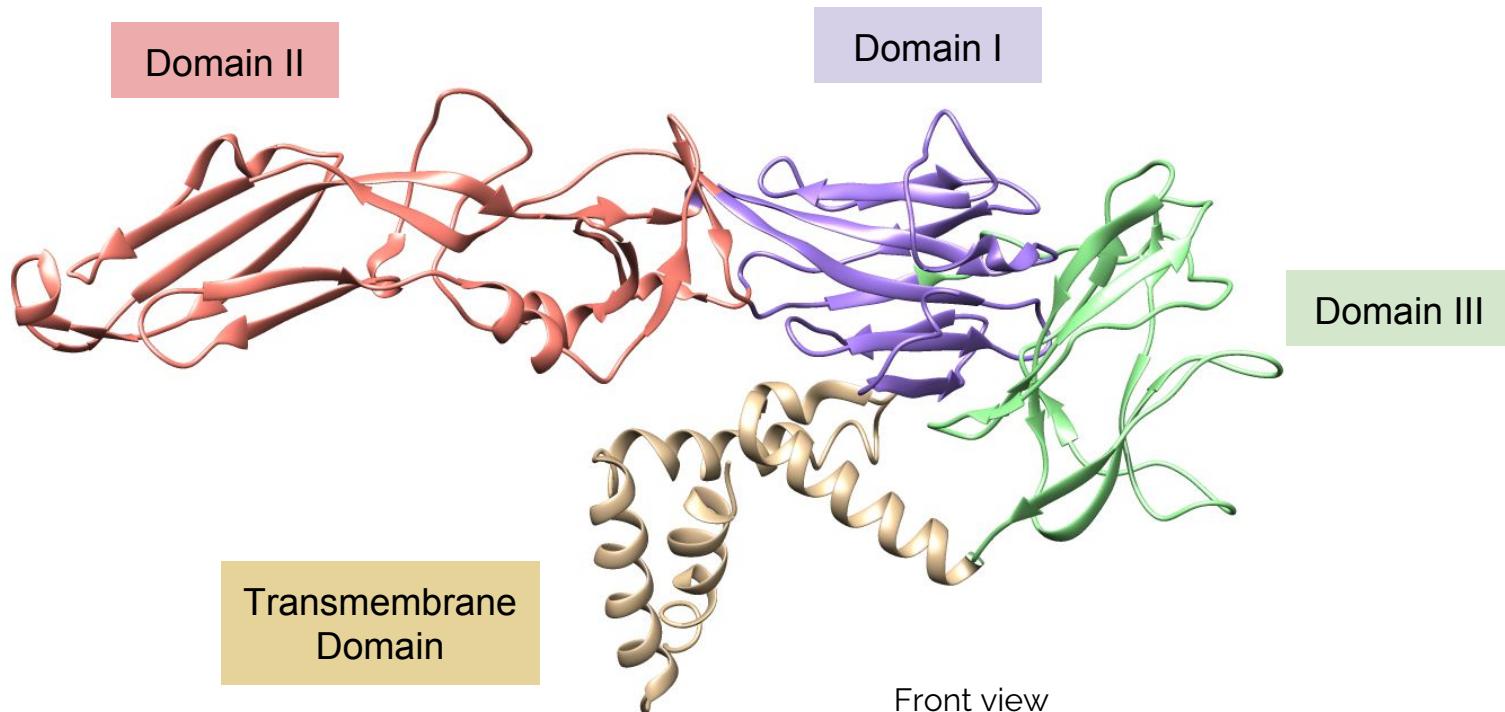


Domain I

Domain II

Domain III

E PROTEIN



E PROTEIN: TOPOLOGICAL DIAGRAM

Domain I

- 9 β strands (A_0 - I_0)
- 3_{10} helix

→ In the N-terminus

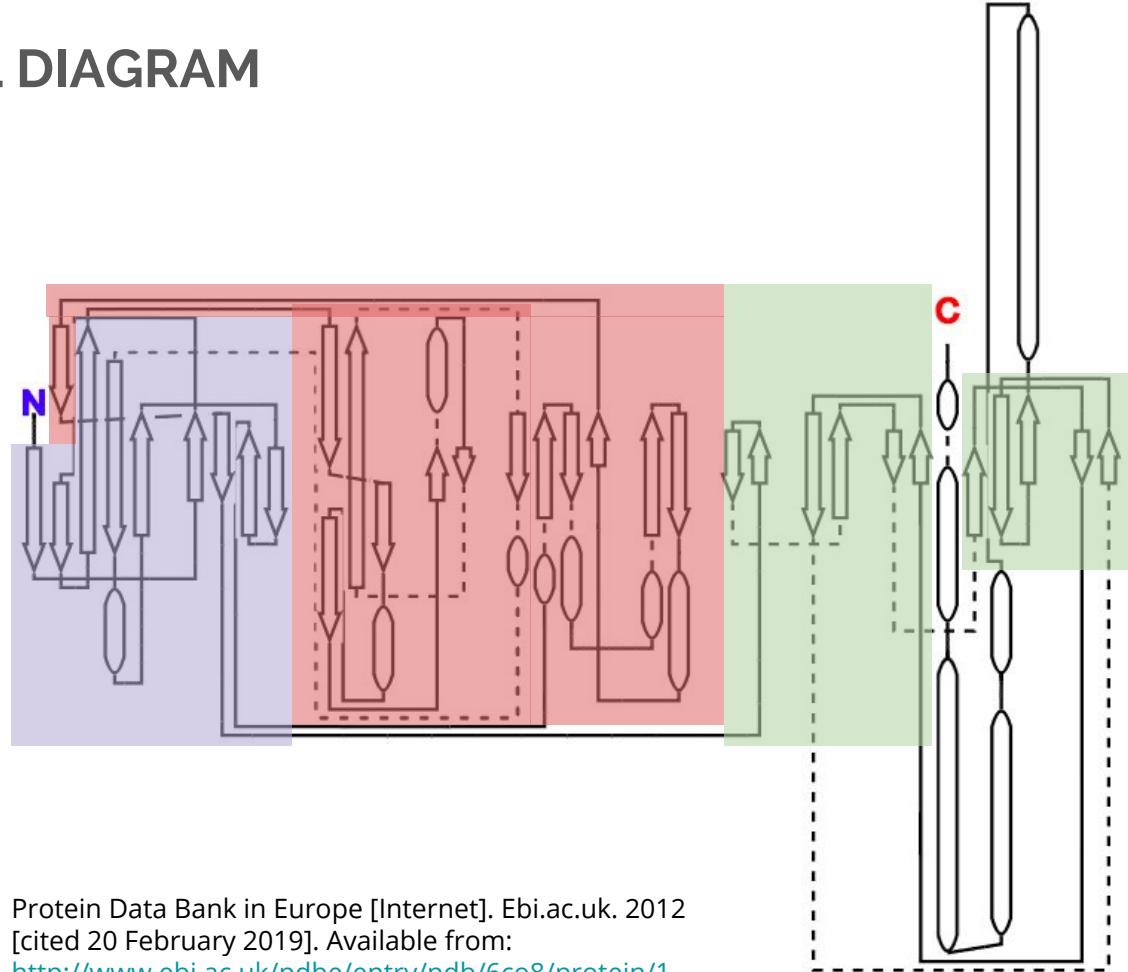
Domain II

- 9 β strands (a-i)
- 2 α helix (A,B)

Domain III

- 7 β strands (A-G)

→ In the C-terminus

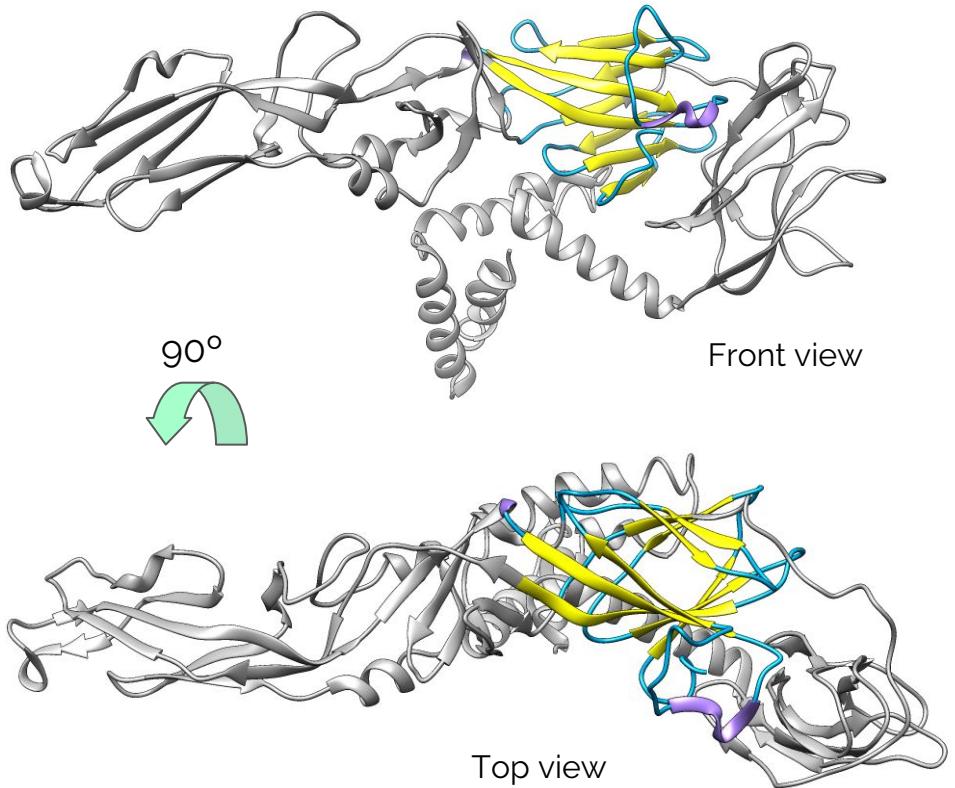


Protein Data Bank in Europe [Internet]. Ebi.ac.uk. 2012 [cited 20 February 2019]. Available from: <http://www.ebi.ac.uk/pdbe/entry/pdb/6co8/protein/1>

E PROTEIN: DOMAINS

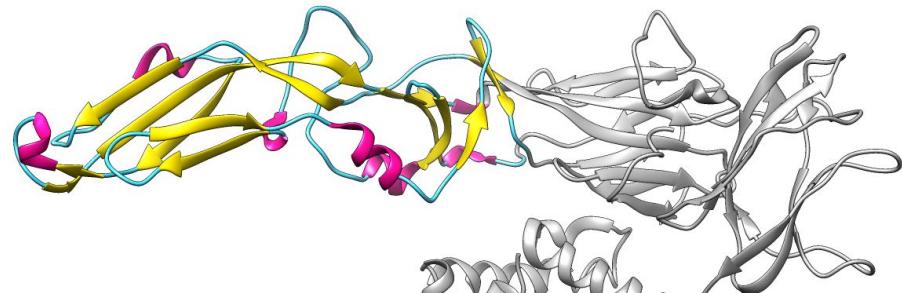
DOMAIN I	
Level	
C	Mainly Beta
A	Sandwich
T	Tick-borne Encephalitis virus Glycoprotein; domain 1
H	Tick-borne Encephalitis virus Glycoprotein; domain 1

Class
Architecture
Topology
Homologous Superfamily



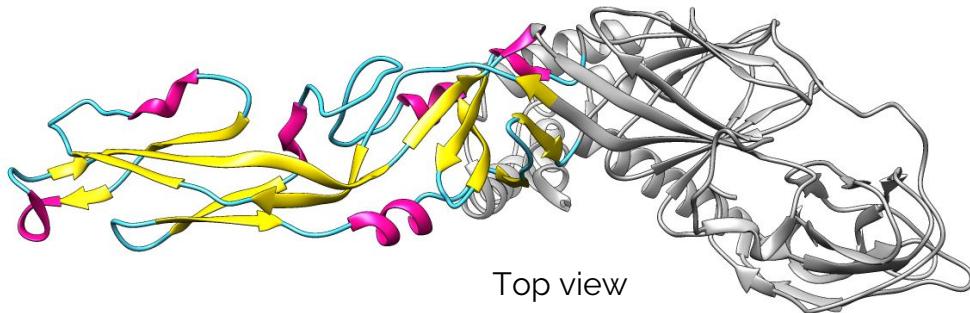
E PROTEIN: DOMAINS

DOMAIN II	
Level	
C	Alpha Beta
A	2-Layer Sandwich
T	Viral Envelope Glycoprotein; domain 2
H	Viral Envelope Glycoprotein; domain 2



90°
↙

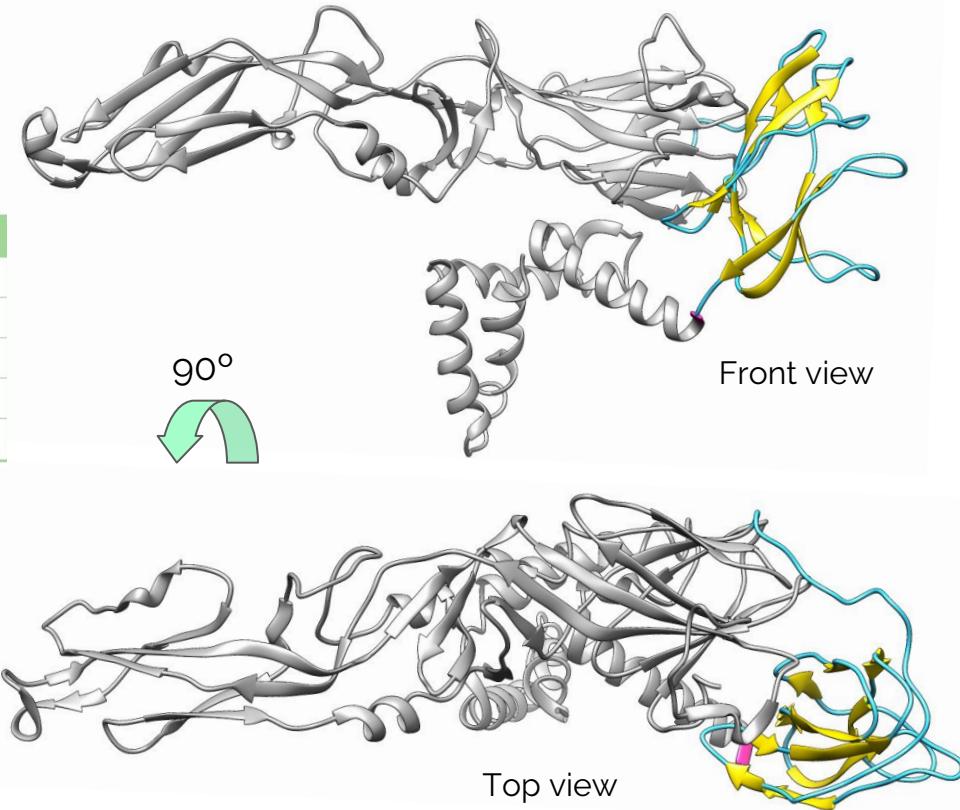
Front view



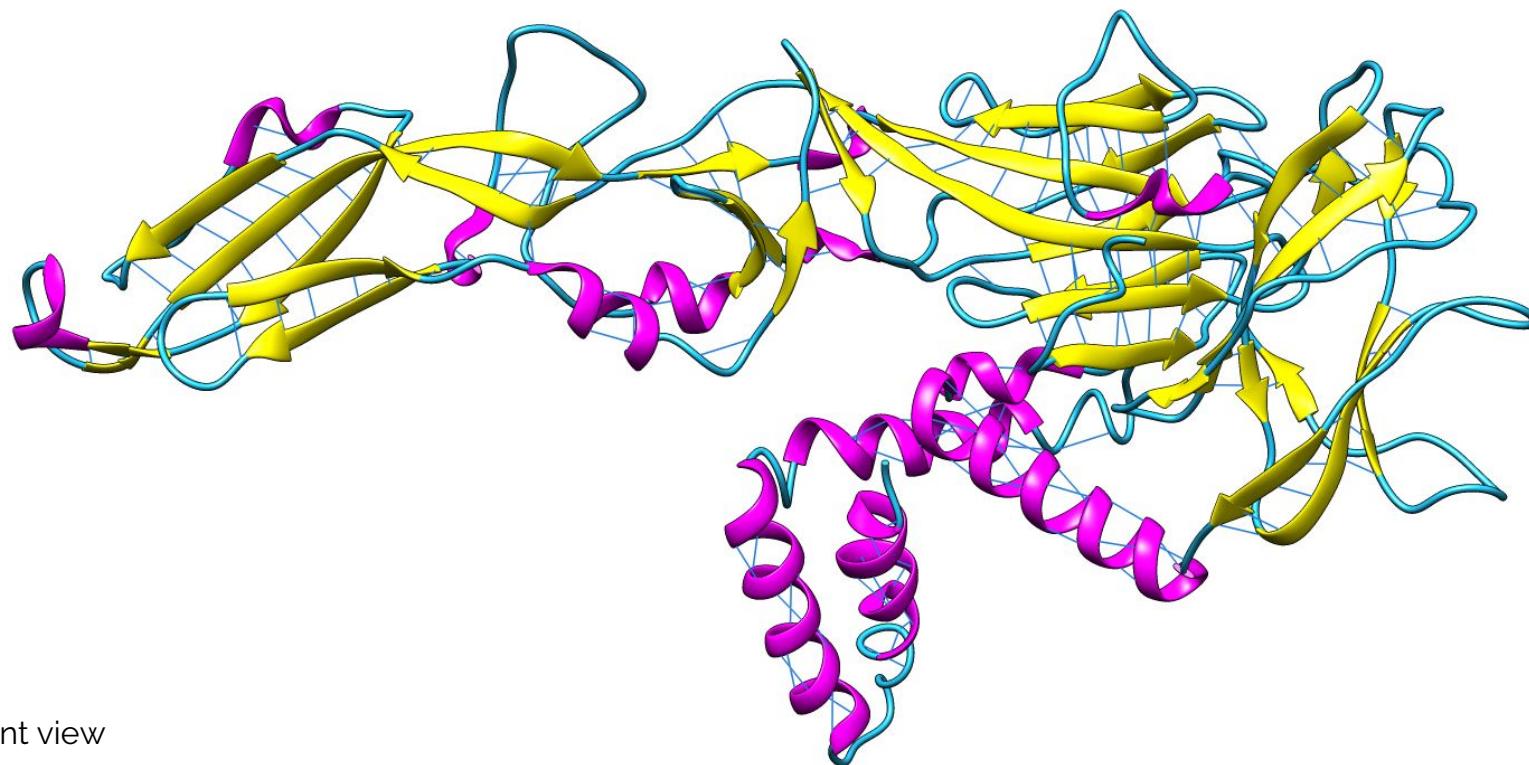
Top view

E PROTEIN: DOMAINS

DOMAIN III	
Level	
C	Alpha Beta
A	Sandwich
T	Immunoglobulin-like
H	

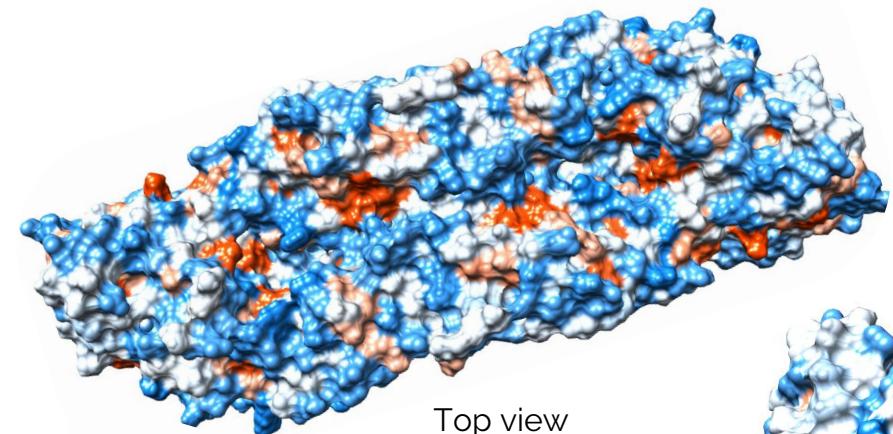


E PROTEIN: DOMAINS INTERACTIONS



Front view

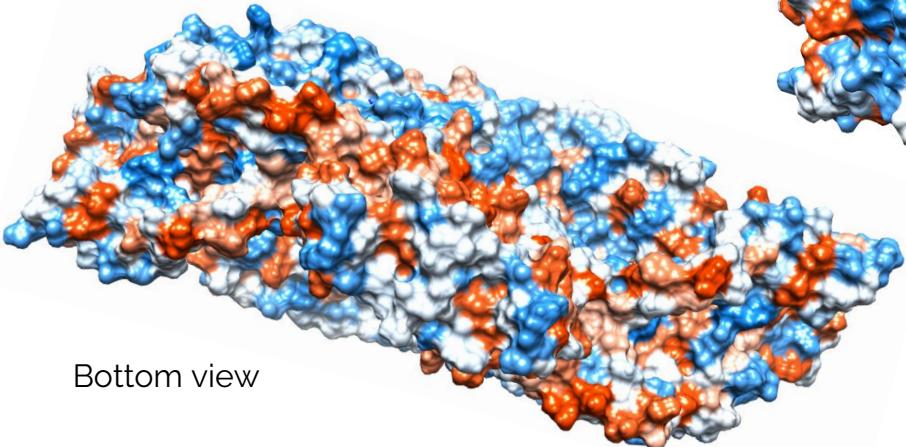
EXPLORING THE E SURFACE



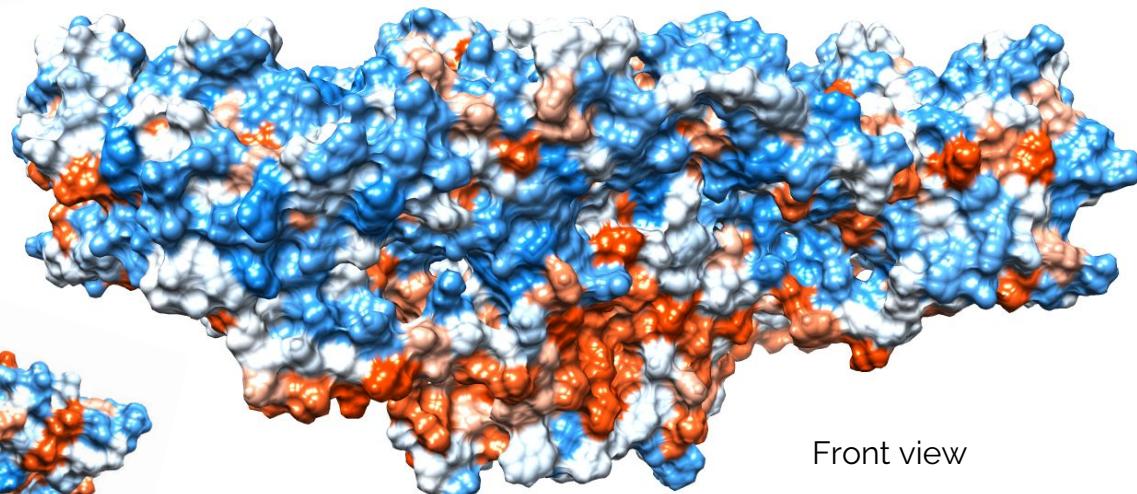
Top view

Hydrophobic regions

Hydrophilic regions

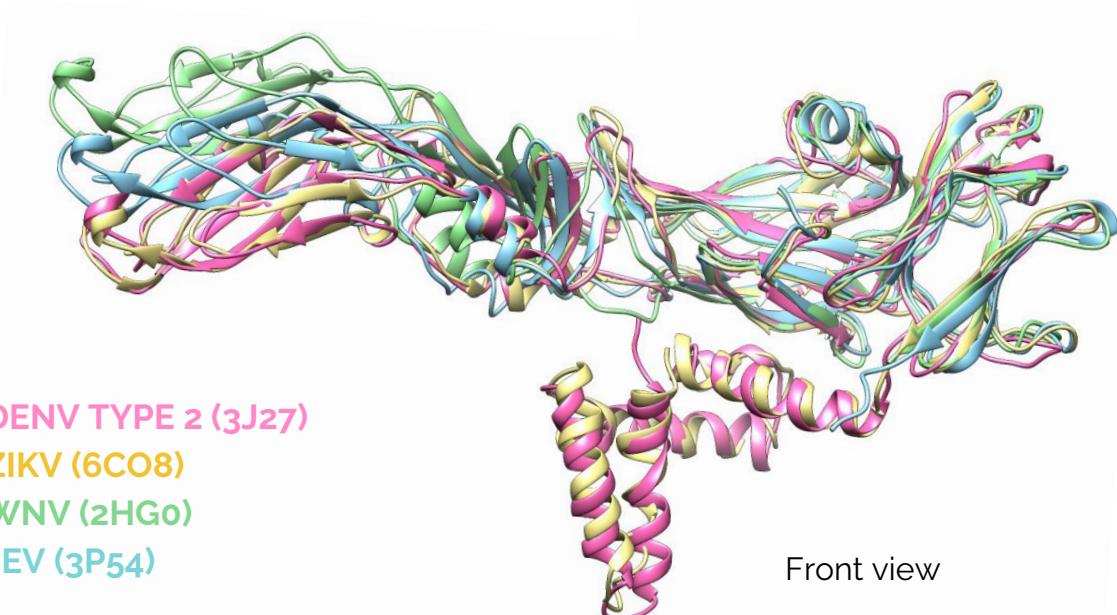


Bottom view

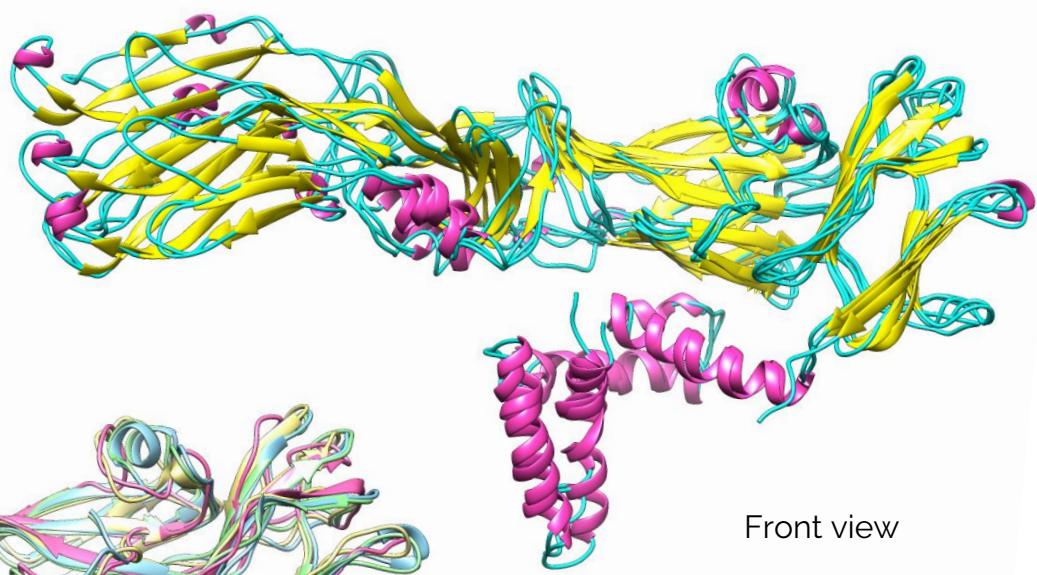


Front view

E PROTEIN: FLAVIVIRUSES SUPERIMPOSITION

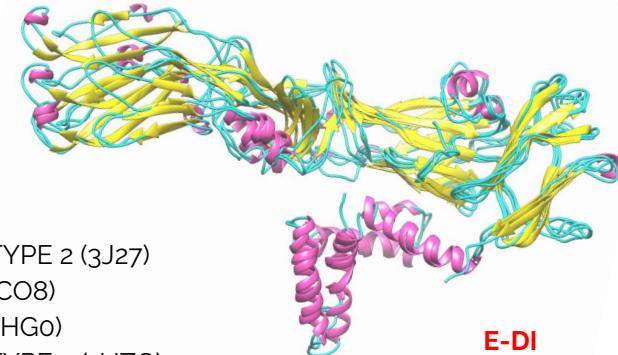
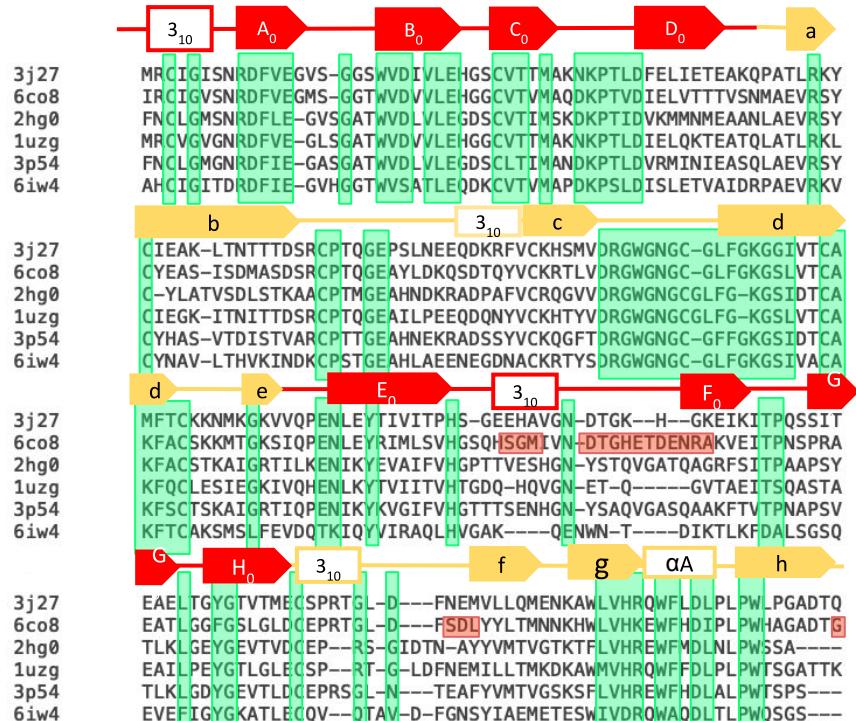


Front view



Score: **7,22**
RMSD: 2,51
Length: 418
nfit: 359 (86%)

E PROTEIN: FLAVIVIRUSES SUPERIMPOSITION



DENV TYPE 2 (3J27)

ZIKV (6CO8)

WNV (2HGo)

DENV TYPE 3 (1UZG)

JEV (3P54)

YFV (6IW4)

3j27 6co8 2hg0 1uzg 3p54 6iw4

GSN/IQKETLVT/K-NPHAK-KD/VV/LGSQEG/AMHT/AL/TG--ATEIQMSSG--NLLF-T
TPH/MNKEALVE/FK-DAHAK-RQ/VV/LGSQEG/AVH/TALAG--ALEAEAM-DGAKR/LS-S
GST/WRNRE-TLMEEFEEPHATKQS/VIALGSQEG/ALHQALAGAIPV/EFFS--N--TVKLTS
TPT/WRKELLVT/K-NAHAK-KD/E/VV/LGSQEG/AMHT/AL/TGATEIQTSG--G--TSIF-A
STA/RNRELLME/F-E-GA/HAT-KQS/VVALGSQEG/GLHQALAG--AIVVEY-SS-SVMLT-S
GGV/REMHHHLVE-E-PPHAA-TLR/V/LALGNQEG/SLK/ALT/TG--AMRVTK-DT-LYKLH-G

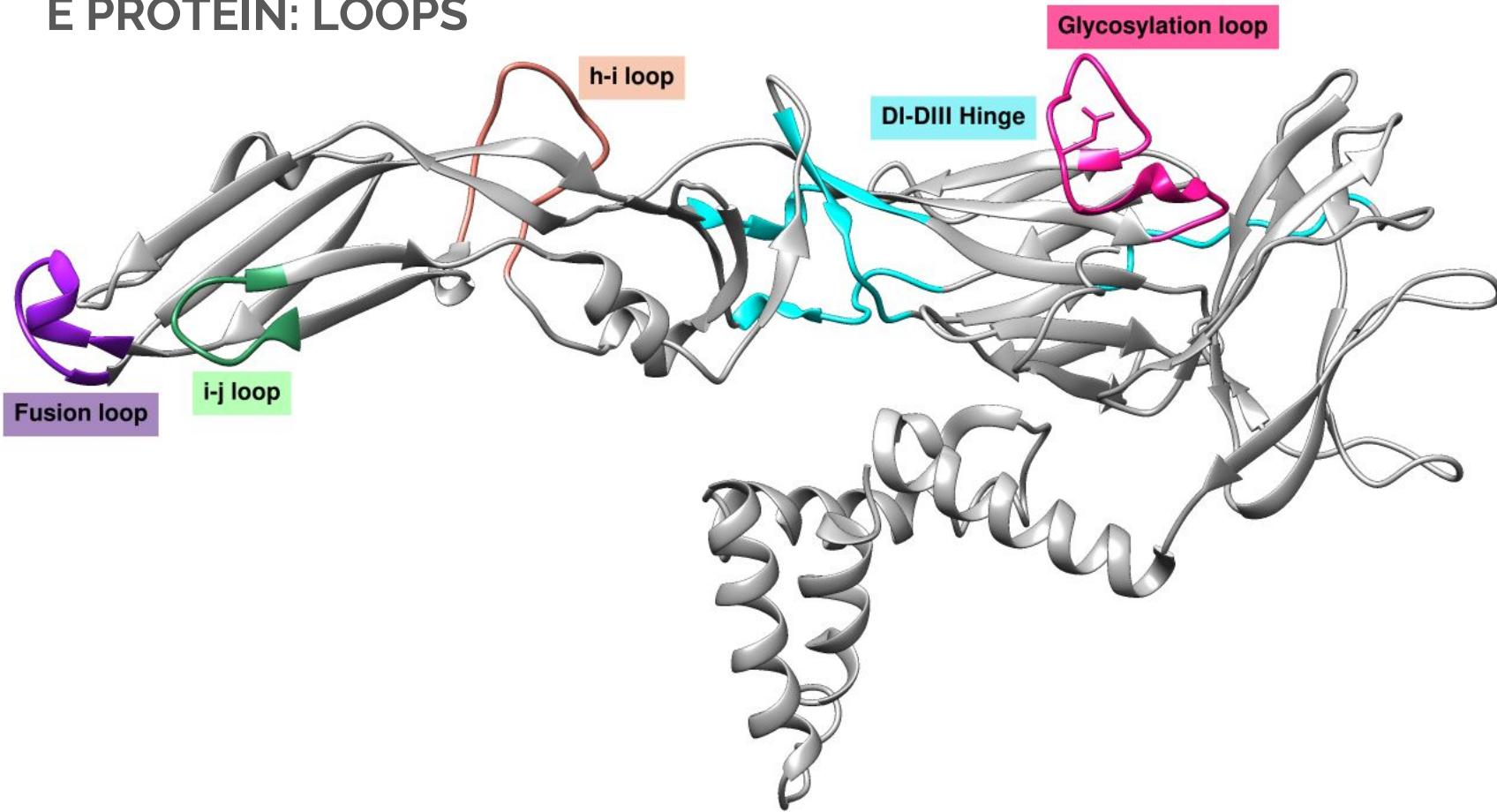
3j27 6co8 2hg0 1uzg 3p54 6iw4

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GHLKCRLLRMDKLQLKGVSYSLCTAAFTFTK/PAET/LHG/T/VTVE/VQ/YAG/TDG/CKPV/AQMA
GHLKCRVKM/MEKLQLKGTTYGVC/SAFK/FLGTP/ADT/CHGT/VVLE/LQY/TG/TDG/CKPV/ISSV
GHLKCRLLRMDKLQLKGMSYSAMCLNT/VLK/KEVSET/TQHG/TILIK/KEVY/KE/DA/CK/CKIP/FSTE
GHLKCRLLRMDKLQLKGTTYGVC/SAFK/FAKNP/VT/CHGT/VVIEL/YS/SG/SDG/CK/CKIP/IVSV
GH/SCRV/KL/SLTLKGTSYK/CTDKM/FFV/KNPTD/TQHG/T/VMQVKVSK-GA/CK/CKIP/VIVA

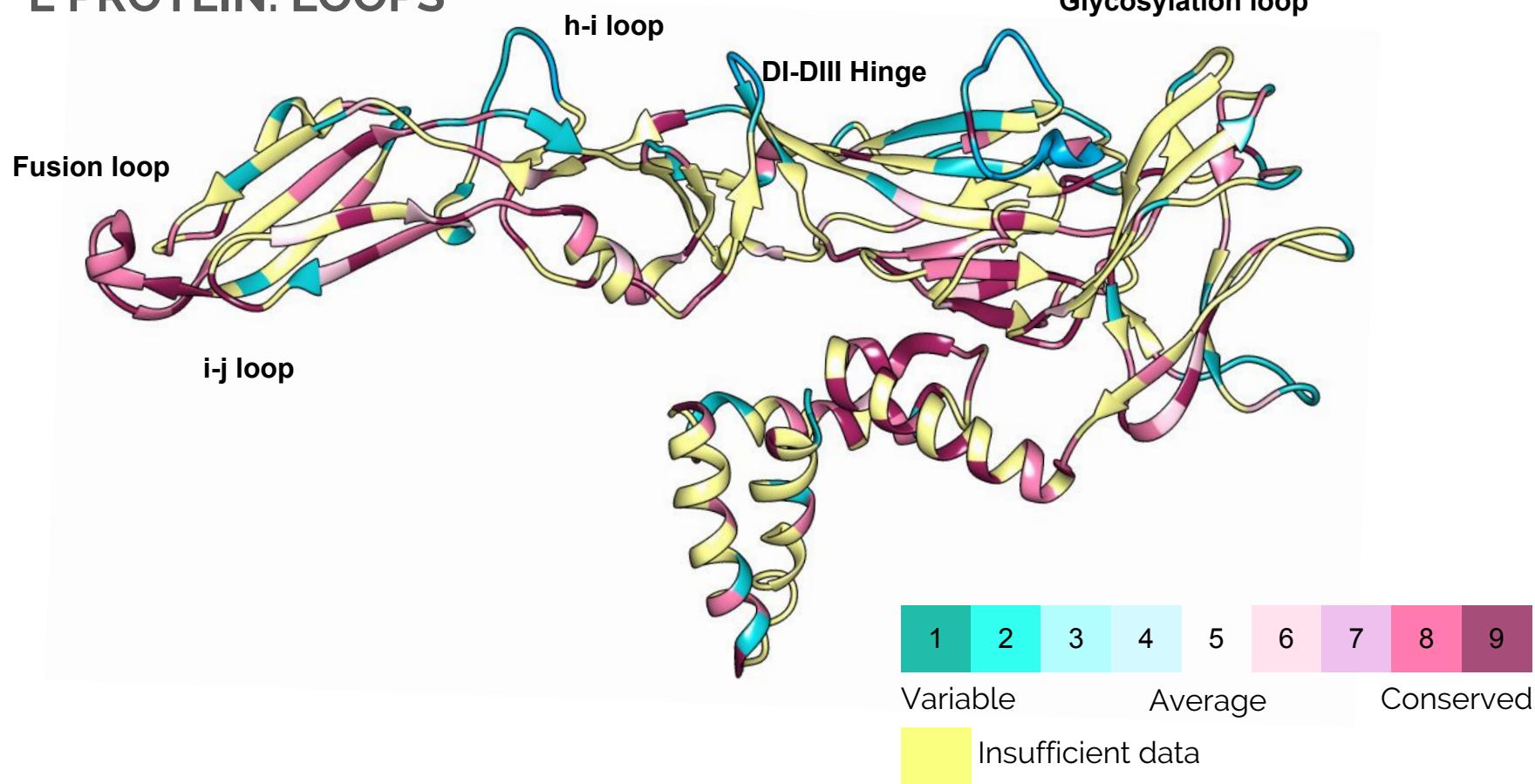
3j27 6co8 2hg0 1uzg 3p54 6iw4

DLEK-R-HVLR/GR/IT/VN/IVTE--KD/SPVNI/EA/PPFGDSY/II/IG/EP/GQ-LKLN/WFKKG
VDMQT/L-TPV/GR/IT/VN/VITESTENSK/MML/ELD/PPFGDSY/IV/VGRG-EKKITHH/WHRSG
ASLNDL-TPV/GR/LVT/VN/FVSVATANAKV/LI/ELE/PPFGDSY/IV/VGRG-EQQINHH/WHRSG
DG-Q-GKAHN/GR/IT/VN/IVTE--KEEPVNI/EA/PPFGESNIV/IG/IG-DKALKIN/WYRK-
ASLNDM-TPV/GR/LVT/VN/FVATSSANSKVL/VME/PPFGDSY/IV/VGRG-DKQINHH/WHAG
DDL/AA-INK/GILVT/VN/IAST--ND/DEV/LI/EV/PPFGDSY/IV/VGRG-DSRL/TYQ/WHKE-

E PROTEIN: LOOPS



E PROTEIN: LOOPS



E PROTEIN: VARIABLE LOOPS

DI-DIII Hinge

Domain movement, transformation of dimer to the fusogenic trimer.

Zika_virus_1/1-504

Zika_virus_2/1-498

Japanese_encephalitis_virus_1/1-500

Japanese_encephalitis_virus_2/1-499

West_Nile_virus_1/1-501

West_Nile_virus_2/1-501

Dengue_virus_4/1-1-495

Dengue_virus_4/2/1-495

Dengue_virus_1/1-1-495

Dengue_virus_1/2/1-495

Dengue_virus_3/1-1-493

Dengue_virus_3/2/1-493

Dengue_virus_2/1-1-495

Dengue_virus_2/2/1-495

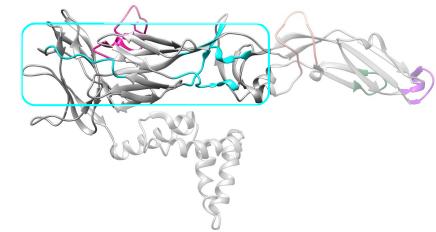
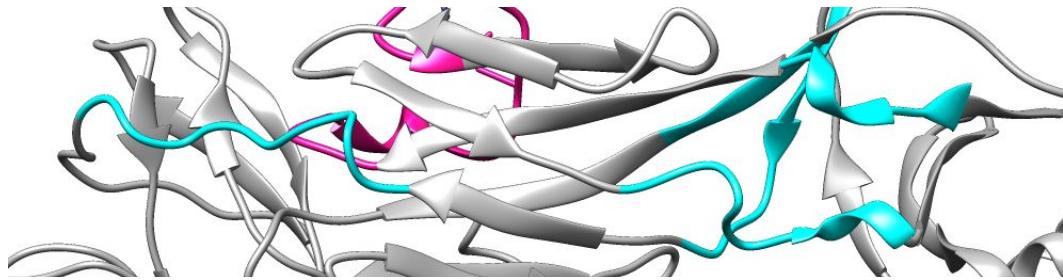
Yellow_fever_virus_1/1-493

Yellow_fever_virus_2/1-493

IRCIIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTV
 IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTV
 FNCLGMGNRDFIEGASGATWDLVLEGDSCLTIMANDKPTLDVRMINIEA
 -NCLGMGNRDFIEGASGATWDLVLEGDSCLTIMANDKPTLDVRMINIEA
 FNCLGMNSNRDFLEGVSATWDLVLEGDSCTVIMSNDKPTIDVKMMNMEA
 FNCLGMNSNRDFLEGVSATWDLVLEGDSCTVIMSNDKPTIDVKMMNMEA
 MRCVGVGNRDFVEGVSGGAWDLVLEHGGCVTTMAQGKPTLDFELTKTTA
 MRCVGVGNRDFVEGVSGGAWDLVLEHGGCVTTMAQGKPTLDFELTKTTA
 MRCVGIGSRDFVEGLSGATWDDVLEHGCCTVTTMAKDPTLDIELLKTEV
 MRCVGIGSRDFVEGLSGATWDDVLEHGCCTVTTMAKDPTLDIELLKTEV
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 MRCIGISNRDFVEGVSGGSWVDIVLEHGCCTVTTMAKNKPTLDIELQKTEA
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 AHCGITDRDFIEGVHGGTWSATLEQDKCVTVMAPDKPSLDISLETVAI
 AHCGITDRDFIEGVHGGTWSATLEQDKCVTVMAPDKPSLDISLETVAI
 .: .***:*** .*:*** .** .*: *: .*:***: .: .

WGNGCGLFGKGSVLTCAKFACTSKKMTGSIQOPEN EYRIMLSVHGSQHSG 150
 WGNGCGLFGKGSVLTCAKFTCSKKMTGSIQOPEN EYRIMLSVHGSQHSG 150
 WGNGCGLFGKGSIDTCAKFSTCSKAICRTIQOPEN KYEVGIFVHGTTSE 150
 WGNGCGLFGKGSIDTCAKFSTCSKAICRTIQOPEN KYEVGIFVHGTTSE 149
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 WGNGCGLFGKGGVVTCAKFSCSGKITQNLVQIEN EYTVVVTVHNGDTH- 149
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 WGNGCGLFGKGSIVACAKFTCAKSMSLFEVDQTK QYVIRAQLHVGAKQE 150
 *****: .:*** *: .: .: *: .: *: .: .: *: .: .: *: .: .: *

Back view



E PROTEIN: VARIABLE LOOPS

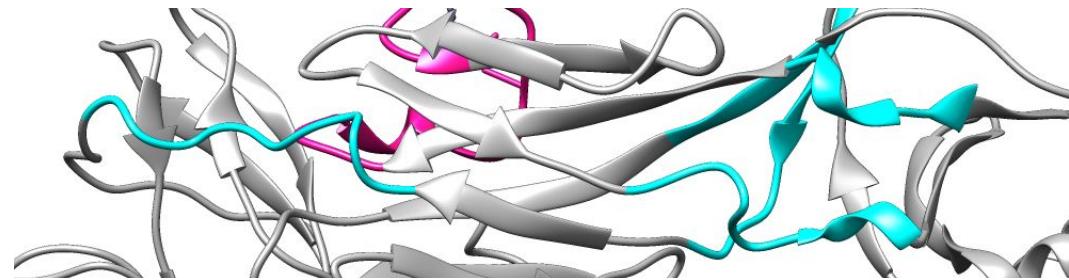
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Zika_virus_1/1-504
 Zika_virus_2/1-498
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 Japanese_encephalitis_virus_2/1-499
 West_Nile_virus_1/1-501
 West_Nile_virus_2/1-501
 Dengue_virus_4_1/1-495
 Dengue_virus_4_2/1-495
 Dengue_virus_1_1/1-495
 Dengue_virus_1_2/1-495
 Dengue_virus_3_1/1-493
 Dengue_virus_3_2/1-493
 Dengue_virus_2_1/1-495
 Dengue_virus_2_2/1-495
 Yellow_fever_virus_1/1-493
 Yellow_fever_virus_2/1-493

MIVNDTGHETDENRAKVEITPNSPRAEATLGGFGLGLDCPRTGLDFSD
 MIVND-----ENRAKVEITPNSPRAEATLGGFGLGLDCPRTGLDFSD
 NHGNYSAQVGASQAAKFTVTPNAPSITLKLGDYEVTLDCPRTGLNTEA
 NHGNYSAQVGASQAAKFTVTPNAPSITLKLGDYEVTLDCPRTGLNTEA
 SHGNYSTQTGATQAGRFGITPAAPSYTLKLGEYEVTLDCPRTSGIDTNA
 SHGNYSTQMGATQAGRFSITPSAPSITLKLGEYEVTLDCPRTSGIDTNA
 AVGNDTS----NHGVATATITPRSPSVEVKLPDYGELTLDCPRTSGIDFNE
 AVGNDTS----NHGVATATITPRSPSVEELPDYGELTLDCPRTSGIDFNE
 QVGNET----EHGTTATITPQAPTSEIQLTDYALTLDCPRTGLDFNE
 QVGNET----EHGTTATITPQAPTSEIQLTDYALTLDCPRTGLDFNE
 QVGNET----QGVTAEITPQASTVEAILPEYGTGLGECPRTGLDFNE
 QVGNDT----QGVTAEITPQASTVEAILPEYGTGLGECPRTGLDFNE
 AVGNDTG----KHGKEIKVTPQSSITEAELTGYGTVTMECPRTGLDFNE
 AVGNDTG----KHGKEIKVTPQSSITEAELTGYGTVTMECPRTGLDFNE
 NW-NTDIK-----TLKFDALSGSQEAEFTGYGRATLECPRTAVDFSN
 NW-NTDIK-----TLKFDALSGSQEAEFTGYGRATLECPRTAVDFSN
 * . . . : : * : :: * : :: : . . .

Back view



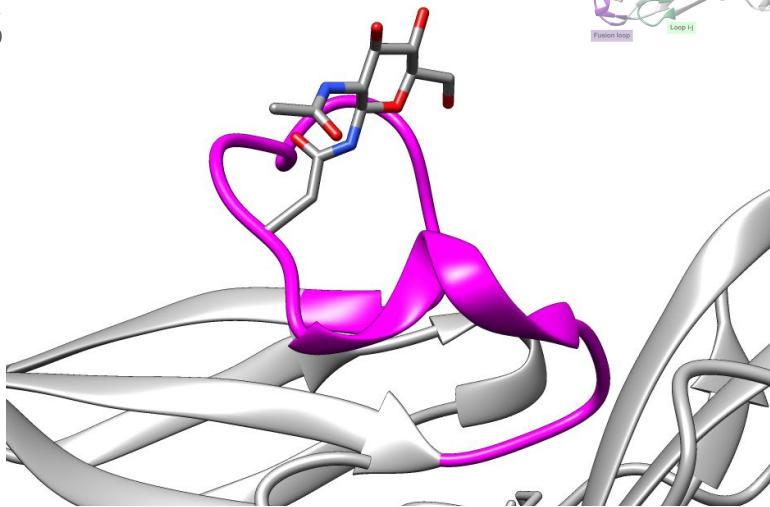
KRQTVVVLGSQEGAVHTALAGALEAEMDGA---KGRLSSGHLKCRLKMDK
 KRQTVVVLGSQEGAVHTALAGALEAEMDGA---KGRLSSGHLKCRLKMDK
 TKQSVVALGSQEGGLHQALAGAIVVEYSS---SVKLTSGHHLKCRLKMDK
 TKQSVVALGSQEGSLHQALAGAIVVEYSS---SVKLTSGHHLKCRLKMDK
 TKQSVIALGSQEGALHQALAGAIPVEFSSN---TVKLTSGHHLKCRVKLEK
 TKQSVVALGSQEGALHQALAGAIPVEFSSN---TVKLTSGHHLKCRVKMEK
 KRQDVTVLGSQEGAMHSALAGATEVDSGD---GNHMFAGHLKCRVMEK
 KRQDVTVLGSQEGAMHSALAGATEVDSGD---GNHMFAGHLKCRVMEK
 KKQEVVVLGSQEGAMHTALTGATEIQTSG---TTTIFAGHLKCRLKMDK
 KKQEVVVLGSQEGAMHTALTGATEIQTSG---TTTIFAGHLKCRLKMDK
 KKQEVVVLGSQEGAMHTALTGATEIQTSG---GTSIFAGHLKCRLKMDK
 KKQEVVVLGSQEGAMHTALTGATEIQNNSG---GTSIFAGHLKCRLKMDK
 KKQDVVVLGSQEGAMHTALTGATEIQMSS---GNLFFGHHLKCRRLRMDK
 KKQDVVVLGSQEGAMHTALTGATEIQMSS---GNLFFGHHLKCRRLRMDK
 ATIKVLALGNQEGSLKALTGAMRVTKDNNSKLYKLHGGHVACRVLSA
 ATIKVLALGNQEGSLKALTGAMRVTKDNNSKLYKLHGGHVACRVLSA
 * . * . * . : : * * : * . . . : * * : * : : : . . .

E PROTEIN: VARIABLE LOOPS

Glycosylation Loop

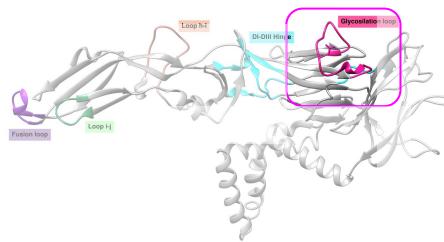
Related to ZIKA virulence pathogenesis and neuroinvasiveness

Zika_virus_1/1-504
Zika_virus_2/1-498
Japanese_encephalitis_virus_1/1-500
Japanese_encephalitis_virus_2/1-499
West_Nile_virus_1/1-501
West_Nile_virus_2/1-501
Dengue_virus_4/1-495
Dengue_virus_4/2-1-495
Dengue_virus_1/1-495
Dengue_virus_1/2-1-495
Dengue_virus_3/1-493
Dengue_virus_3/2-1-493
Dengue_virus_2/1-495
Dengue_virus_2/2-1-495
Yellow_fever_virus_1/1-493
Yellow_fever_virus_2/1-493



WGNGCGLFGKGSVLTCAKFACSKKMTGKSIQOPENLEYRIMLSVHGSQHSG MIVNDTGHETDENRAKVEITPNSPRAEATLG
WGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQOPENLEYRIMLSVHGSQHSG MIVND-----ENRAKVEITPNSPRAEATLG
WGNGCGLFGKGSIDTCAKFSCSTSKAIGRTIQOPENIYEVGIFVHGTTSSE NHGNYSAQVGASQAAKFTVTPNAPSITLKLGI
WGNGCGLFGKGSIDTCAKFSCSTSKAIGRTIQOPENIYEVGIFVHGTTSSE NHGNYSAQVGASQAAKFTVTPNAPSITLKLGI
WGNGCGLFGKGSIDTCAKFACSTNATGRTILKENIKYEVAIFVHGPTTVE SHGNYSTQTGATQAGRGFTPAAPSYTTLKLGI
WGNGCGLFGKGSIDTCAKFACTTKATGWIQKENIKYEVAIFVHGPTTVE SHGNYSTQMGTQAGRFSITPSAPSYTTLKLGI
WGNGCGLFGKGGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTH- AVGNDTS---NHGVATATITPRSPSVEVKLP
WGNGCGLFGKGGVVTCAKFSCSGKITGNLVQIENLEYTVVTVHNGDTH- AVGNDTS---NHGVATATITPRSPSVEVELP
WGNGCGLFGKGSLLTCAFKFCVTKLEGKIVQYENLKYSVIVTVHGDQH- QVGNET-----EHGTTATITPQAPTSEIQLT
WGNGCGLFGKGSLLTCAFKFCVTKLEGKIVQYENLKYSVIVTVHGDQH- QVGNET-----EHGTTATITPQAPTSEIQLT
WGNGCGLFGKGSVLTCAKFQCLELIEGKVVQHENLKYTVIITVHGDQH- QGVNET-----QGVTAEITPQASTVEAILP
WGNGCGLFGKGSVLTCAKFQCLESIEGKVVQHENLKYTVIITVHGDQH- QGVNDT-----QGVTAEITPQASTVEAILP
WGNGCGLFGKGGIVTCAMFTCKKNMEGKIVQOPENLEYTIVTPHSGEEH- AVGNDTG----KHGKEIKVTPQSSITEAELT
WGNGCGLFGKGGIVTCAMFTCKKNMEGKIVQOPENLEYTIVTPHSGEEH- AVGNDTG----KHGKEIKITPQSSITEAELT
WGNGCGLFGKGSIVACAKFTCAKMSLFEVDQTKIQYVIRQLHVGAQKE NW-NTDIK-----TLKFDALSGSQEAFT
WGNGCGLFGKGSIVACAKFTCAKMSLFEVDQTKIQYVIRQLHVGAQKE NW-NTDIK-----TLKFDALSGSQEAFT
*****: :** * * : : ::* : * * . : :

E PROTEIN: VARIABLE LOOPS



Glycosylation Loop

Asn 154 in ZIKV
Asn 153 in DENV

DENV TYPE 2 (3J27)

ZIKV (6CO8)

WNV (2HGo)

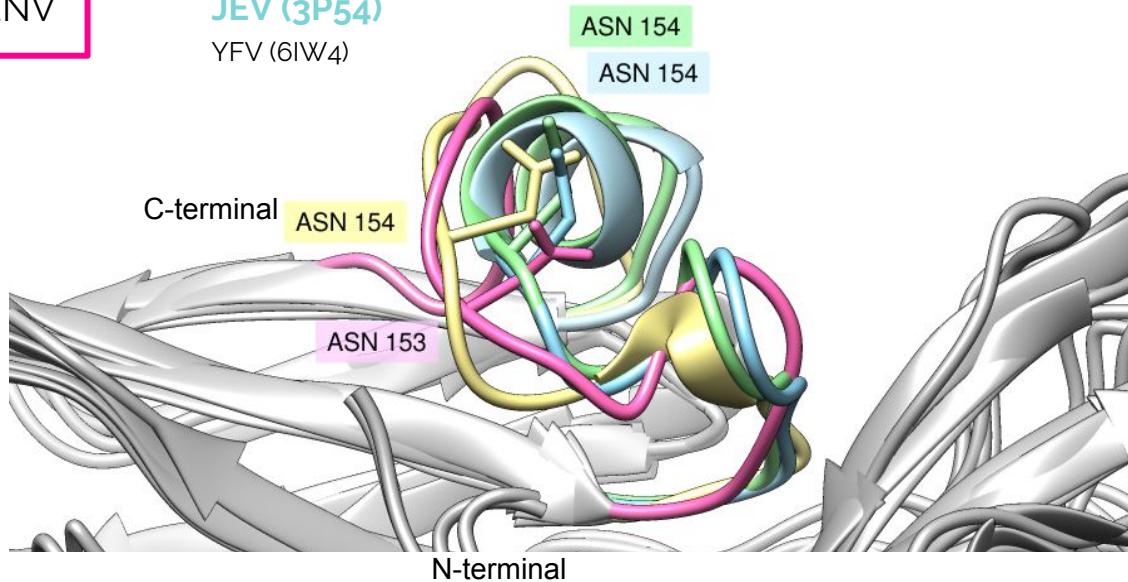
DENV TYPE 3 (1UZG)

JEV (3P54)

YFV (6IW4)

3j27
6co8
2hg0
1uzg
3p54
6iw4

MFTCKKNMKGKVQOPENLEYTIVITPHS-GEEHAVCN-DTGK--H--GKEIKITPQSSIT
KFACSKKMTGKSIQOPENLEYRIMLSVHGSGMIVN-DTGHETDENRAKVEITPNSPRA
KFACSTKAIGRTILKENIKYEVAIFVHGPTTVESHCN-YSTQVGATQAGRFSITPAAPSY
KFQCLESIEGKIVQHENLKYTVIITVHTGQD-HQVGN-ETQ-----GTAEITSQASTA
KFSCTSKAIGRTIQOPENIKYKVGIFVHGTTSENHCN-YSAQVGASQAAKFTVTPNAPSV
KFTCAKSMMSLFEVDQTKIQYVIRAQLHVGAK---QEWNTD-----IKTLKFDALSGS



E PROTEIN: VARIABLE LOOPS

Glycosylation Loop

Asn 154 in ZIKV

Asn 153 in DENV

ZIKV (6CO8)

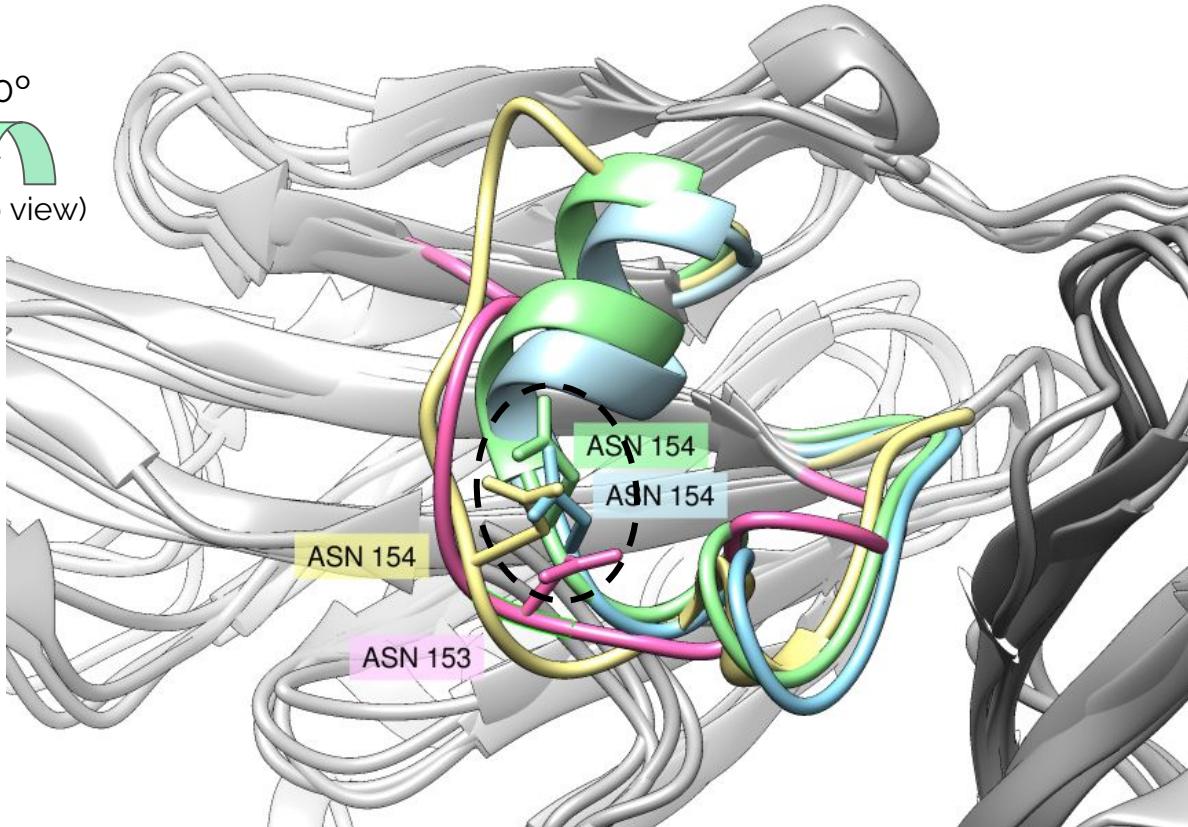
DENV TYPE 2 (3J27)

JEV (3P54)

WNV (2HGo)

**Conserved
glycosylation site**

90°
(Top view)

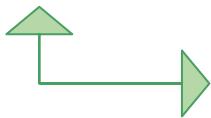


E PROTEIN: VARIABLE LOOPS

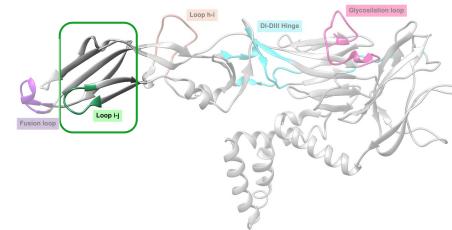
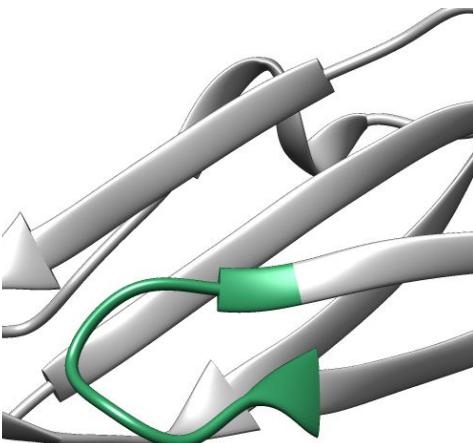
i-j loop

Related to **large conformational changes** during transformation from immature to mature forms.

Larger differences between *Flaviviruses*



Differences in binding of **neutralizing antibodies.**



Zika_virus_1/1-504
Zika_virus_2/1-498
Japanese_encephalitis_virus_1/1-500
Japanese_encephalitis_virus_2/1-499
West_Nile_virus_1/1-501
West_Nile_virus_2/1-501
Dengue_virus_4_1/1-495
Dengue_virus_4_2/1-495
Dengue_virus_1_1/1-495
Dengue_virus_1_2/1-495
Dengue_virus_3_1/1-493
Dengue_virus_3_2/1-493
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Yellow_fever_virus_1/1-493
Yellow_fever_virus_2/1-493

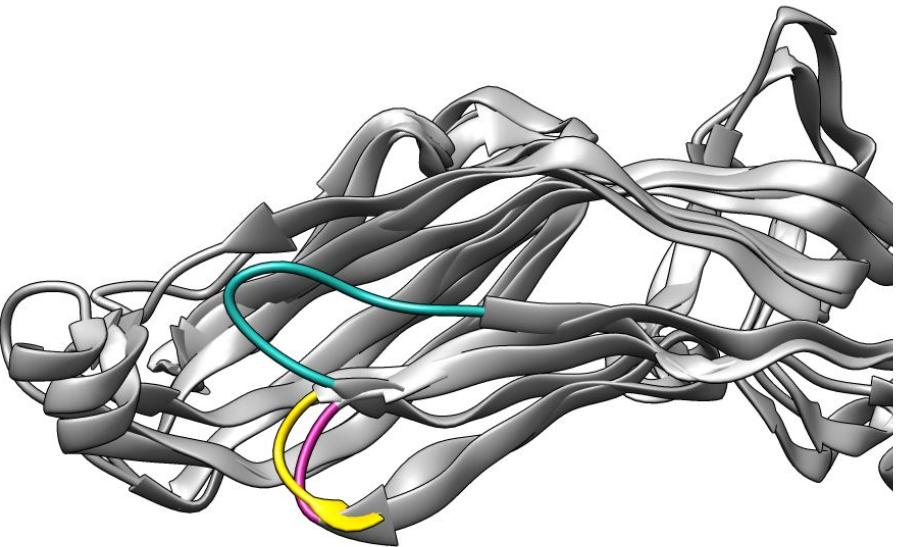
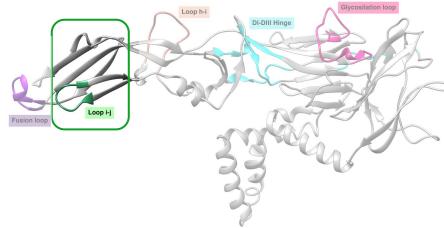
E PROTEIN: VARIABLE LOOPS

i-j loop

Similar closed conformation in **ZIKV** and **DENV**, whereas in **JEV** this loop has an open conformation.



The differences in these loop conformations might account for differences in binding of neutralizing antibodies.

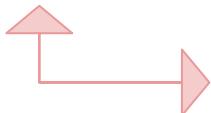


E PROTEIN: VARIABLE LOOPS

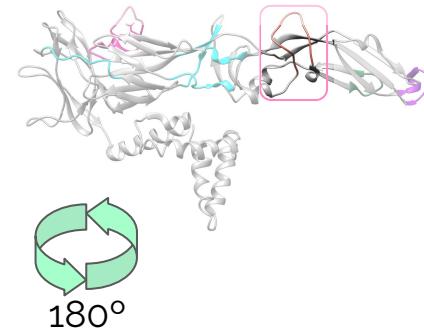
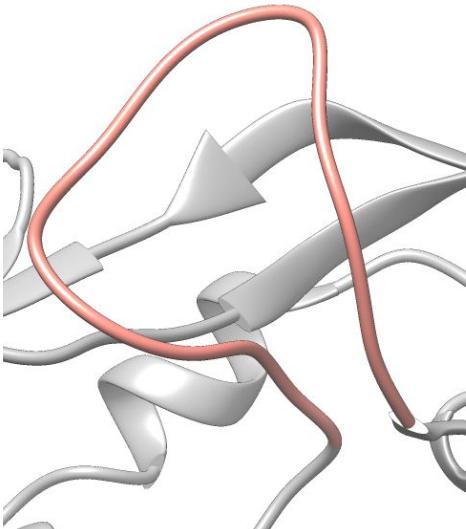
h-i loop

Related to **large conformational changes** during transformation from immature to mature forms.

Larger differences between *Flaviviruses*



Differences in binding of **neutralizing antibodies**.



Back view

Zika_virus_1/1-504
Zika_virus_2/1-498
Japanese_encephalitis_virus_1/1-500
Japanese_encephalitis_virus_2/1-499
West_Nile_virus_1/1-501
West_Nile_virus_2/1-501
Dengue_virus_4_1/1-495
Dengue_virus_4_2/1-495
Dengue_virus_1_1/1-495
Dengue_virus_1_2/1-495
Dengue_virus_3_1/1-493
Dengue_virus_3_2/1-493
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Dengue_virus_2_2/1-495
Yellow_fever_virus_1/1-493
Yellow_fever_virus_2/1-493

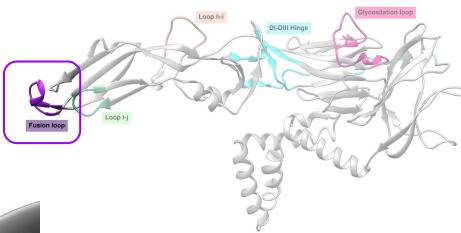
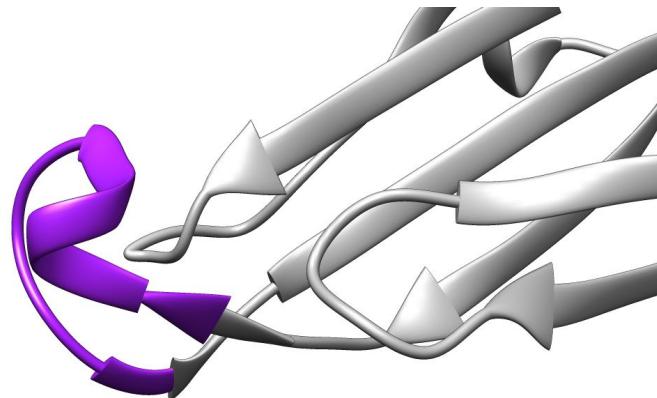
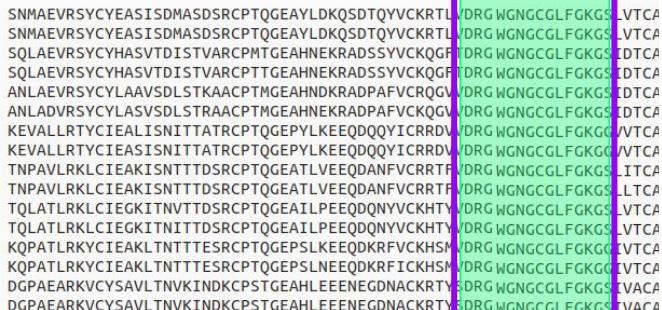
LYYLTMMNNKKHVLVHKEWFHDIPLPW	HAGADGTPH	HNKNEALVEFKDAHA	256
LYYLTMMNNKKHVLVHKEWFHDIPLPW	HAGADGTPH	HNKNEALVEFKDAHA	244
FWMTVMTGSKSFLVHREWFLHDLALP	PTPSST	AIRNRRELLMEEFAA	247
FWMTVMTGSKSFLVHREWFLHDLALP	PTPSST	AIRNRRELLMEEFAA	246
YYVMTVGTKLFLVHREWFMDLNLPW	PSAGST	TWNRRETLMEEFEEPA	247
YYVMTVGSKFLVHREWFMDLNLPW	PSAGST	TWNRRETLMEEFEEPA	247
YYVMSVGAKSFLVHREWFMDLNLPW	PSAGST	TWNRRETLMEEFEEPA	247
MILMKMKKKKTWLVHKQWFQLDLPW	PTTGADTSE	HINYKERMVTFKVPHA	245
MILMKMKKKKTWLVHKQWFQLDLPW	PTTGADTSE	HINYKERMVTFKVPHA	245
MVLTTMKEKSFLVHJKQWFQLDLPW	TSGASTSQE	TWNRQDQLLVTFKTAHA	245
MVLTTMKEKSFLVHJKQWFQLDLPW	TSGASTSQE	TWNRQDQLLVTFKTAHA	245
MILLTMMNKNAWMVHQRWFQFLDLPW	TSGATTETP	TWINKKELLLVTFKNAHA	243
MILLLTMNKNAWMVHQRWFQFLDLPW	TSGATTETP	TWINKKELLLVTFKNAHA	243
MVLLQMGKENKAWLVRHQWFQFLDLPW	PGADKQES	NIQKETLVTFKFNPNA	245
MVLLQMGEDKAWLVRHQWFQFLDLPW	PGADKQES	NIQKETLVTFKFNPNA	245
SYIAEMEKESWIVDQKQAWQADLTLW	PGSGSGG	VIRMEMHLLVFEFPNA	239
SYIAEMEKESWIVDQKQAWQADLTLW	PGSGSGG	VIRMEMHLLVFEFPNA	239

E PROTEIN: CONSERVED LOOPS

Fusion Loop

Virus mediated membrane fusion

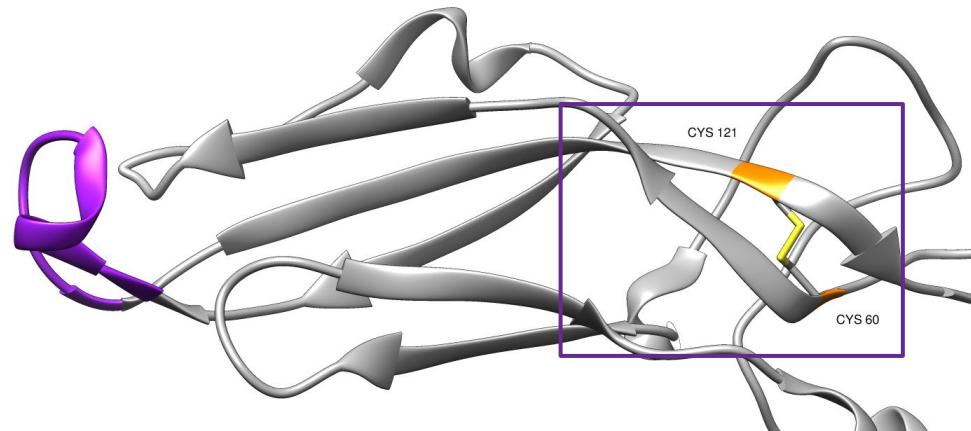
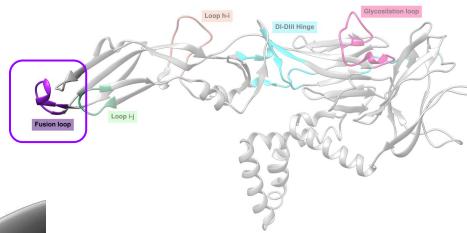
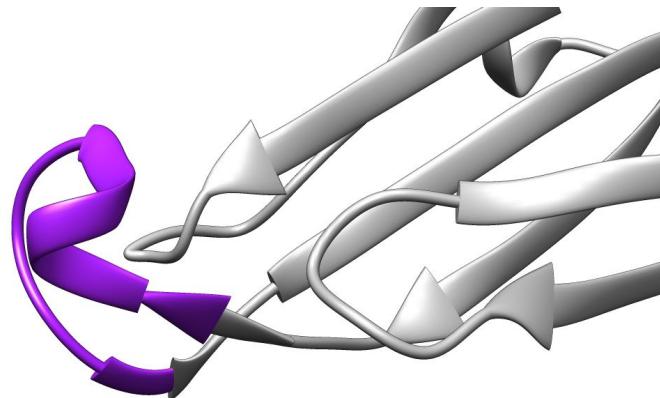
Zika_virus_1/1-504
Zika_virus_2/1-498
Japanese_encephalitis_virus_1/1-500
Japanese_encephalitis_virus_2/1-499
West_Nile_virus_1/1-501
West_Nile_virus_2/1-501
Dengue_virus_4_1/1-495
Dengue_virus_4_2/1-495
Dengue_virus_1_1/1-495
Dengue_virus_1_2/1-495
Dengue_virus_3_1/1-493
Dengue_virus_3_2/1-493
Dengue_virus_2_1/1-495
Dengue_virus_2_2/1-495
Yellow_fever_virus_1/1-493
Yellow_fever_virus_2/1-493



E PROTEIN: CONSERVED LOOPS

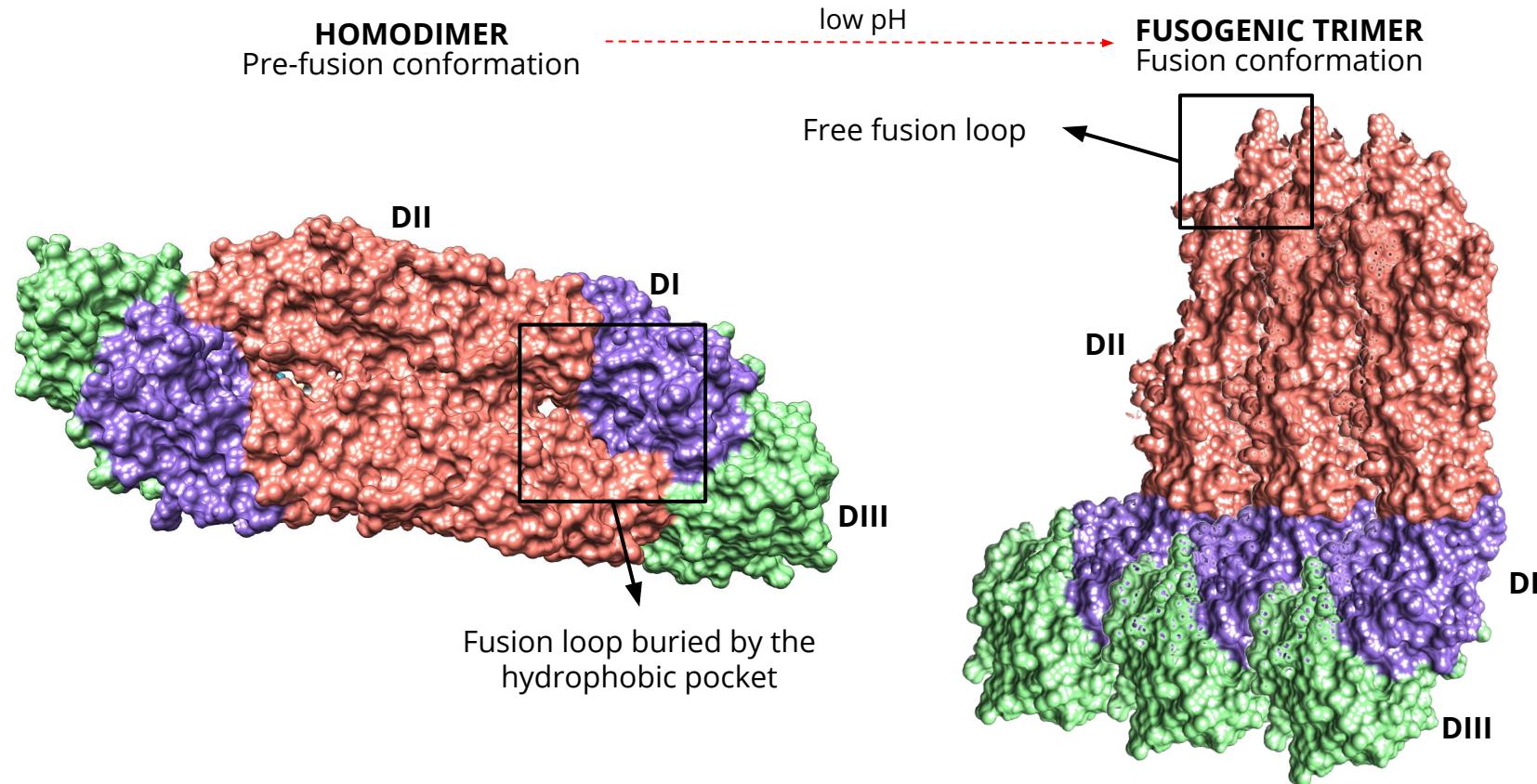
Fusion Loop

Virus mediated
membrane fusion



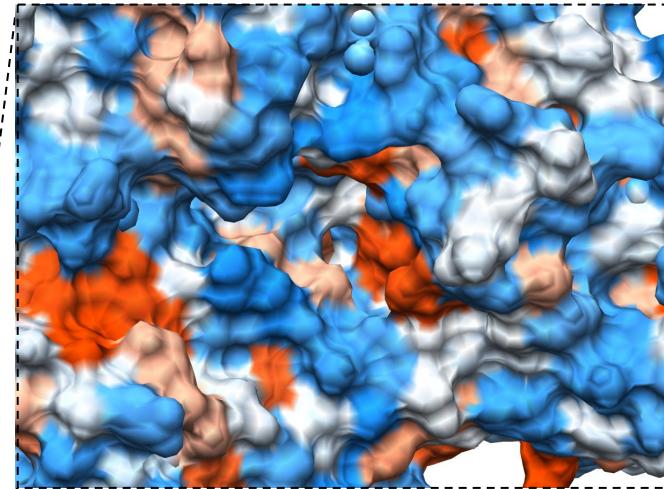
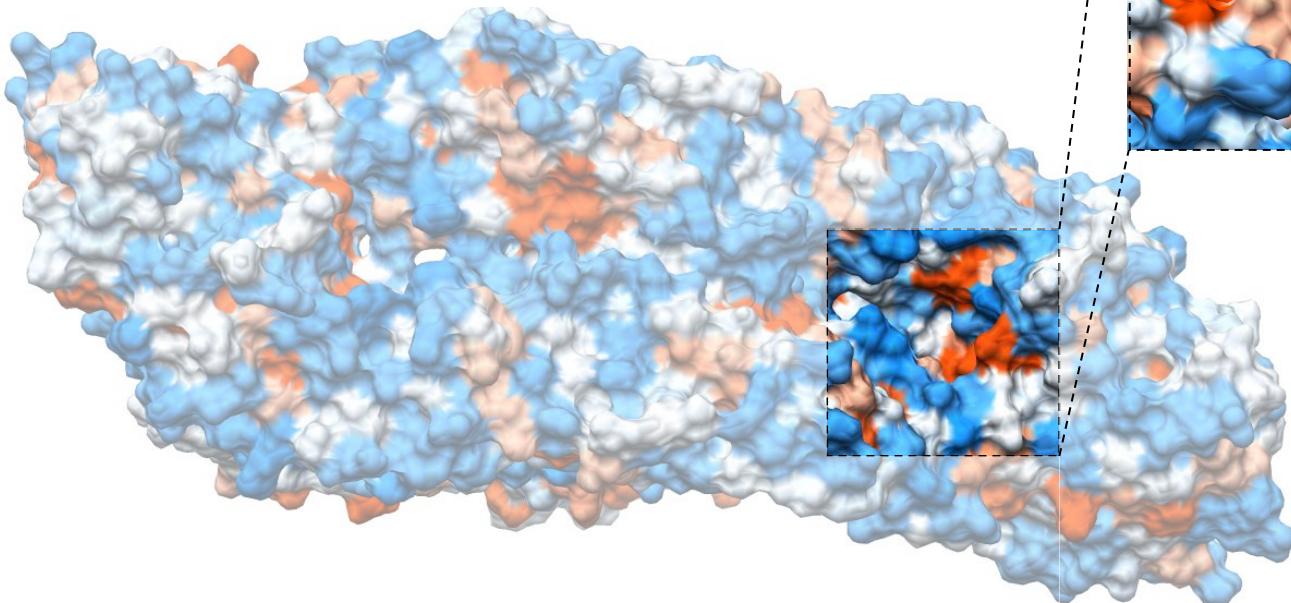
HYDROPHOBIC POCKET

VIRUS MEDIATED MEMBRANE FUSION AND DRUG TARGET



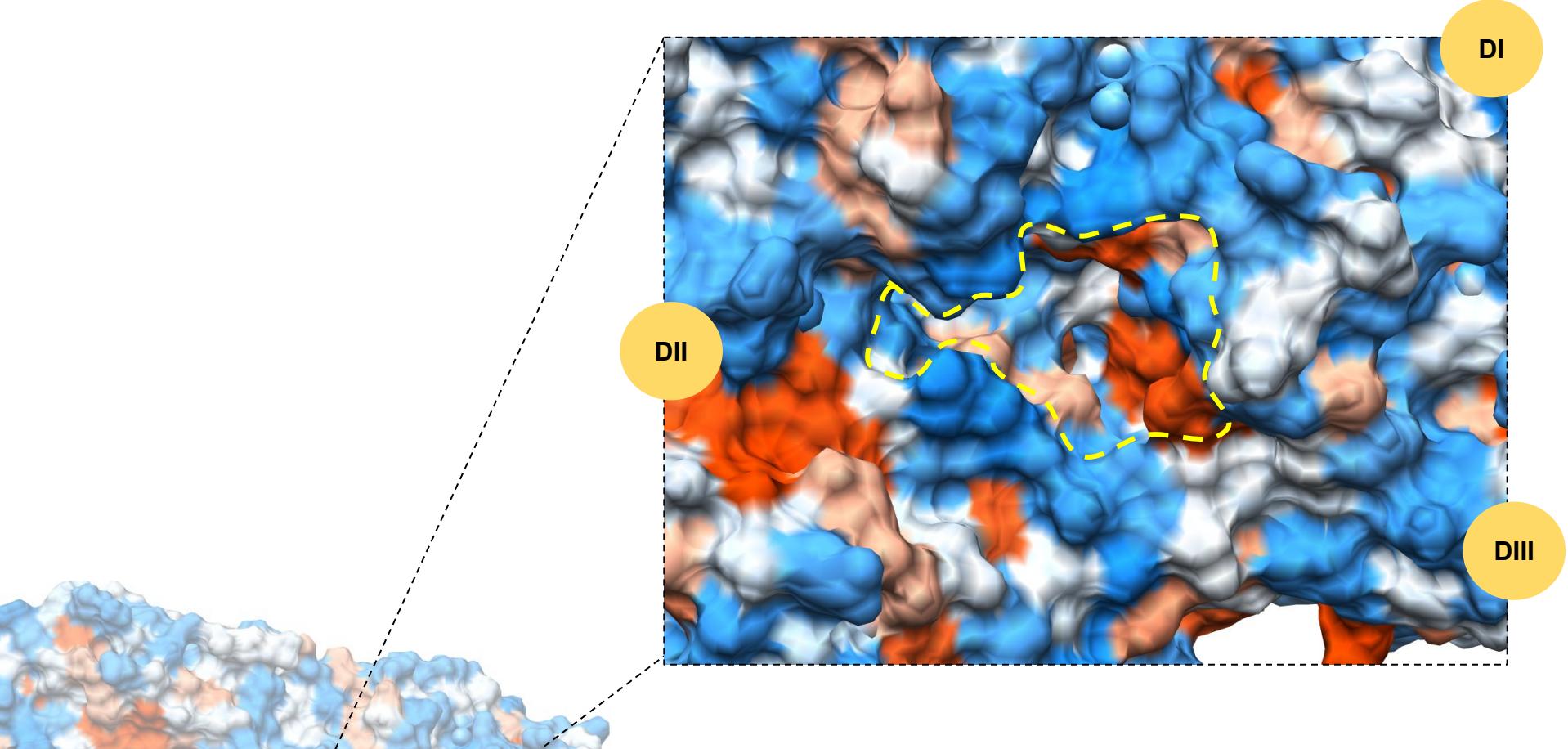
HYDROPHOBIC POCKET

VIRUS MEDIATED MEMBRANE FUSION
AND DRUG TARGET



HYDROPHOBIC POCKET

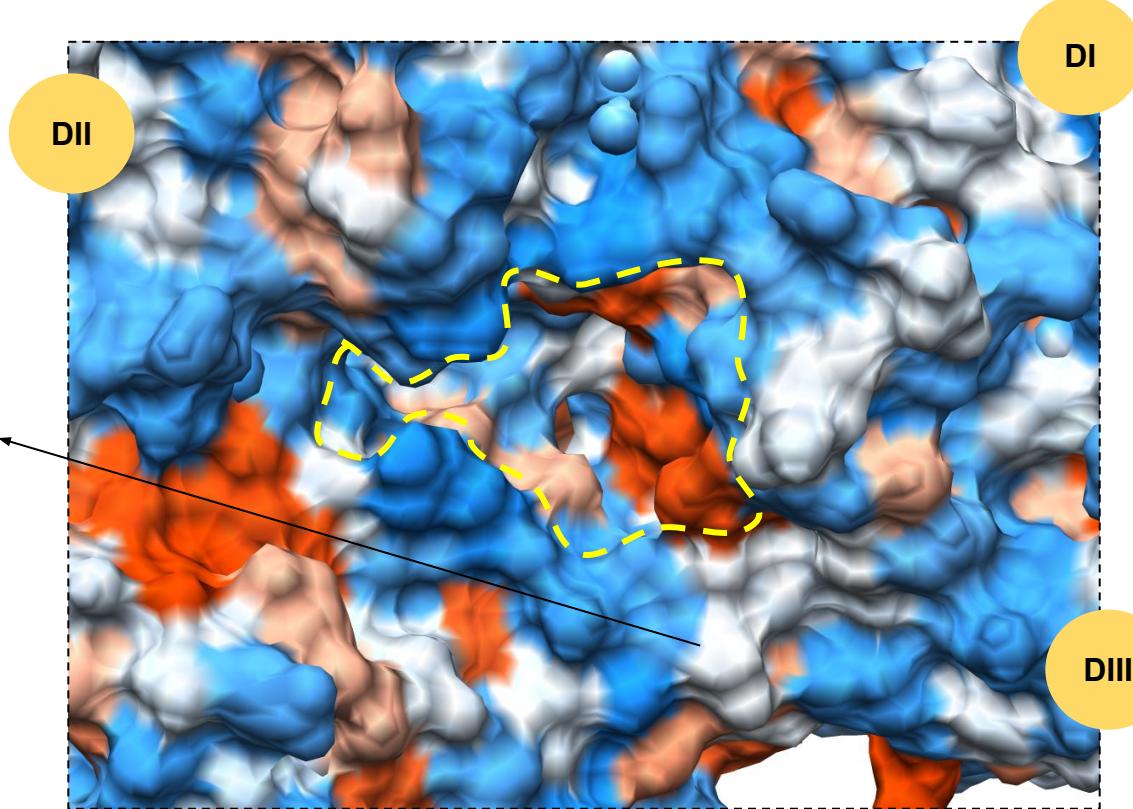
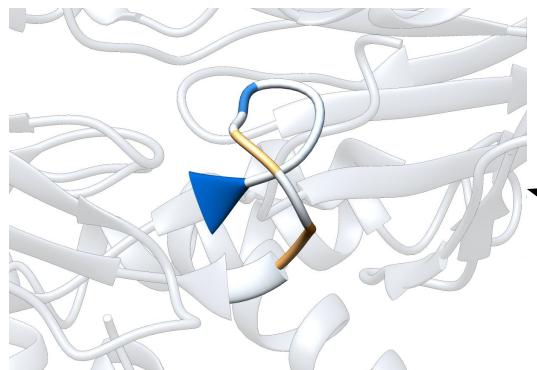
VIRUS MEDIATED MEMBRANE FUSION AND DRUG TARGET



HYDROPHOBIC POCKET

VIRUS MEDIATED MEMBRANE FUSION AND DRUG TARGET

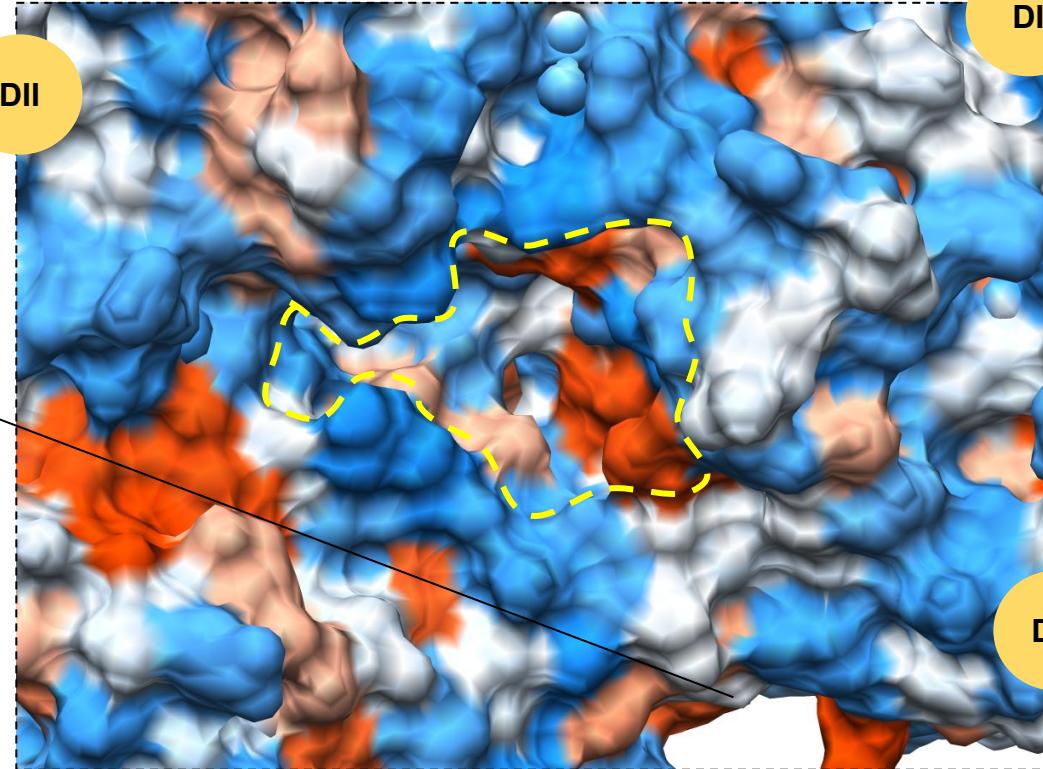
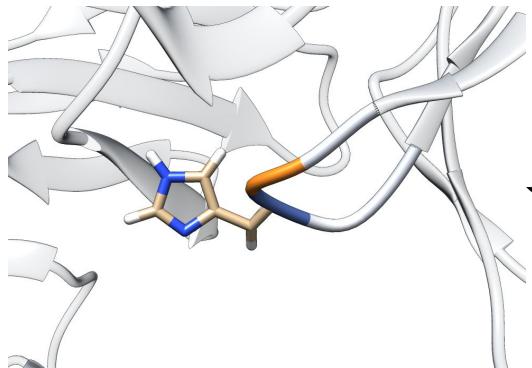
fusion-loop



HYDROPHOBIC POCKET

VIRUS MEDIATED MEMBRANE FUSION AND DRUG TARGET

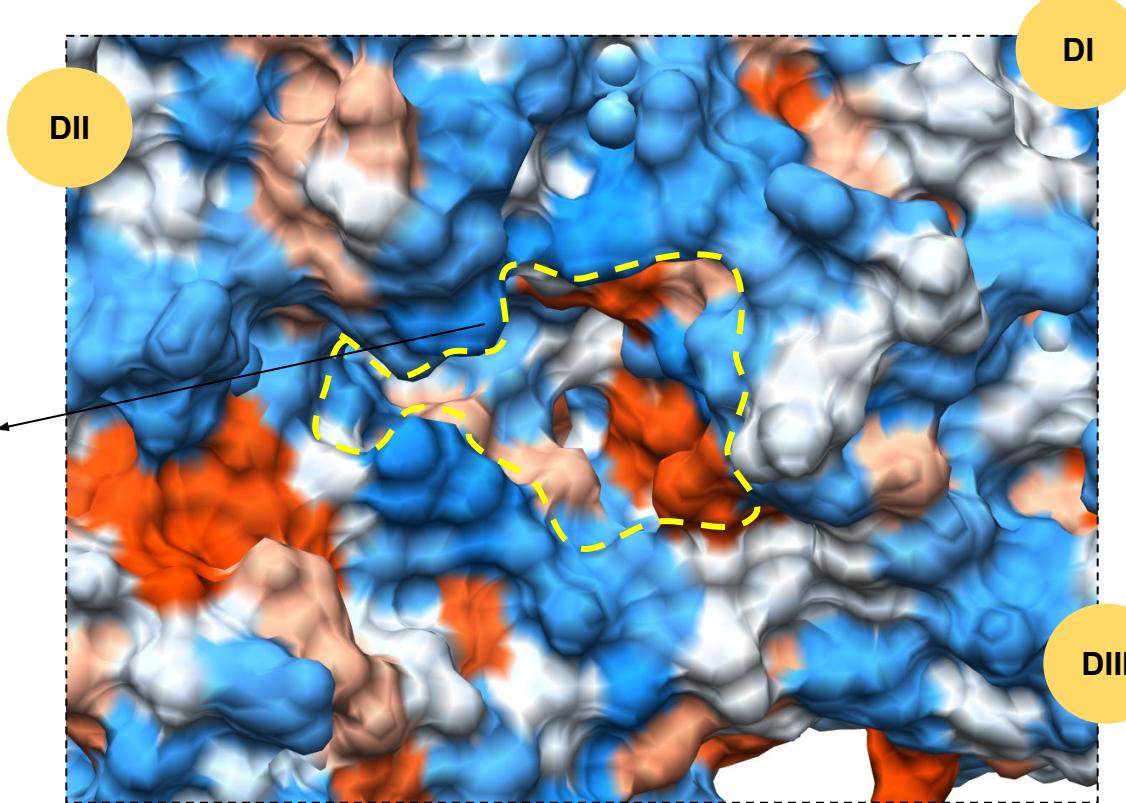
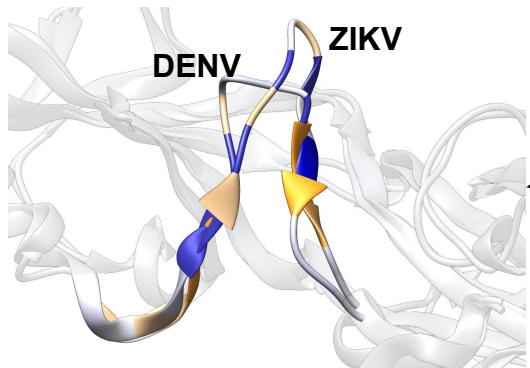
HIS 323



HYDROPHOBIC POCKET

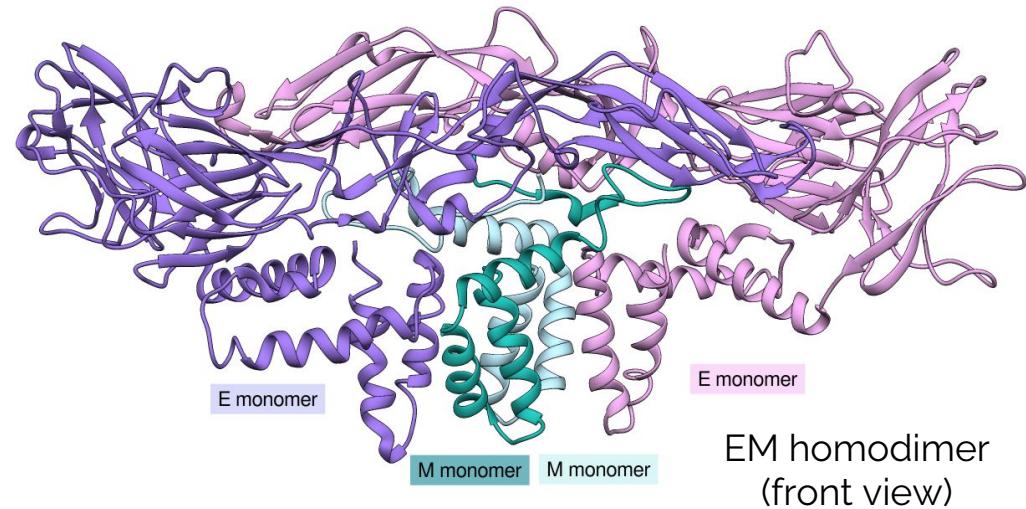
VIRUS MEDIATED MEMBRANE FUSION AND DRUG TARGET

(K-I Loop)
beta-hairpin

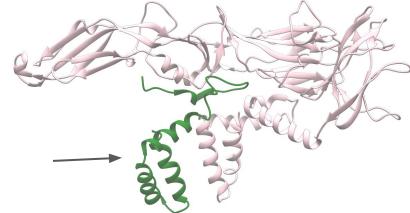


Envelope elements

M protein

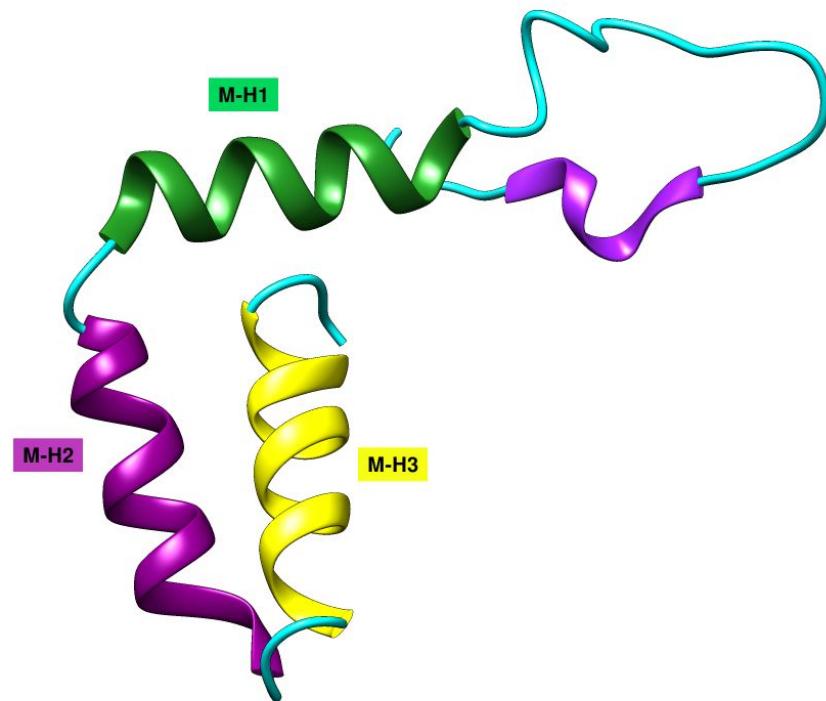
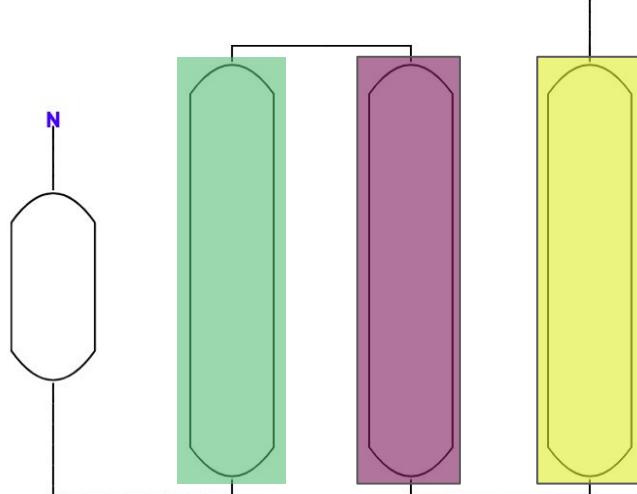


M PROTEIN: TOPOLOGICAL DIAGRAM

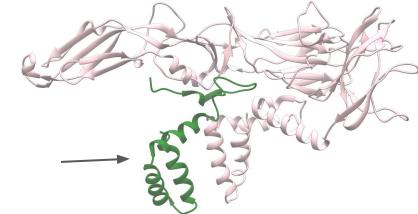
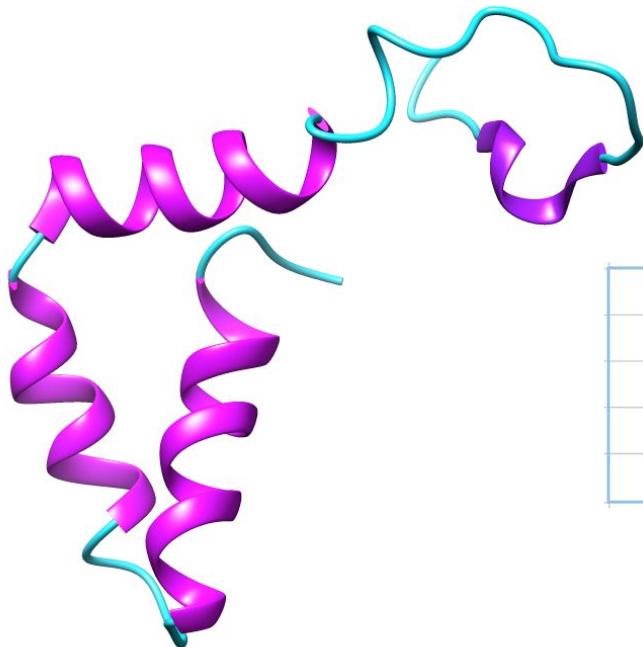


Has three helices: M-H1, M-H2, and M-H3.

The helices **M-H2** and **M-H3** are transmembrane helices.

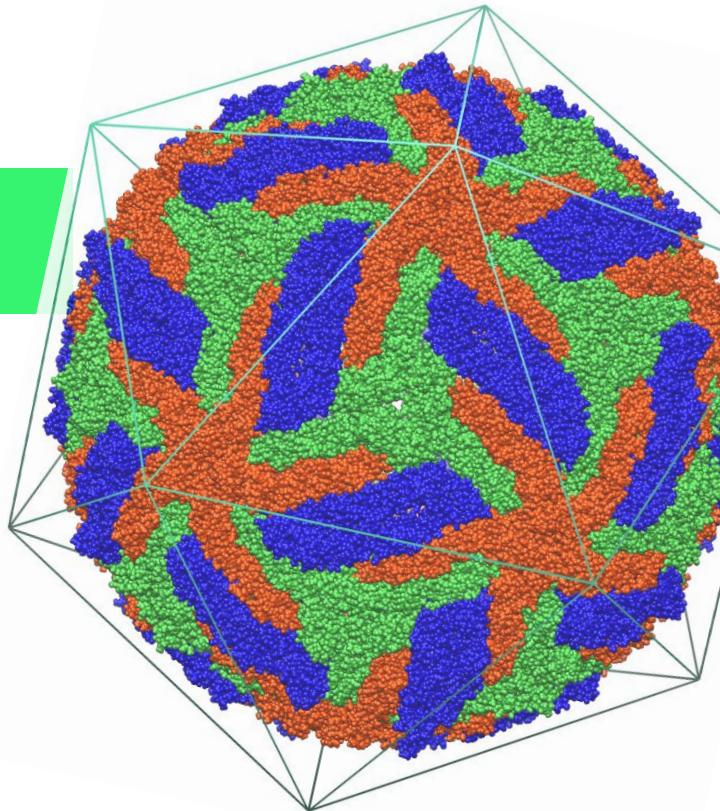


M PROTEIN



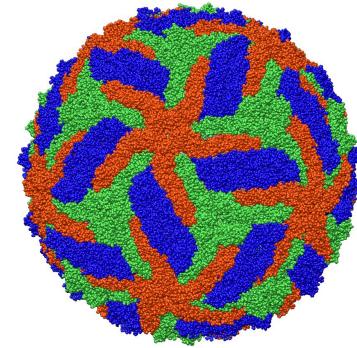
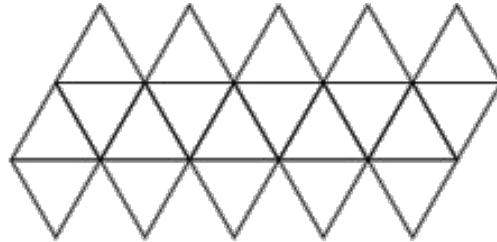
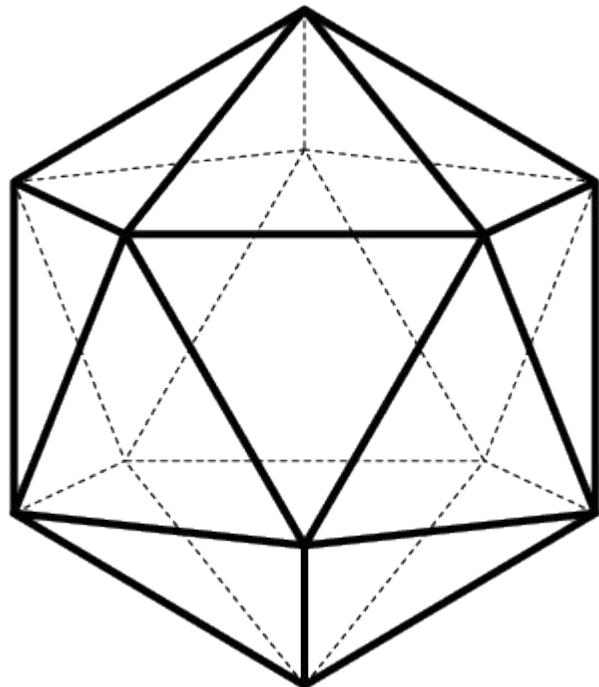
Level	
C	Mainly Alpha
A	Orthogonal Bundle
T	Helicase, Ruva Protein; domain 3
H	Flavivirus envelope glycoprotein M-like

Envelope symmetry



ENVELOPE SYMMETRY

ICOSAHEDRAL ASSEMBLY

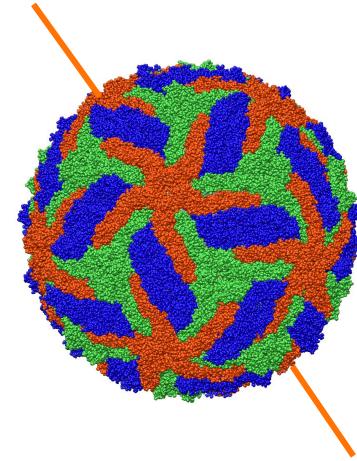
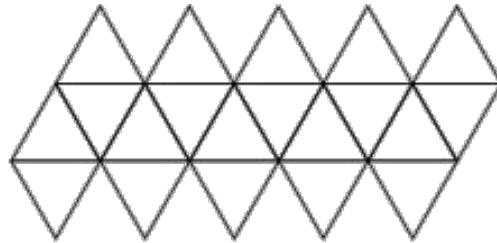
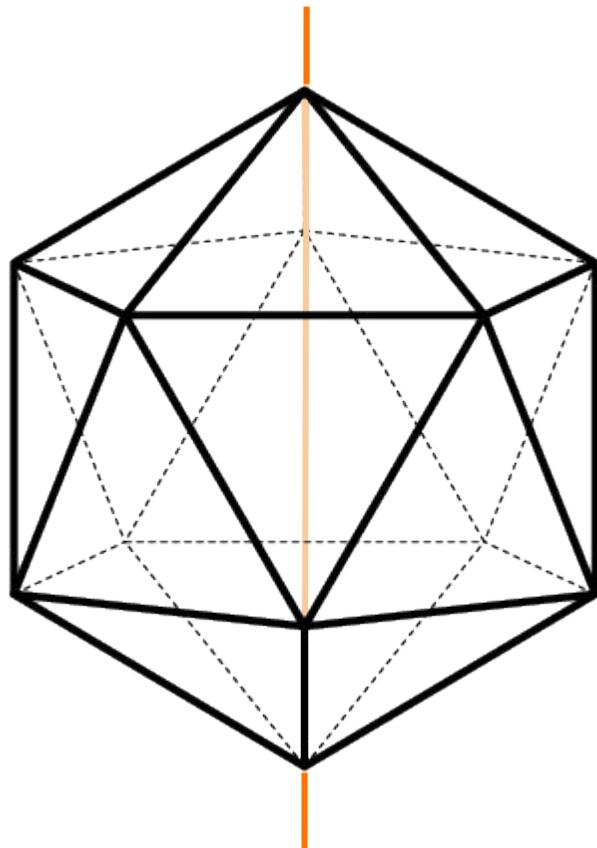


Symmetry axes:

- **Six 5-fold axes through the 12 vertices**
- **Ten 3-fold axes through the 20 triangular faces**
- **Fifteen 2-fold axes through the 30 edges**

ENVELOPE SYMMETRY

ICOSAHEDRAL ASSEMBLY

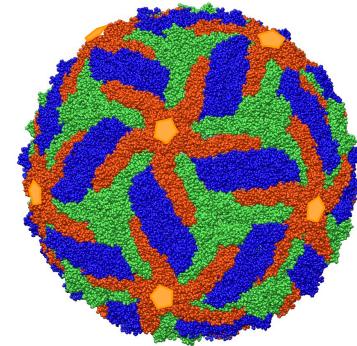
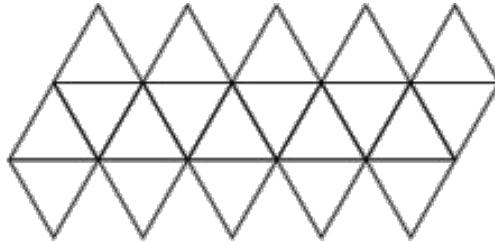
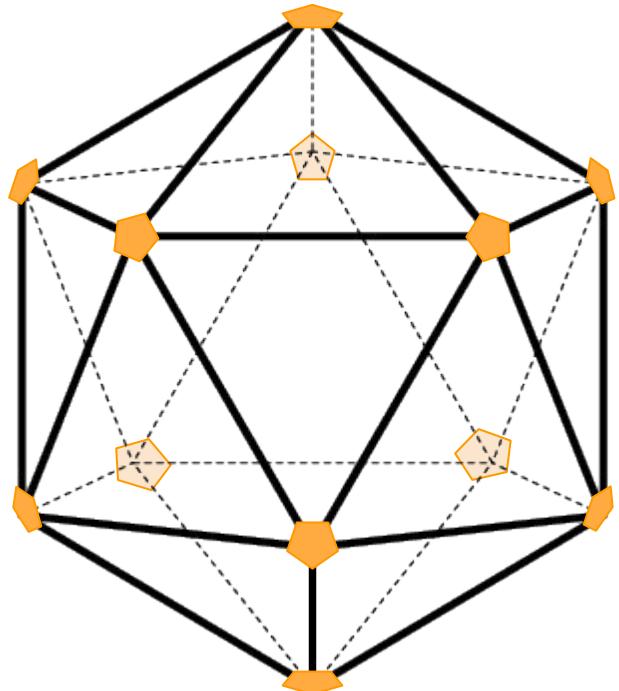


Symmetry axes:

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- Fifteen 2-fold axes through the 30 edges

ENVELOPE SYMMETRY

ICOSAHEDRAL ASSEMBLY

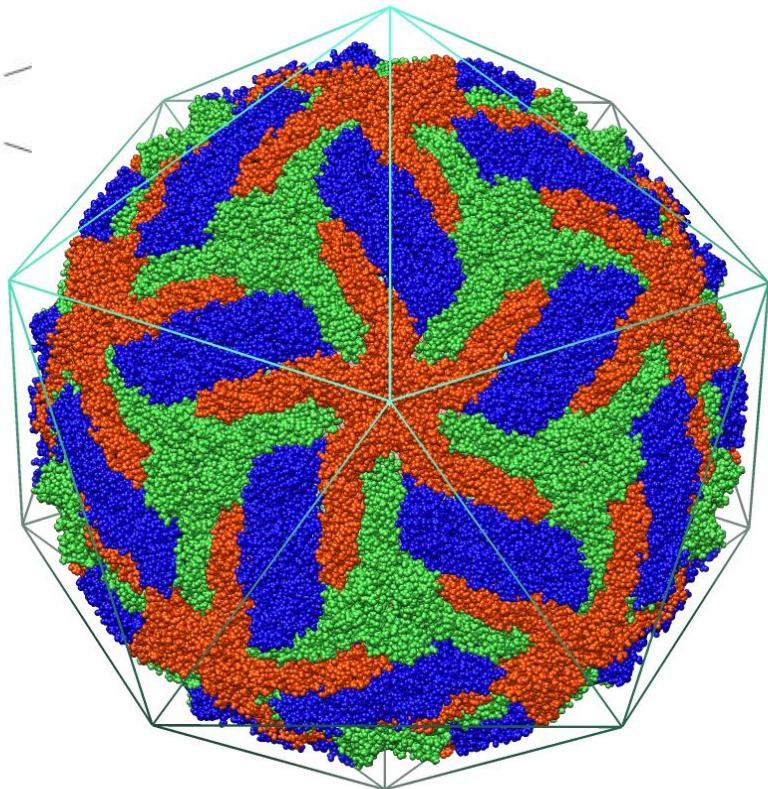
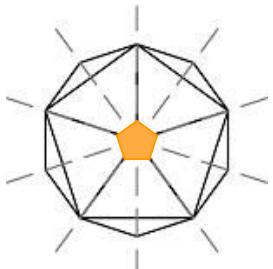
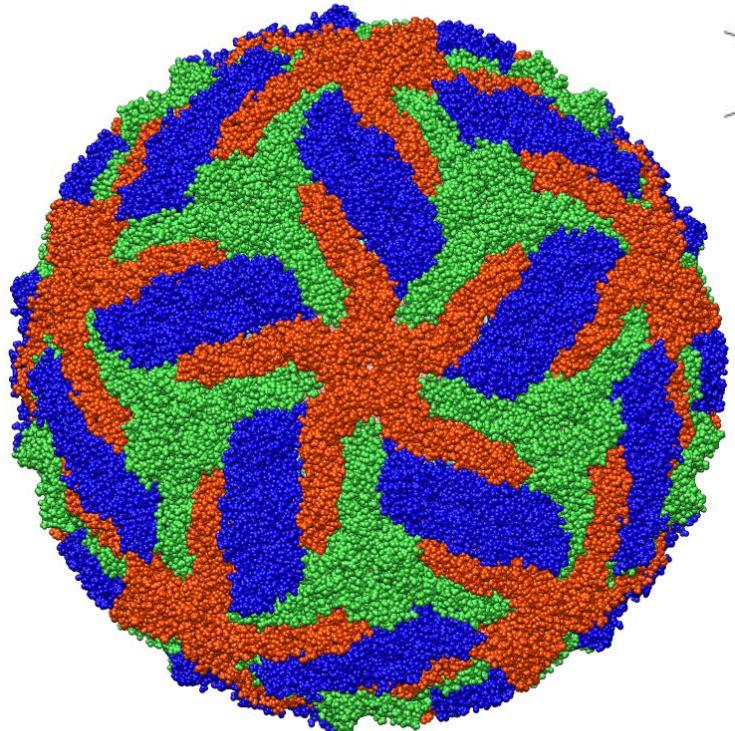


Symmetry axes:

- Six 5-fold axes through the 12 vertices
- Ten 3-fold axes through the 20 triangular faces
- Fifteen 2-fold axes through the 30 edges

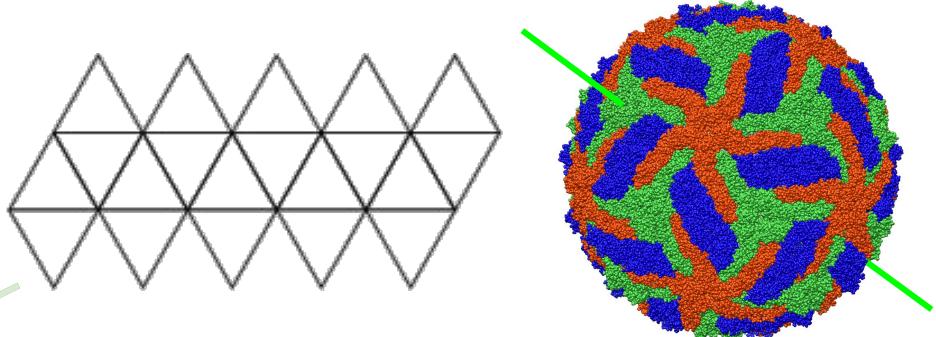
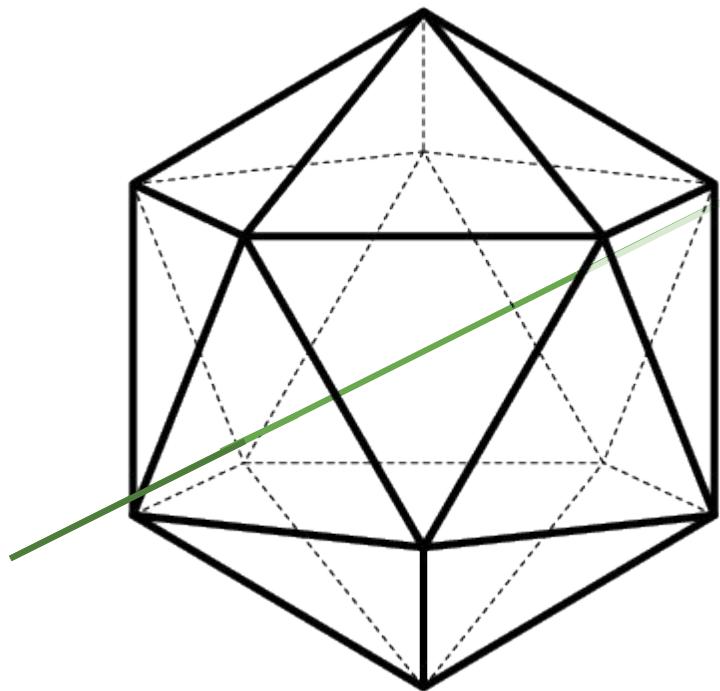
ENVELOPE SYMMETRY

5-FOLD AXIS



ENVELOPE SYMMETRY

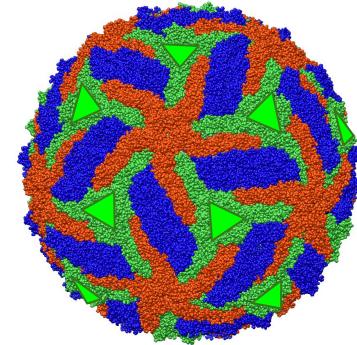
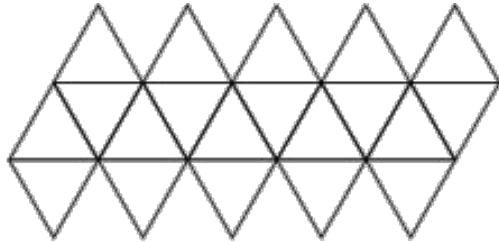
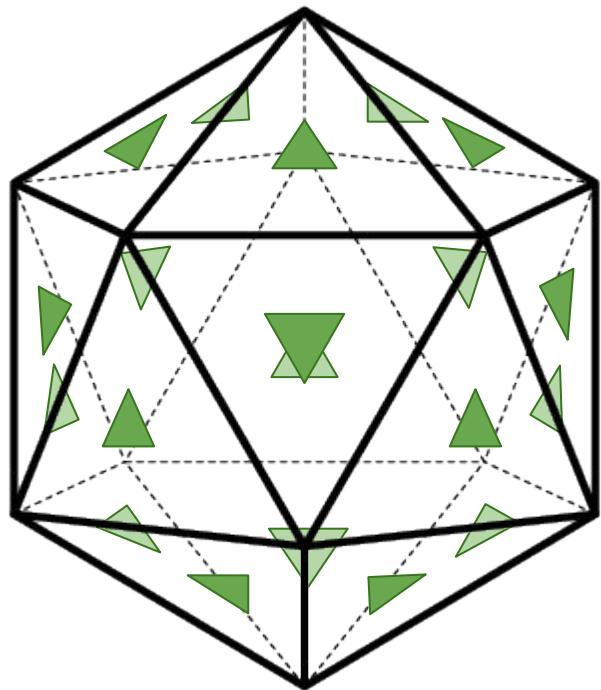
ICOSAHEDRAL ASSEMBLY



Symmetry axes:

- Six 5-fold axes through the 12 vertices
- Ten 3-fold axes through the 20 triangular faces
- Fifteen 2-fold axes through the 30 edges

ENVELOPE SYMMETRY ICOSAHEDRAL ASSEMBLY

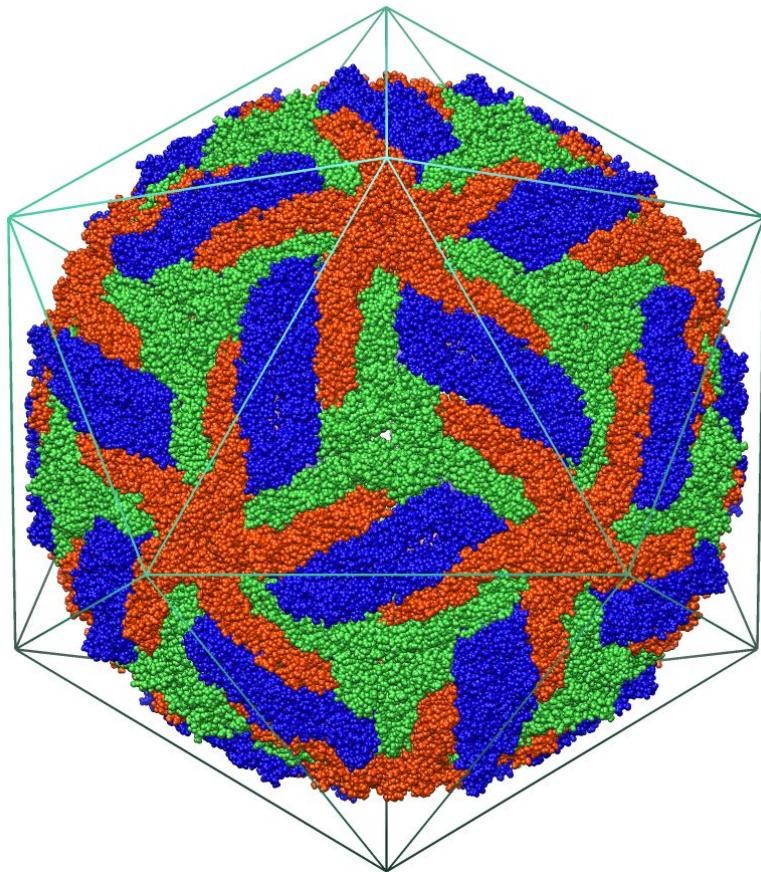
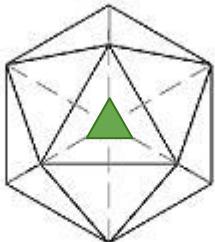
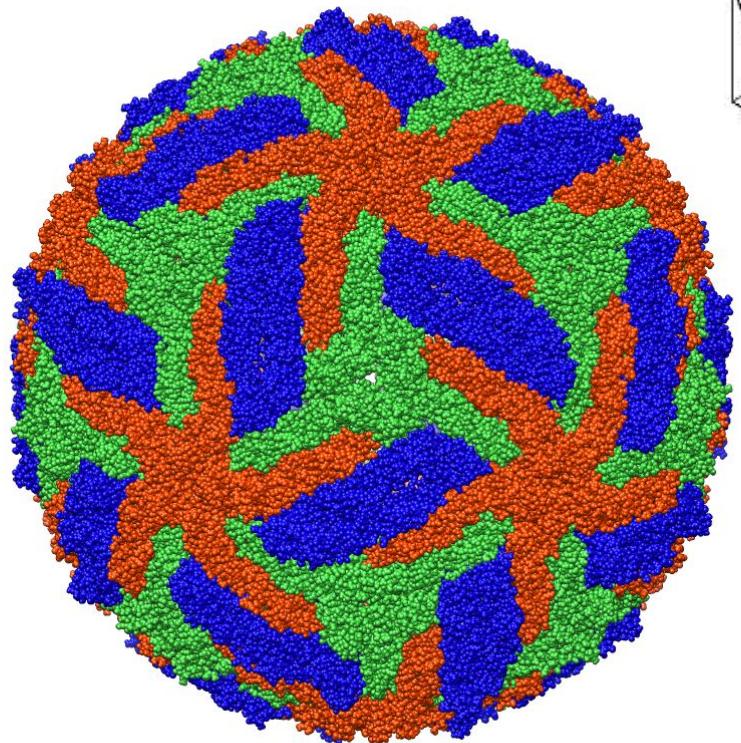


Symmetry axes:

- Six 5-fold axes through the 12 vertices
- Ten 3-fold axes through the 20 triangular faces
- Fifteen 2-fold axes through the 30 edges

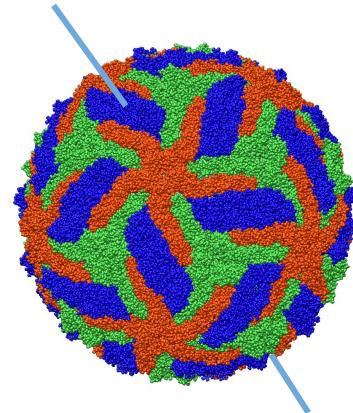
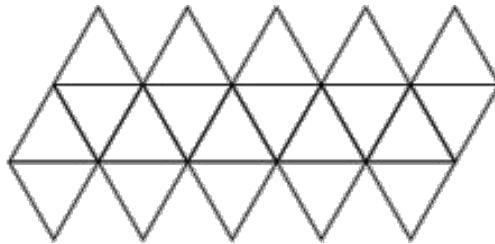
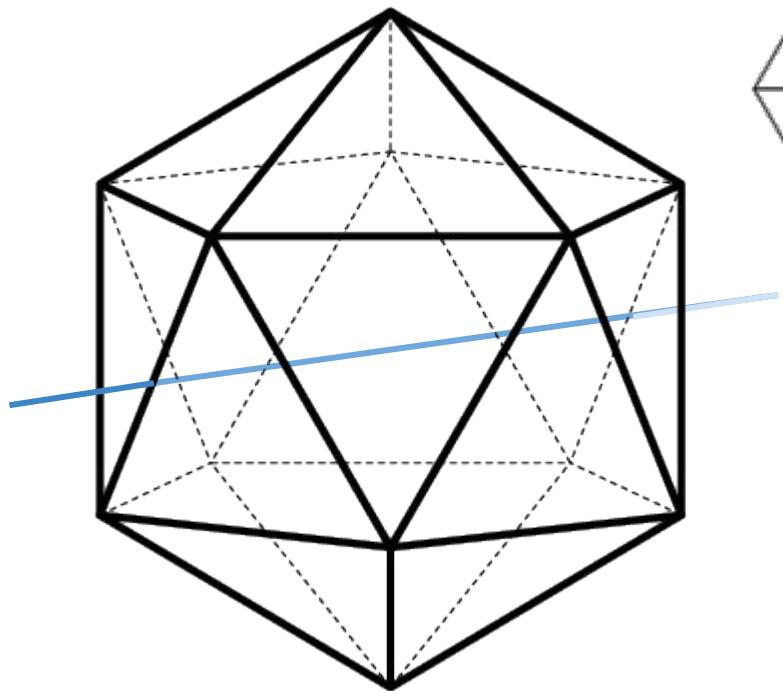
ENVELOPE SYMMETRY

3-FOLD AXIS



ENVELOPE SYMMETRY

ICOSAHEDRAL ASSEMBLY

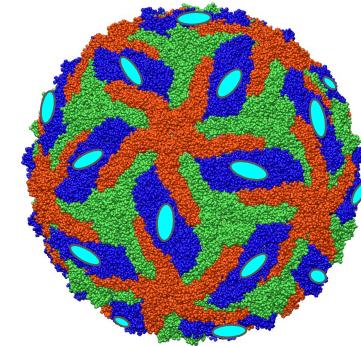
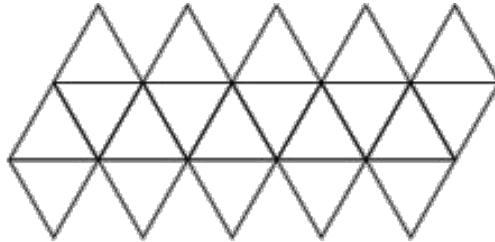
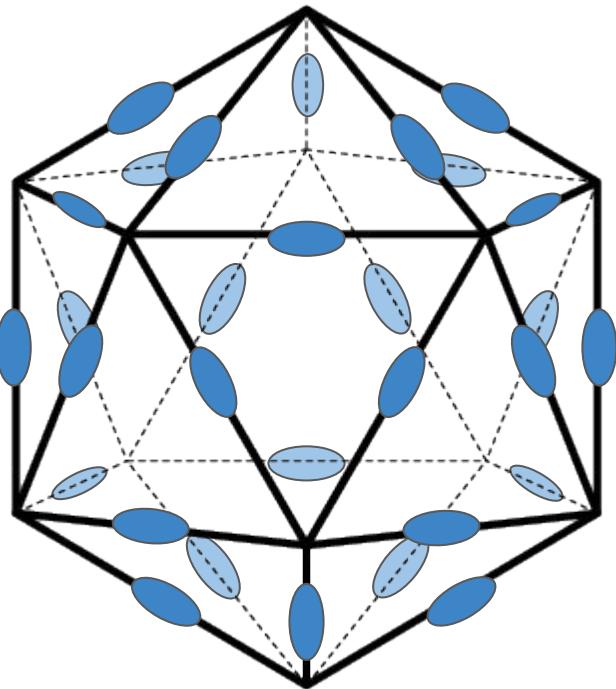


Symmetry axes:

- Six 5-fold axes through the 12 vertices
- Ten 3-fold axes through the 20 triangular faces
- Fifteen 2-fold axes through the 30 edges

ENVELOPE SYMMETRY

ICOSAHEDRAL ASSEMBLY

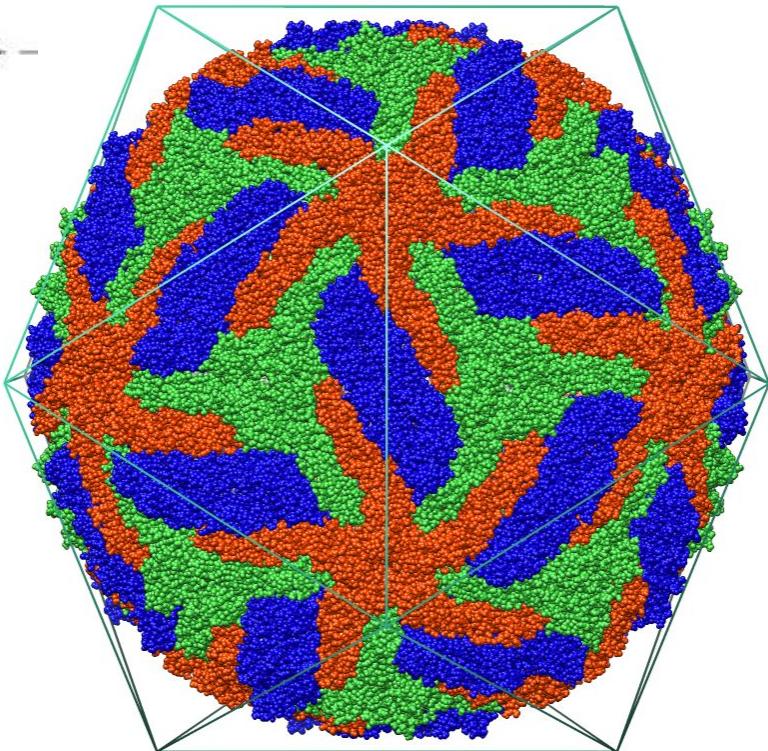
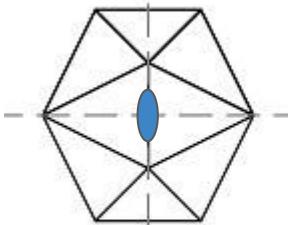
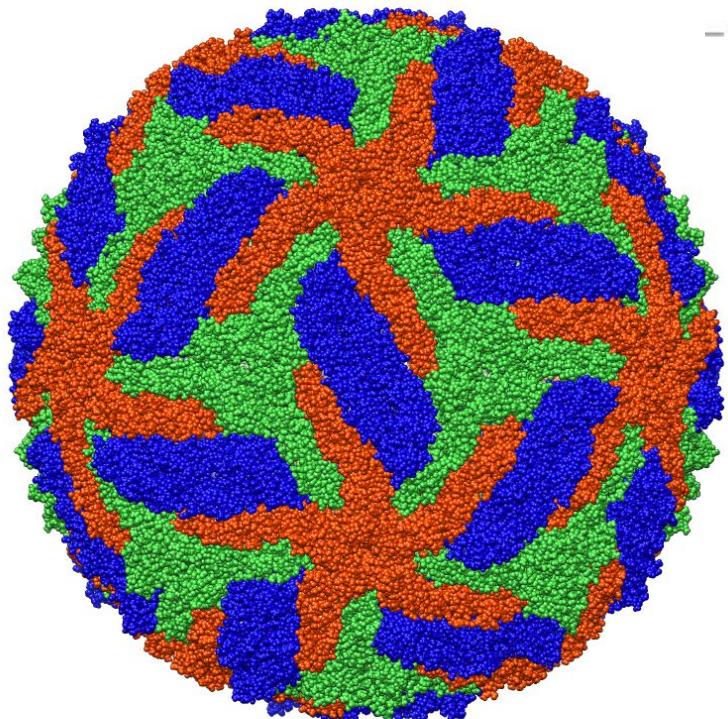


Symmetry axes:

- Six 5-fold axes through the 12 vertices
- Ten 3-fold axes through the 20 triangular faces
- Fifteen 2-fold axes through the 30 edges

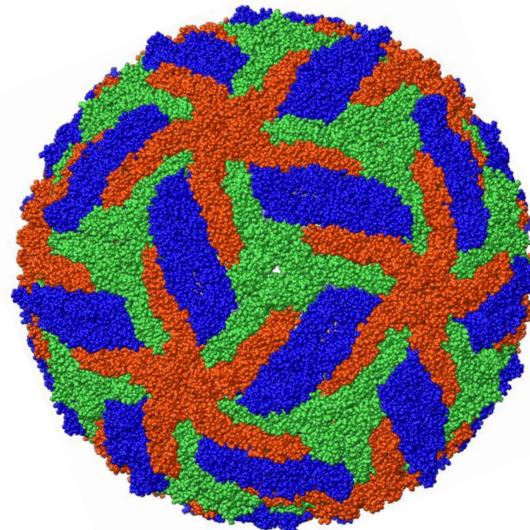
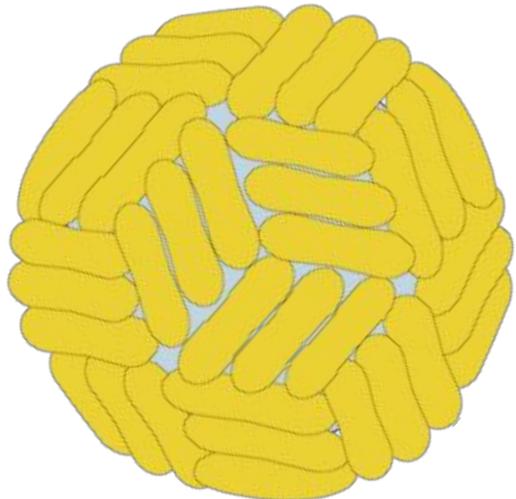
ENVELOPE SYMMETRY

2-FOLD AXIS

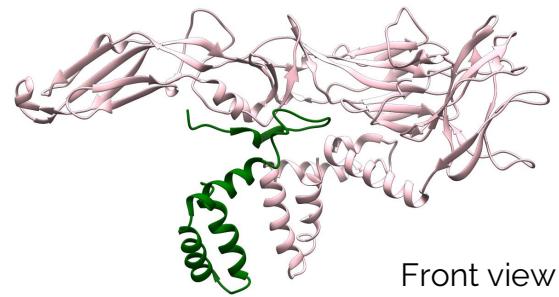


ENVELOPE SYMMETRY GLYCOPROTEIN SHELL

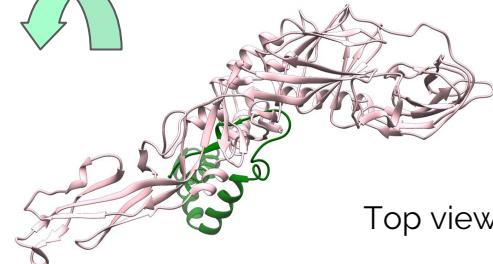
**Herringbone pattern of 180 E proteins
(90 antiparallel dimers of E protein)**



Unit structure: E-M heterodimer



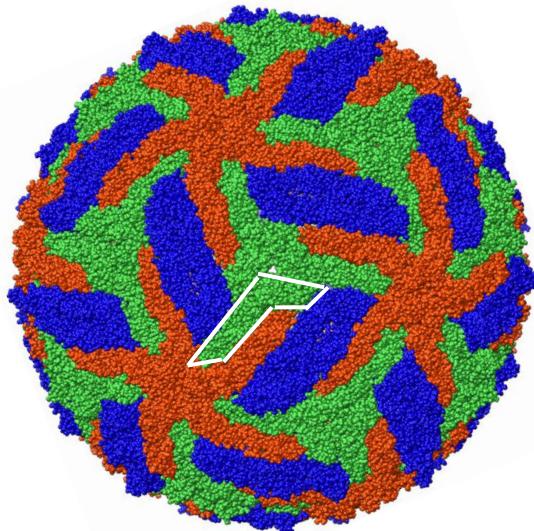
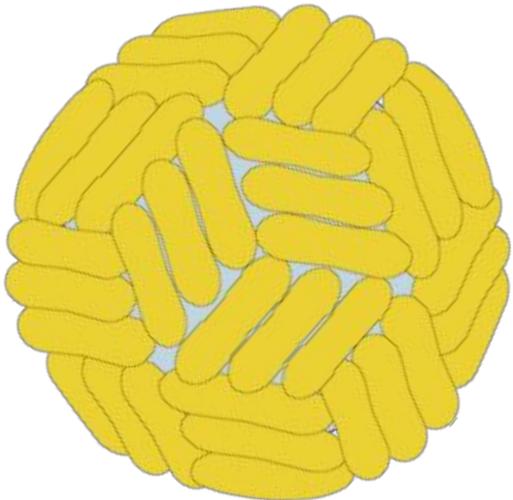
Front view



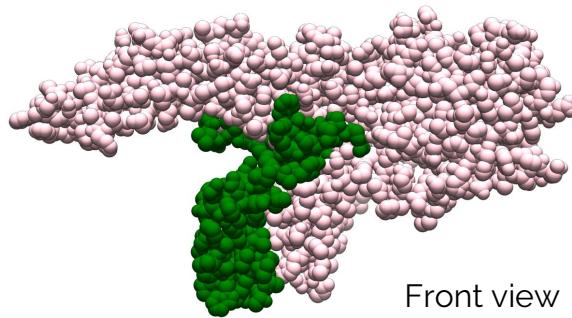
Top view

ENVELOPE SYMMETRY GLYCOPROTEIN SHELL

Herringbone pattern of 180 E proteins (90 antiparallel dimers of E protein)



Unit structure: E-M heterodimer



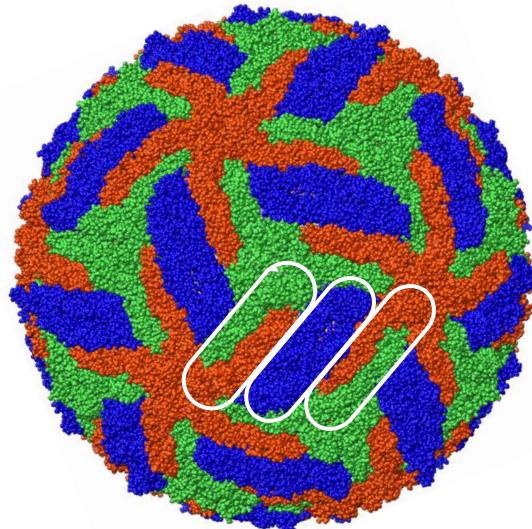
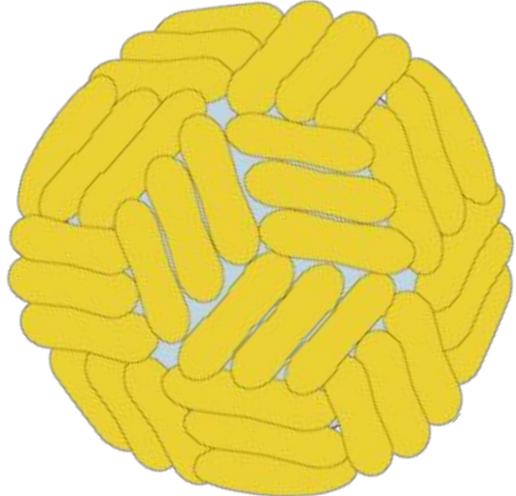
Front view



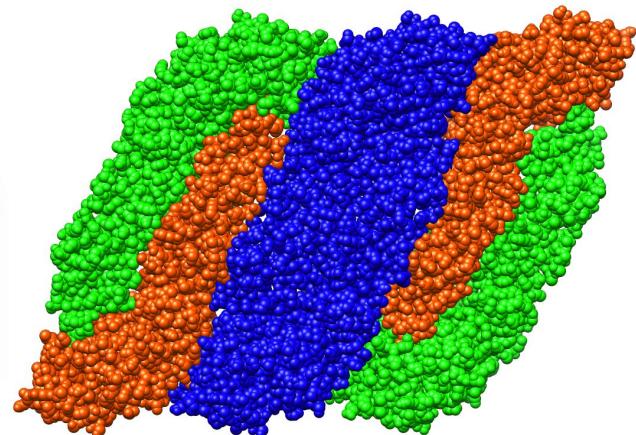
Top view

ENVELOPE SYMMETRY GLYCOPROTEIN SHELL

**Herringbone pattern of 180 E proteins
(90 antiparallel dimers of E protein)**



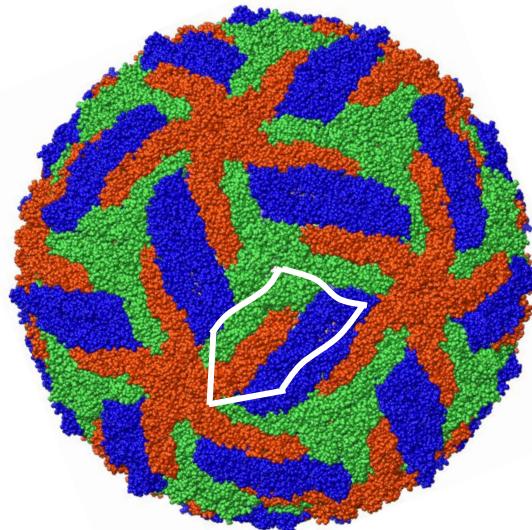
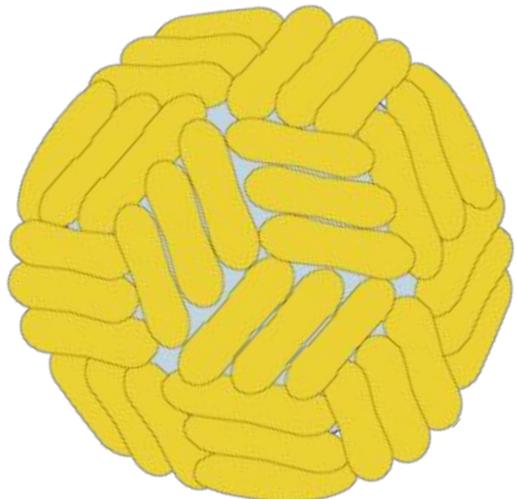
**Three E dimers
form a raft**



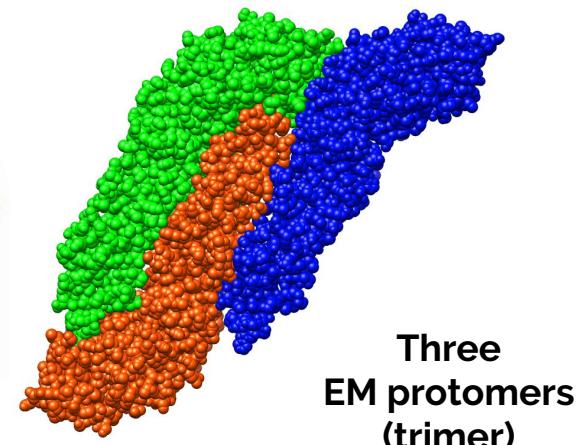
ENVELOPE SYMMETRY

ASYMMETRIC UNIT

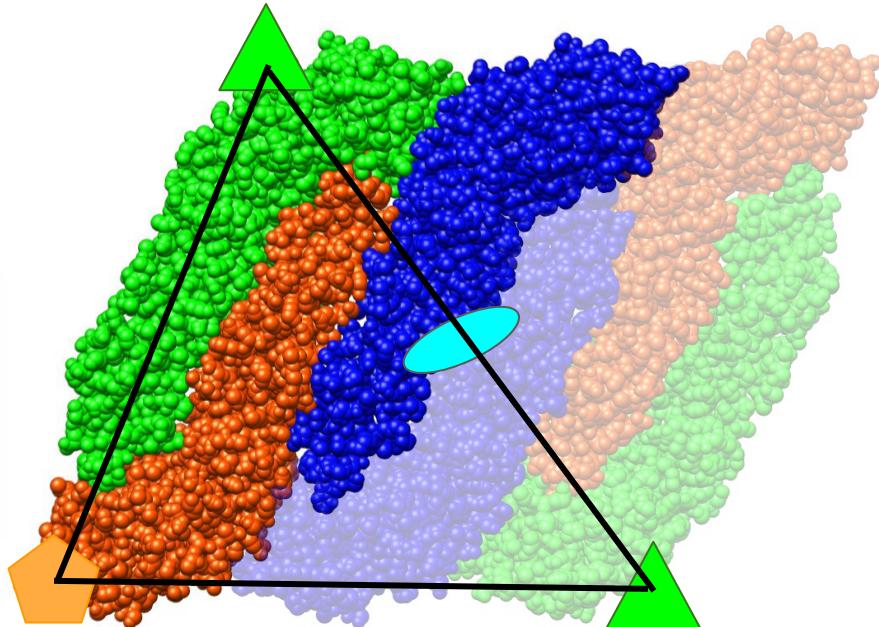
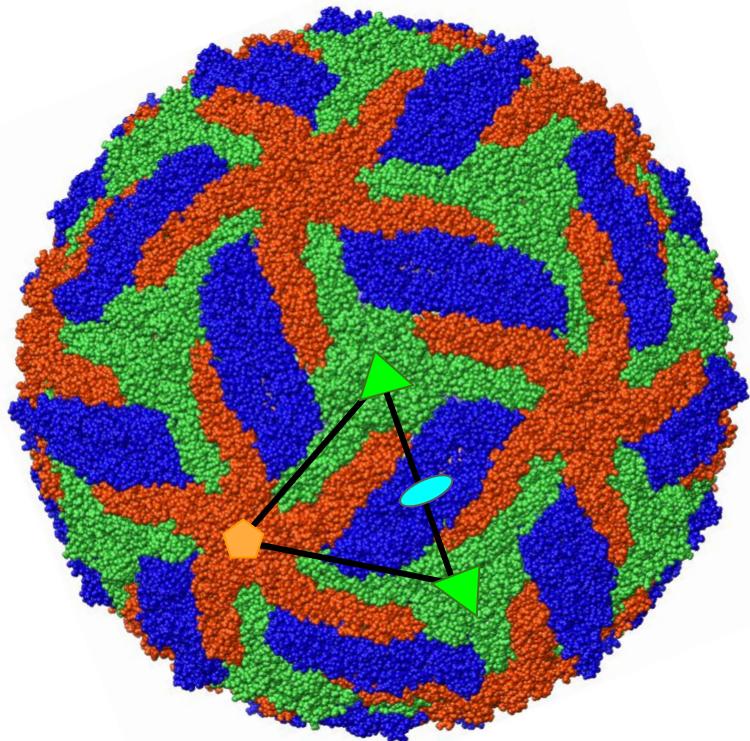
**Herringbone pattern of 180 E proteins
(90 antiparallel dimers of E protein)**



**60 asymmetric units
(T=3-like organization of surface
EM heterodimers)**

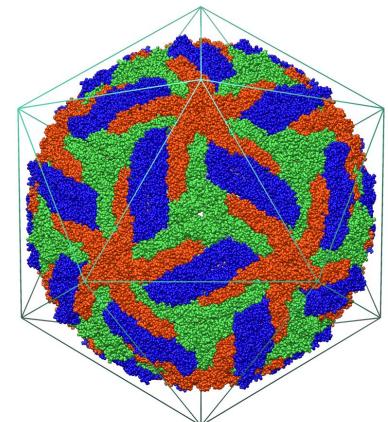
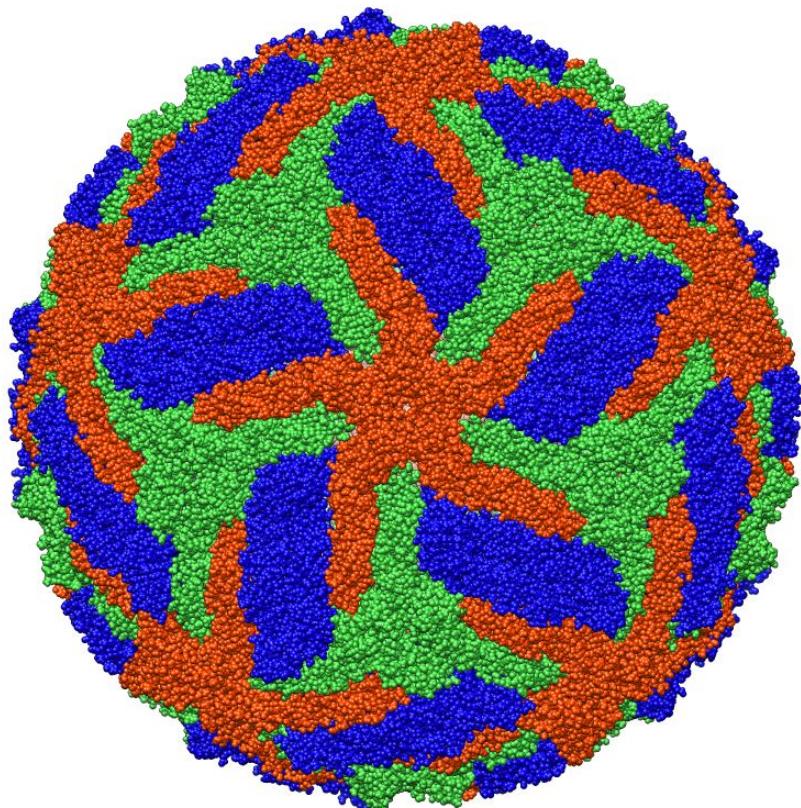


ENVELOPE SYMMETRY ASYMMETRIC UNIT

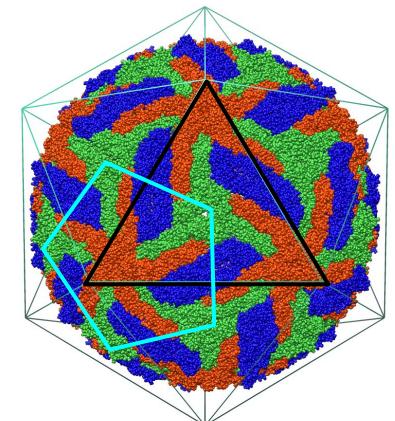
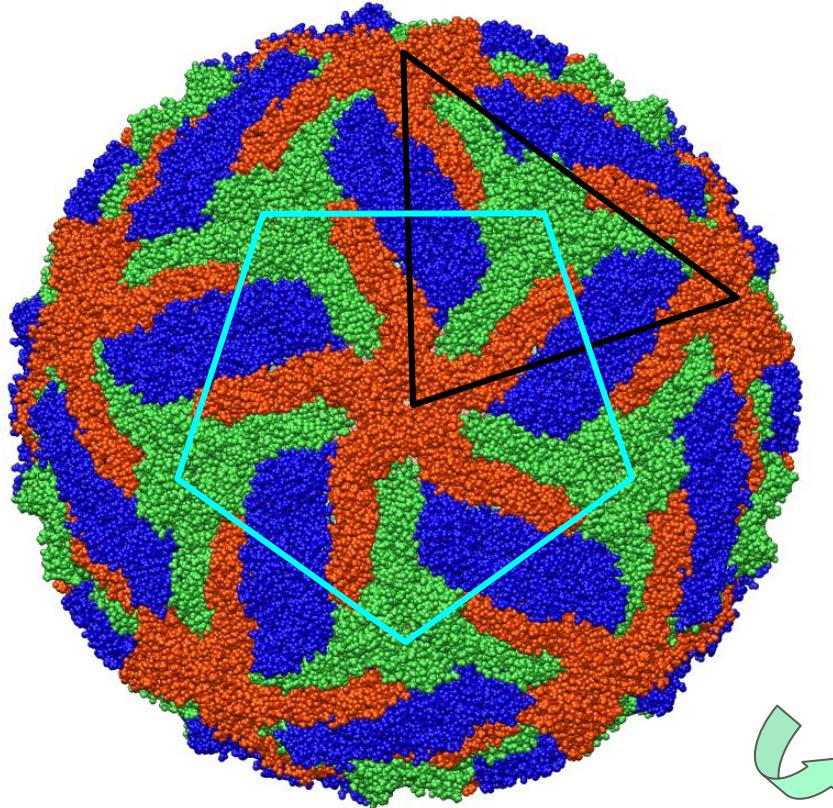


ENVELOPE SYMMETRY

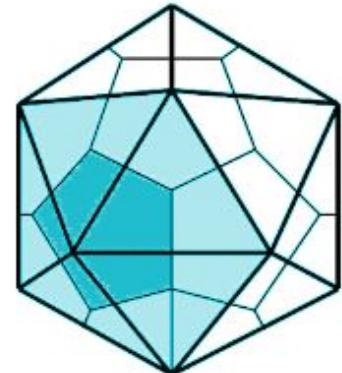
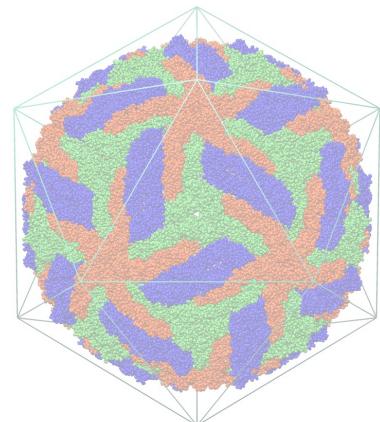
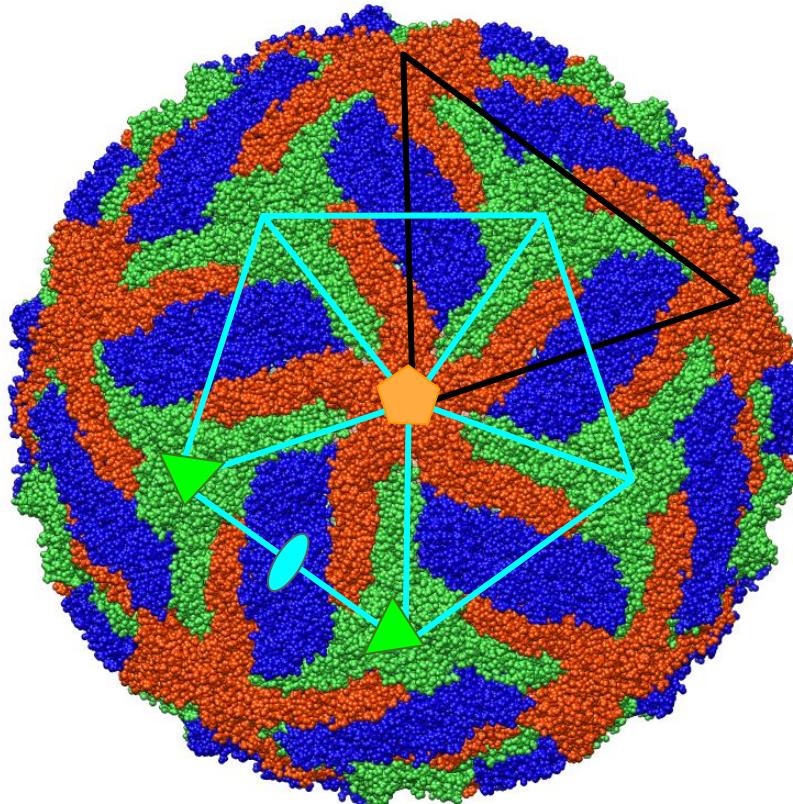
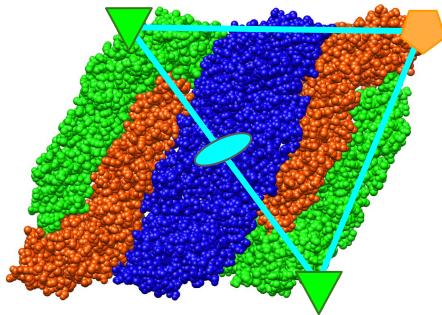
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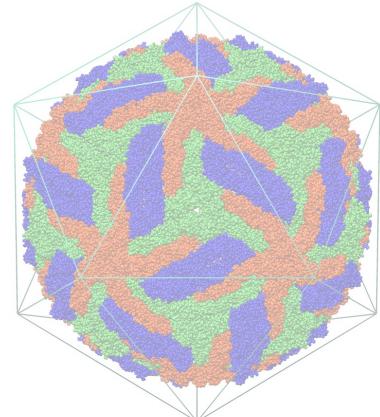
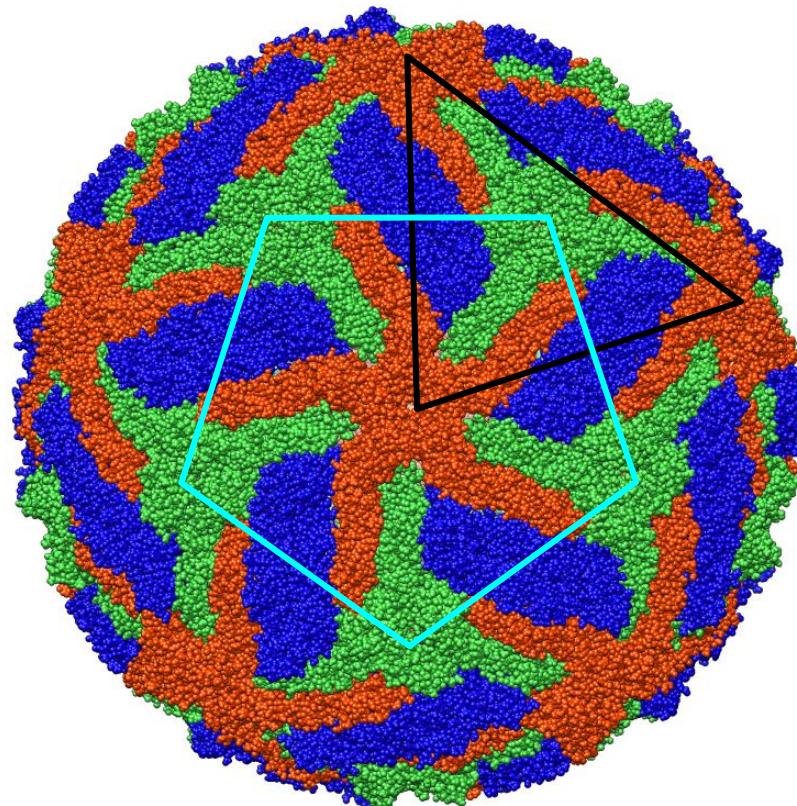
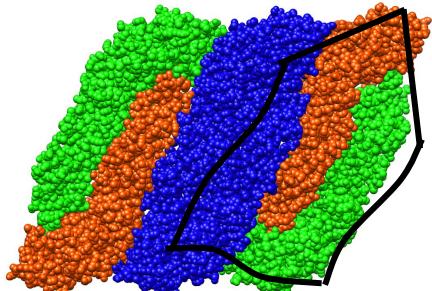
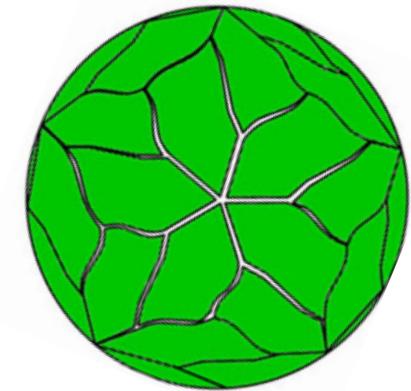
ENVELOPE SYMMETRY ASYMMETRIC UNIT



ENVELOPE SYMMETRY ASYMMETRIC UNIT

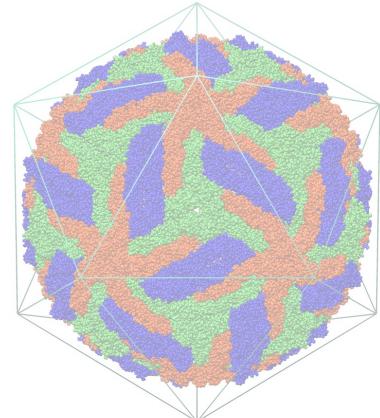
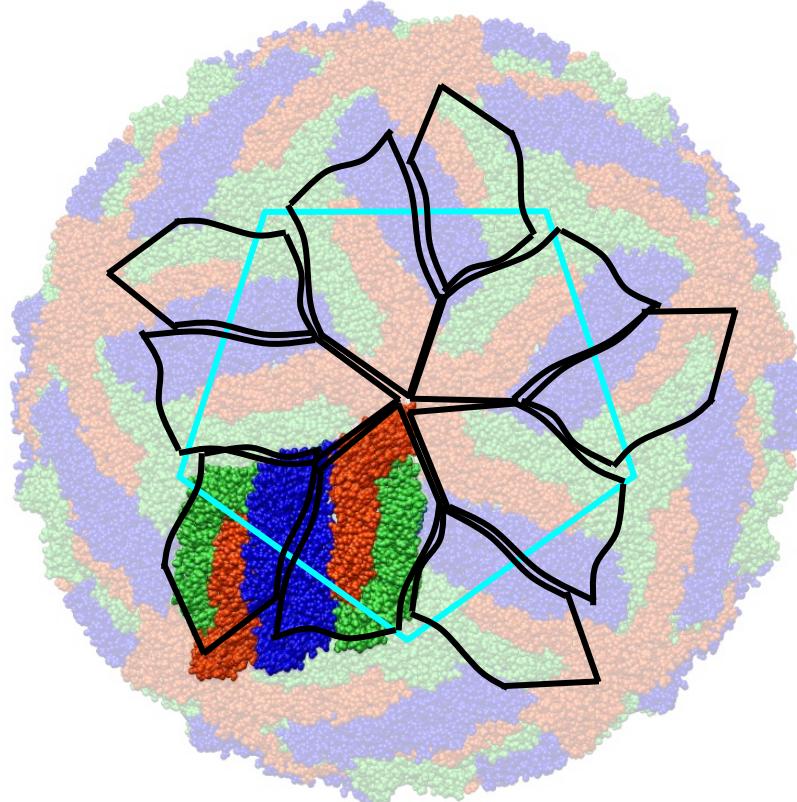
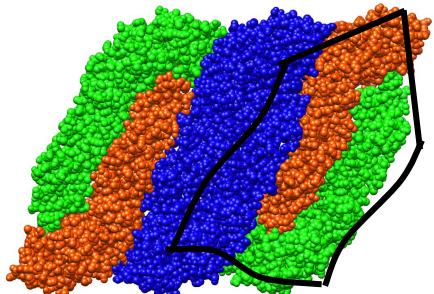
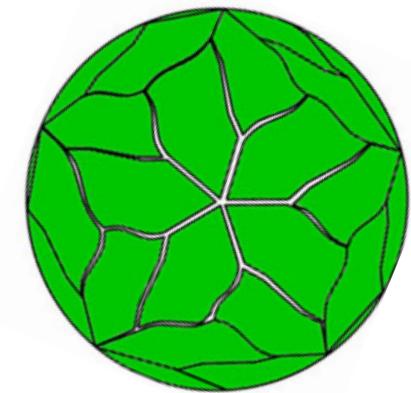


ENVELOPE SYMMETRY ASYMMETRIC UNIT



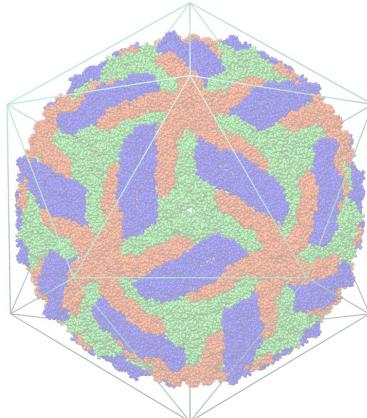
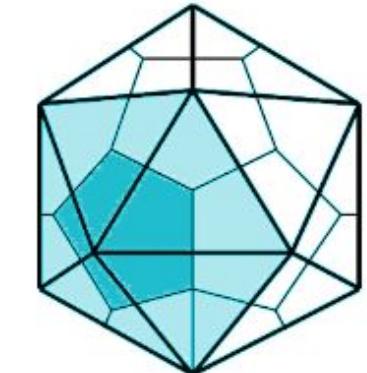
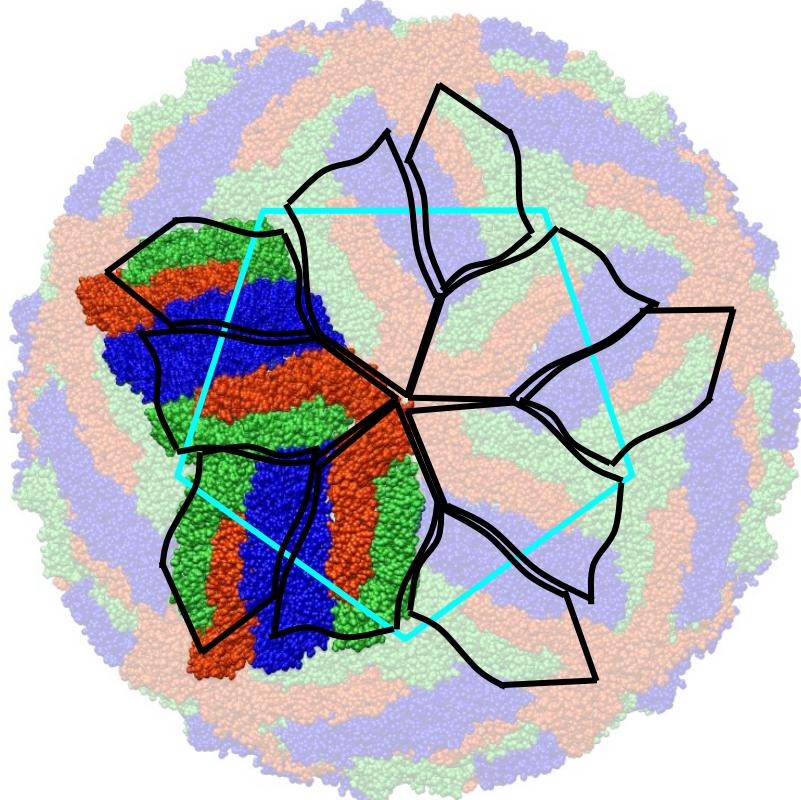
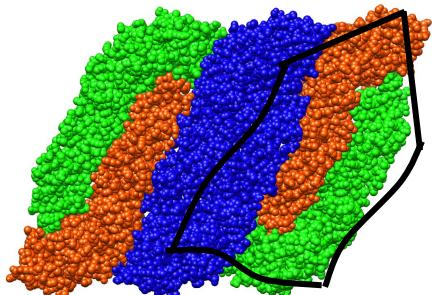
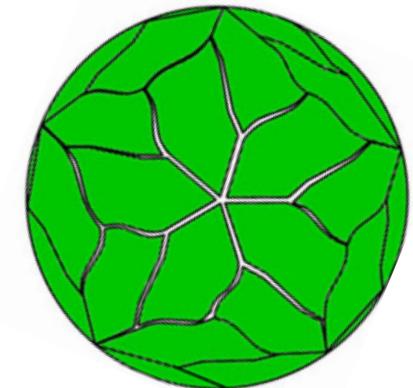
ENVELOPE SYMMETRY

ASYMMETRIC UNIT



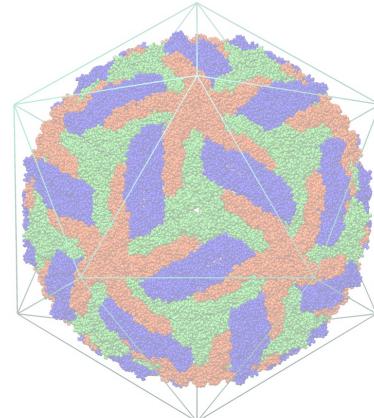
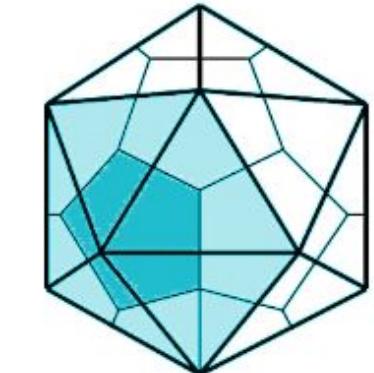
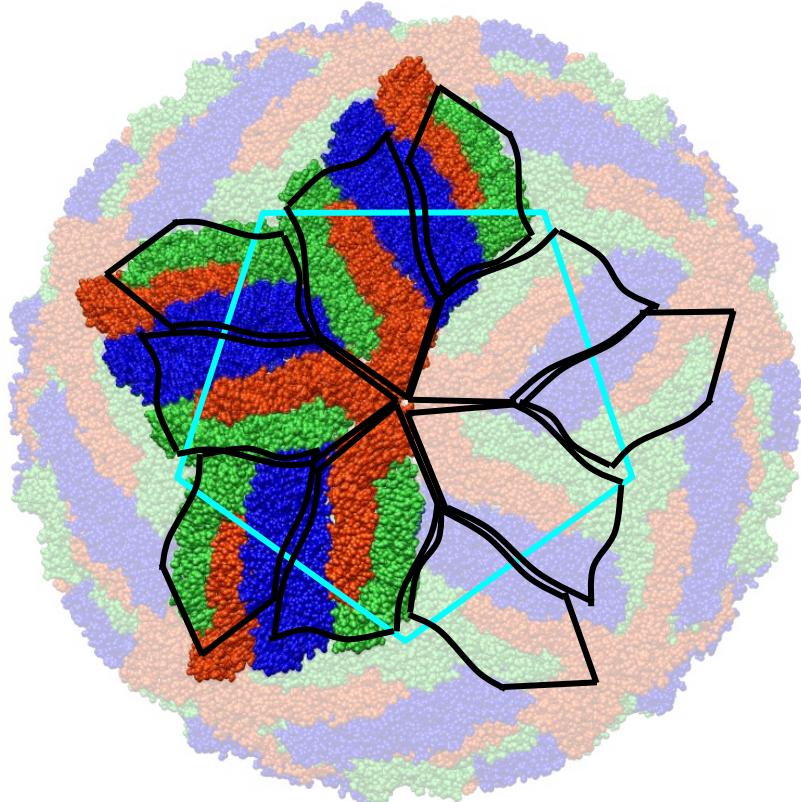
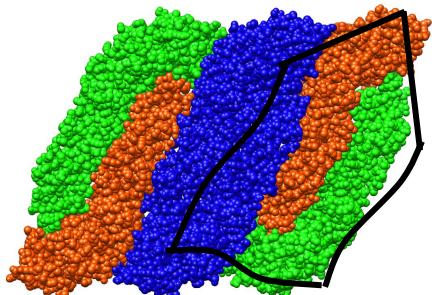
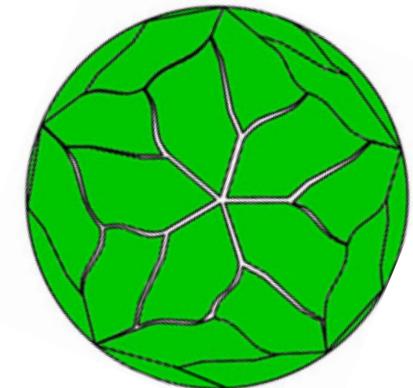
ENVELOPE SYMMETRY

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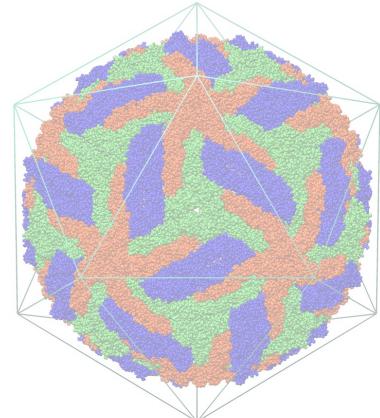
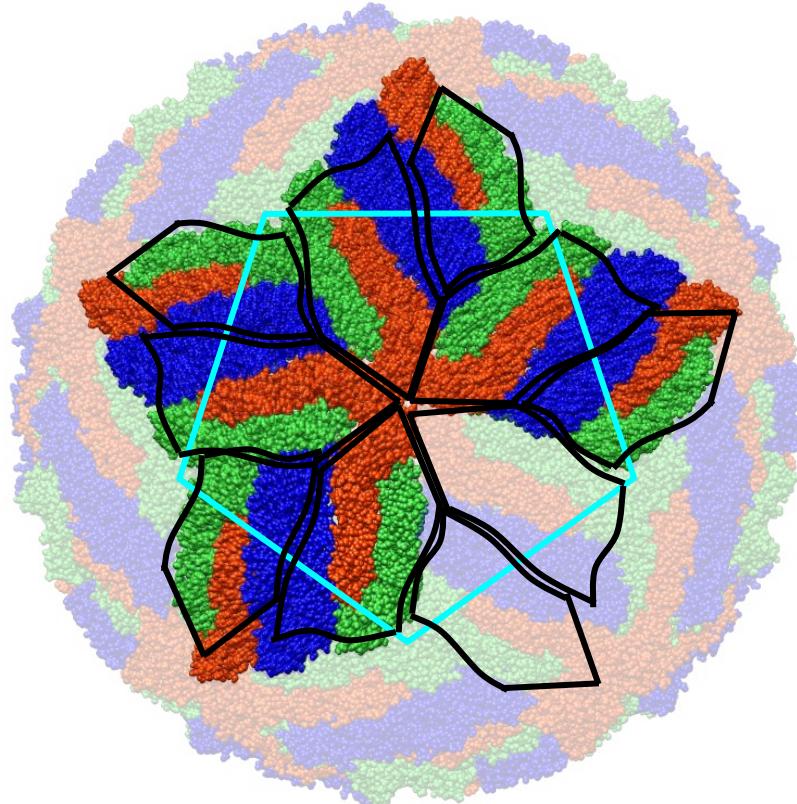
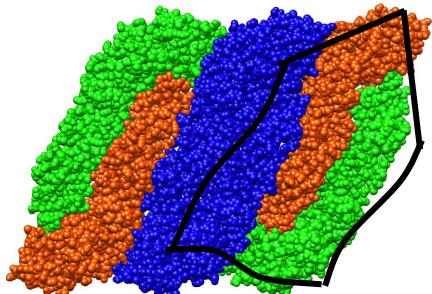
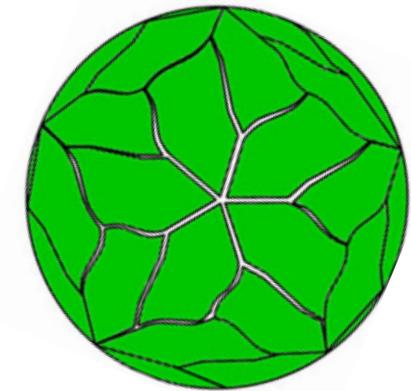
ENVELOPE SYMMETRY

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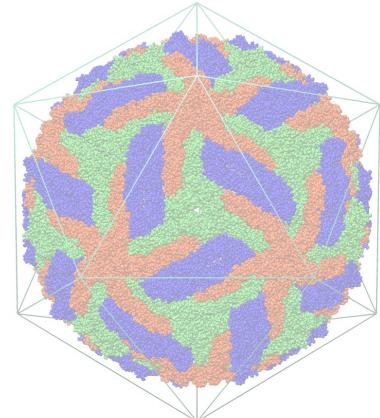
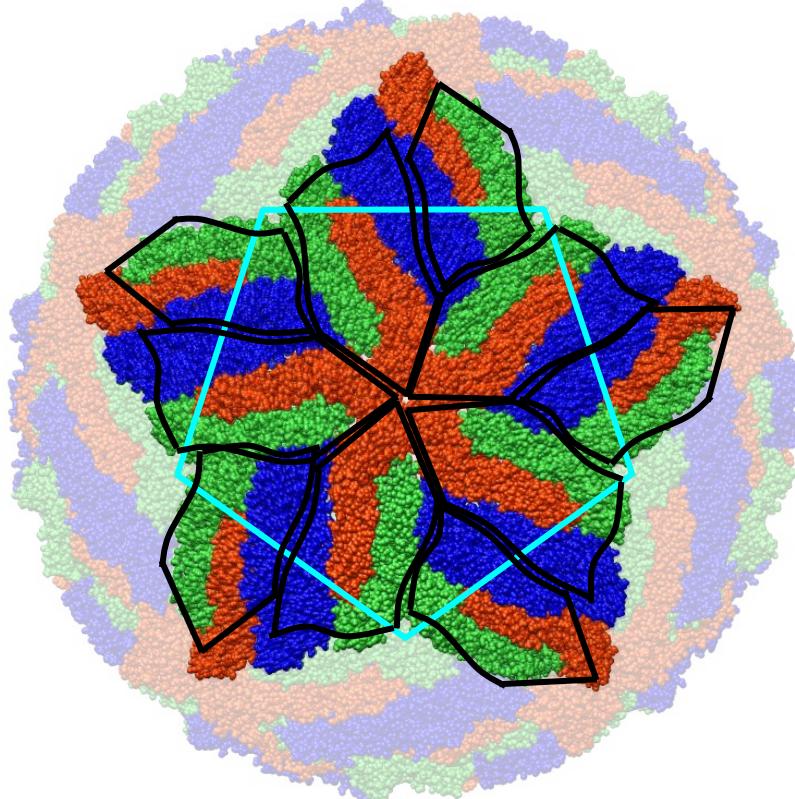
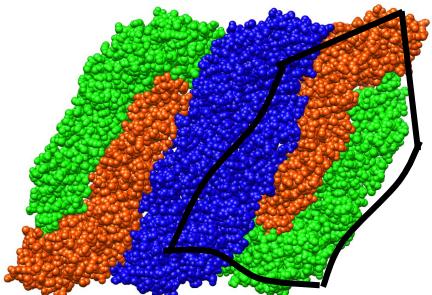
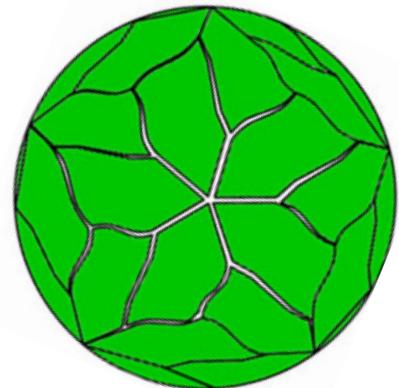
ENVELOPE SYMMETRY

ASYMMETRIC UNIT



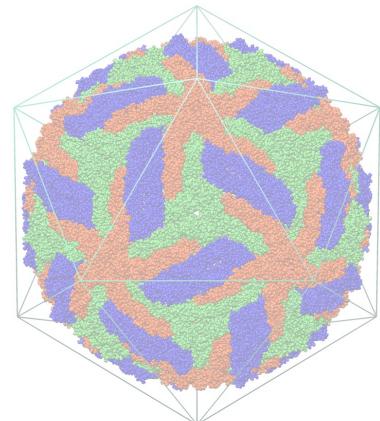
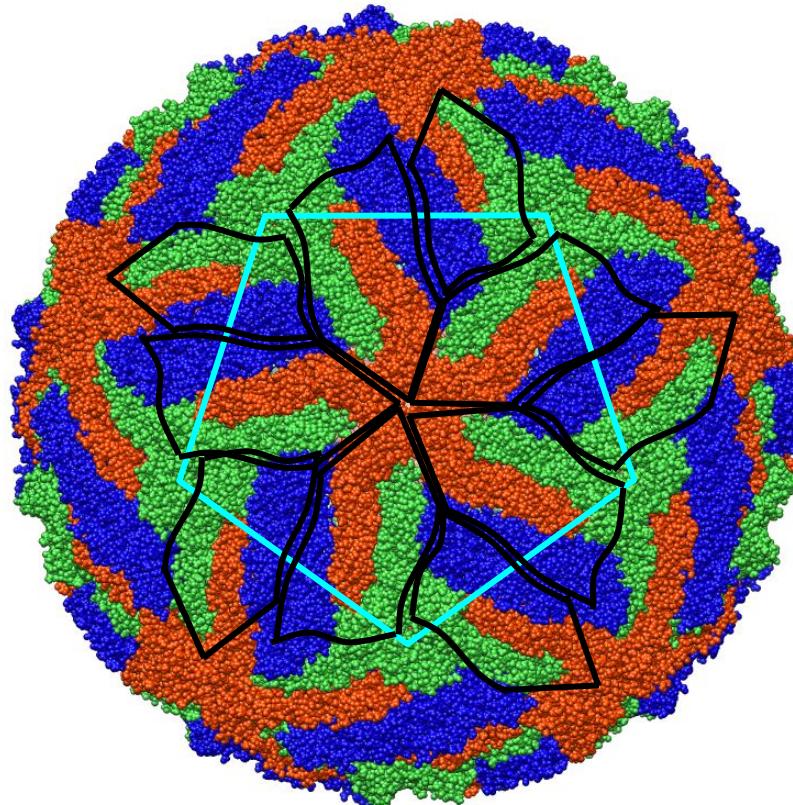
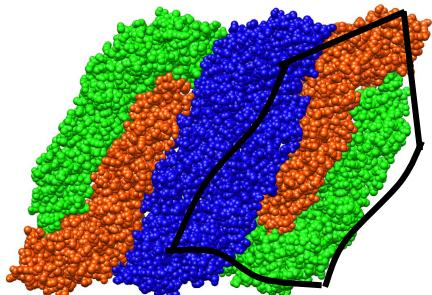
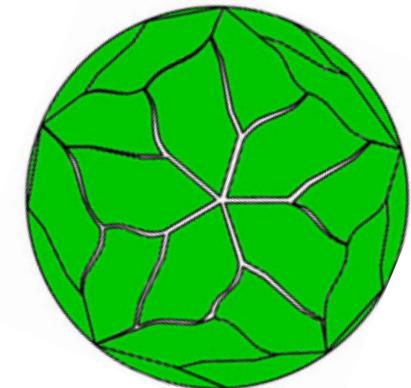
ENVELOPE SYMMETRY

ASYMMETRIC UNIT

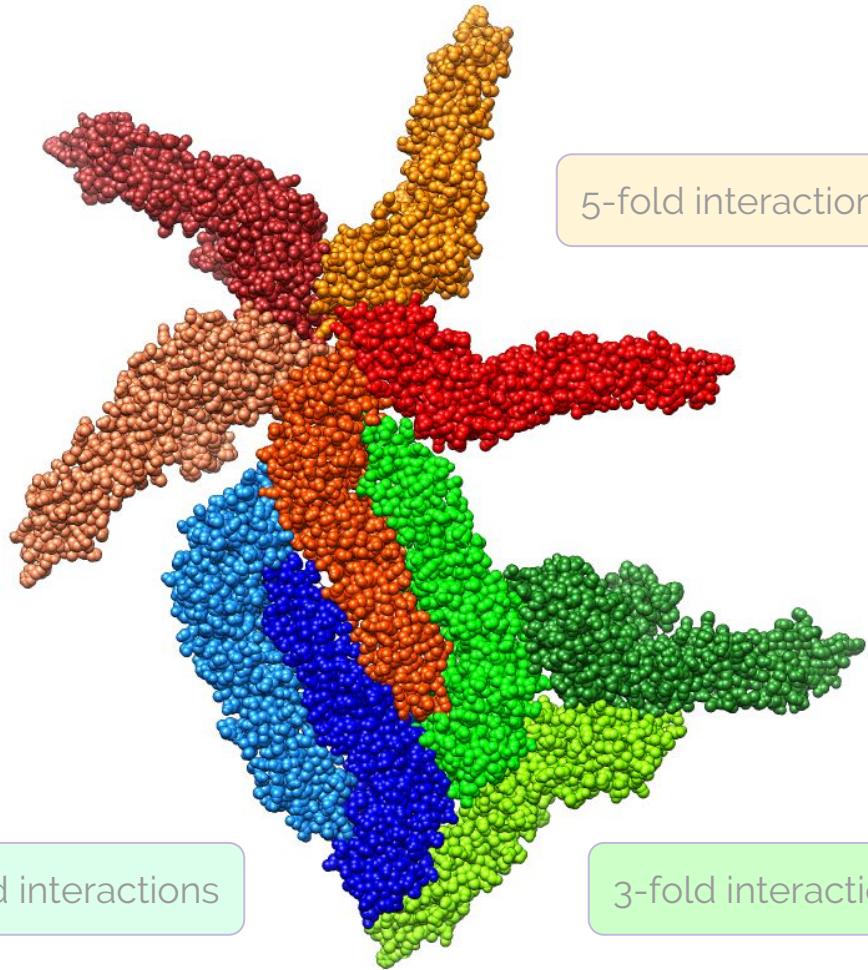
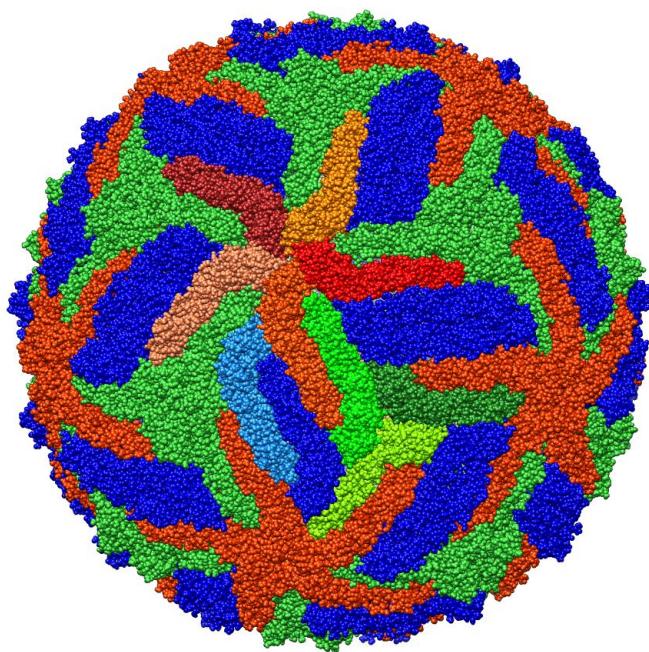


ENVELOPE SYMMETRY

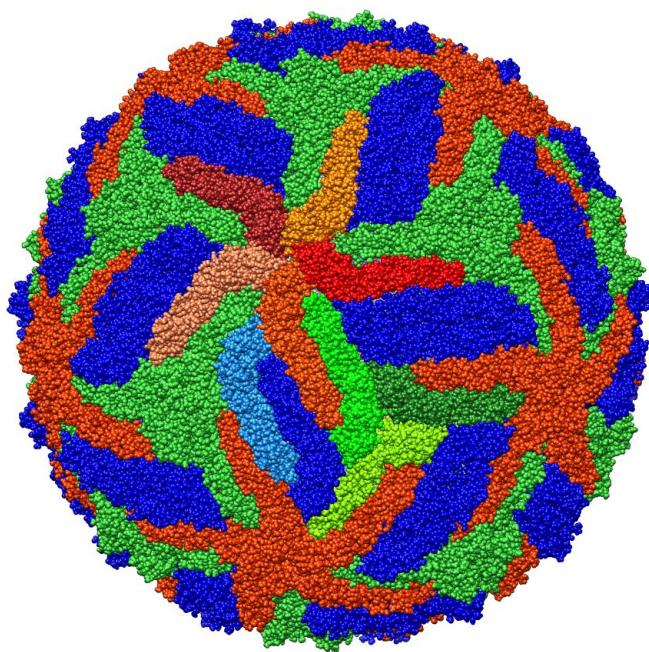
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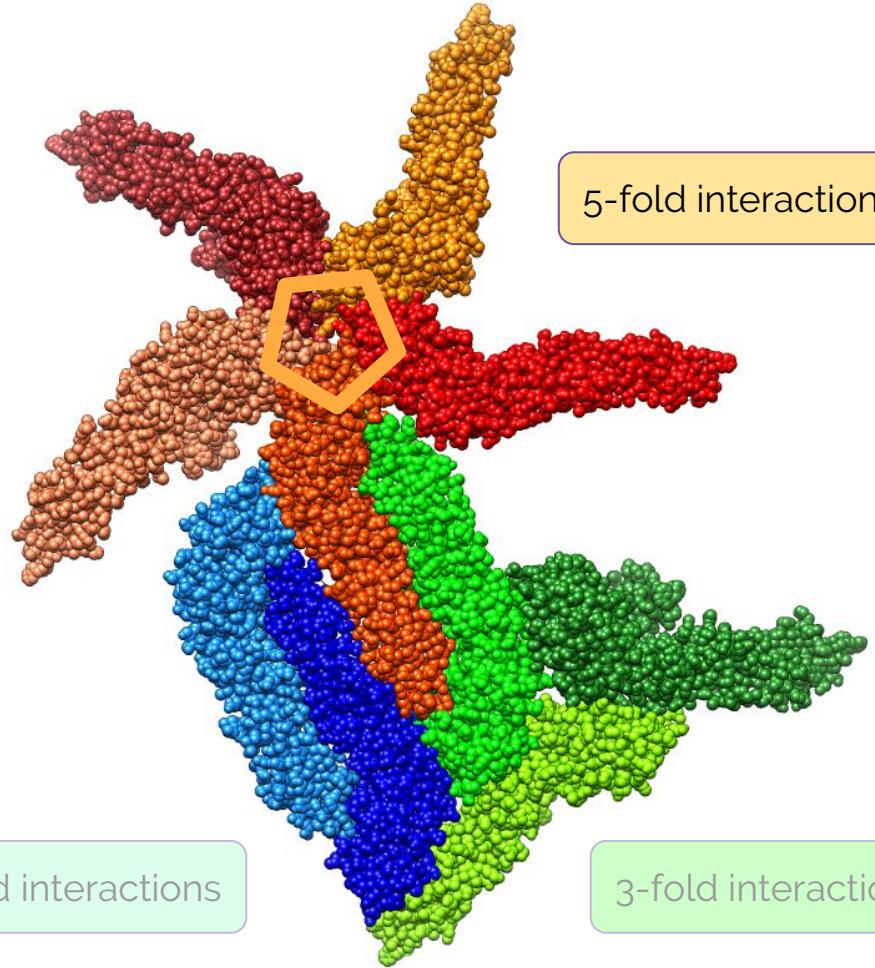
ENVELOPE SYMMETRY INTERFACES



ENVELOPE SYMMETRY INTERFACES



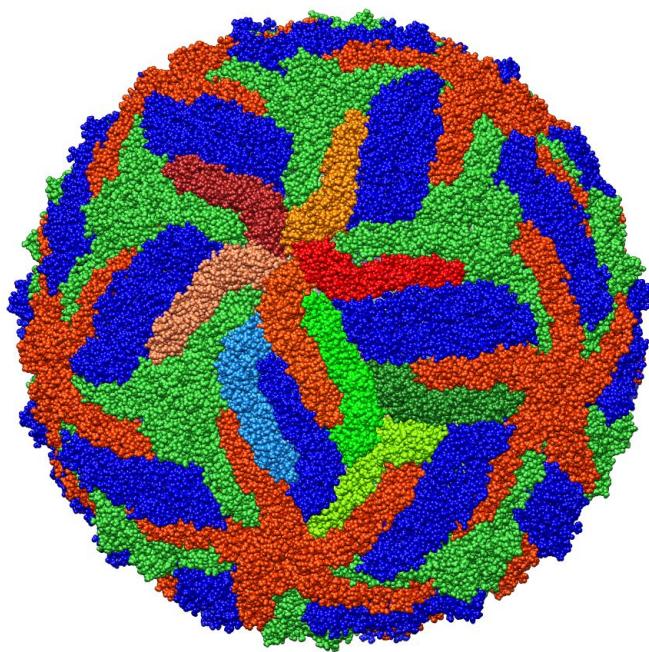
2-fold interactions



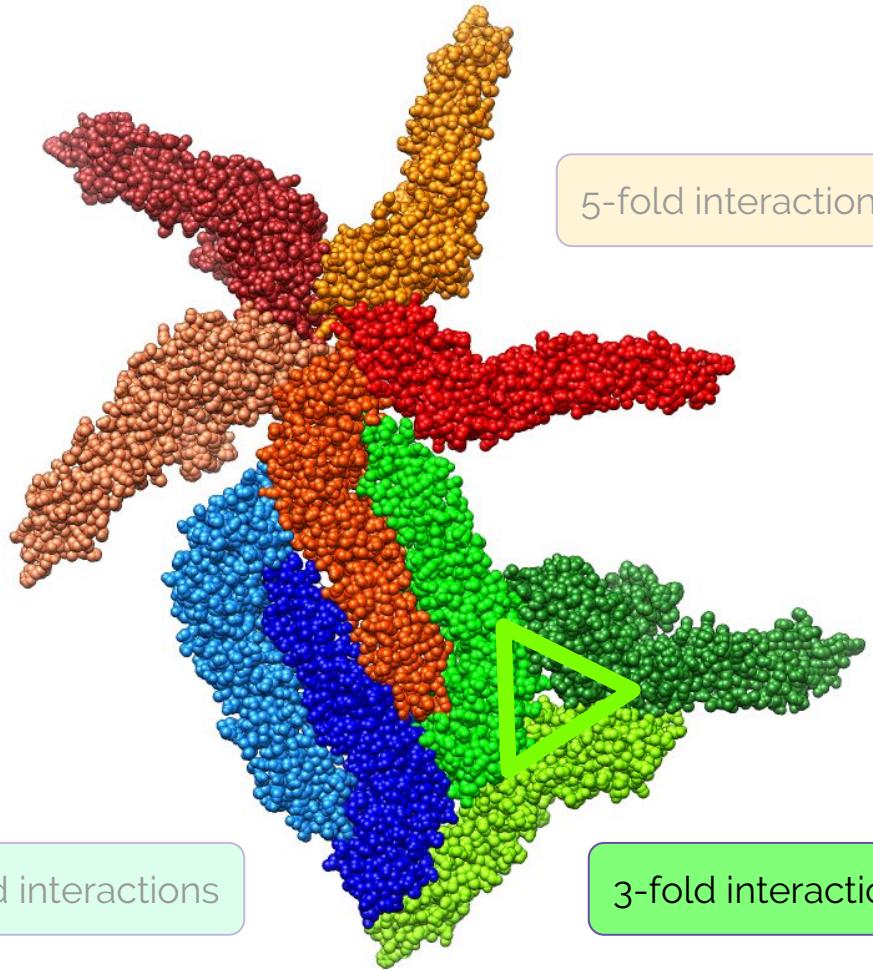
3-fold interactions

5-fold interactions

ENVELOPE SYMMETRY INTERFACES



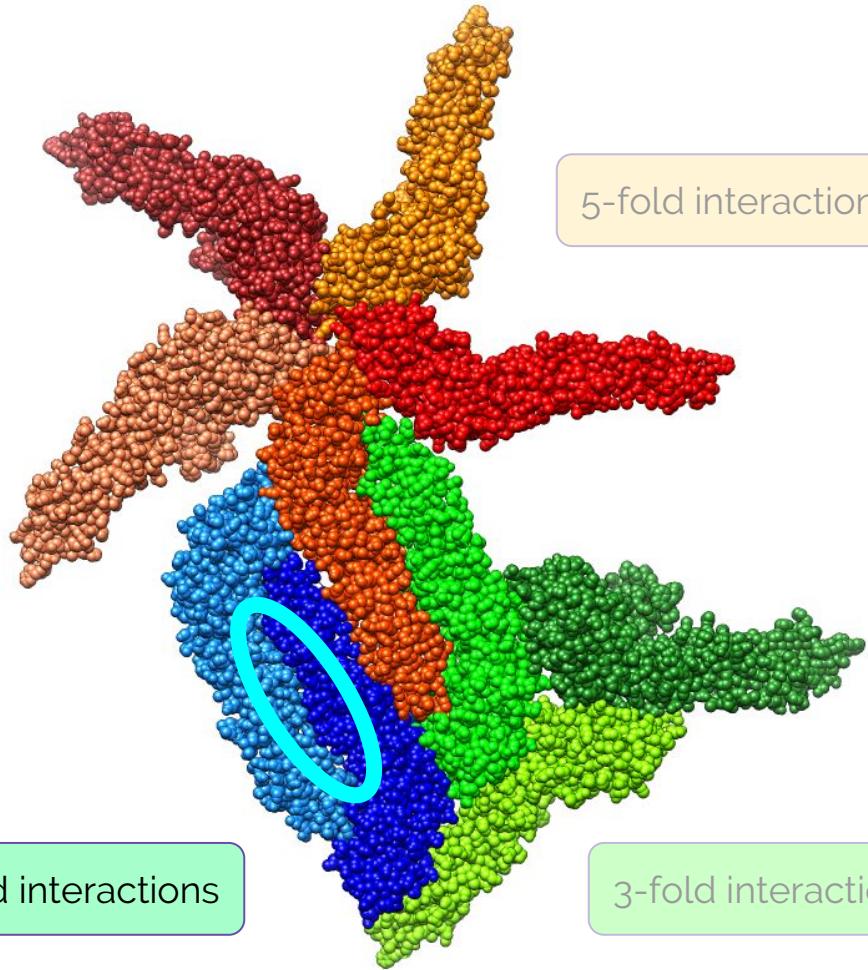
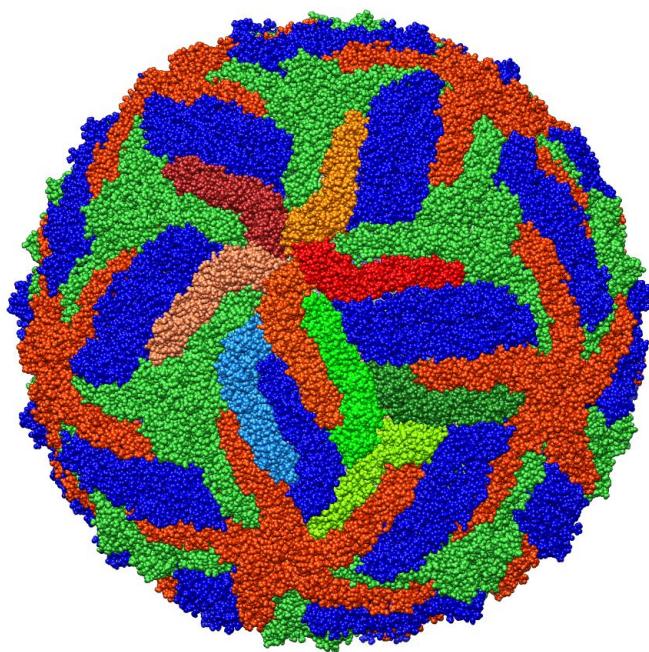
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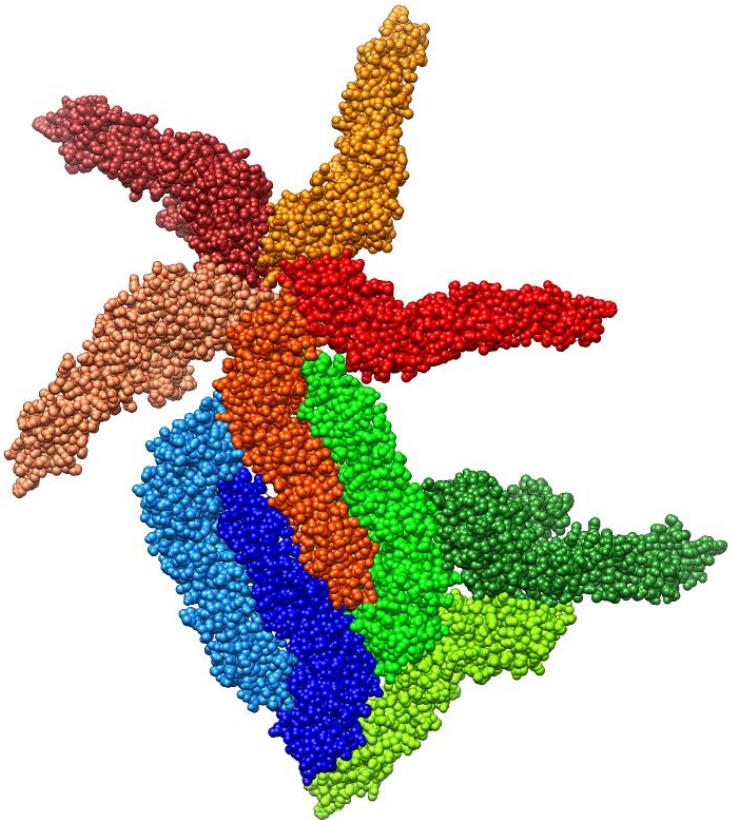
3-fold interactions

5-fold interactions

ENVELOPE SYMMETRY INTERFACES

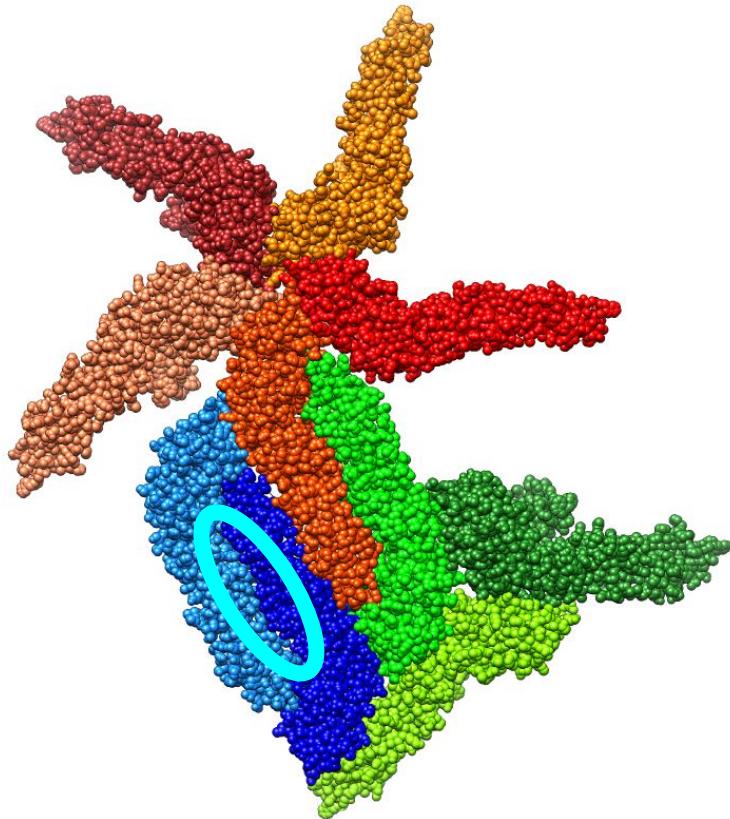


Interactions

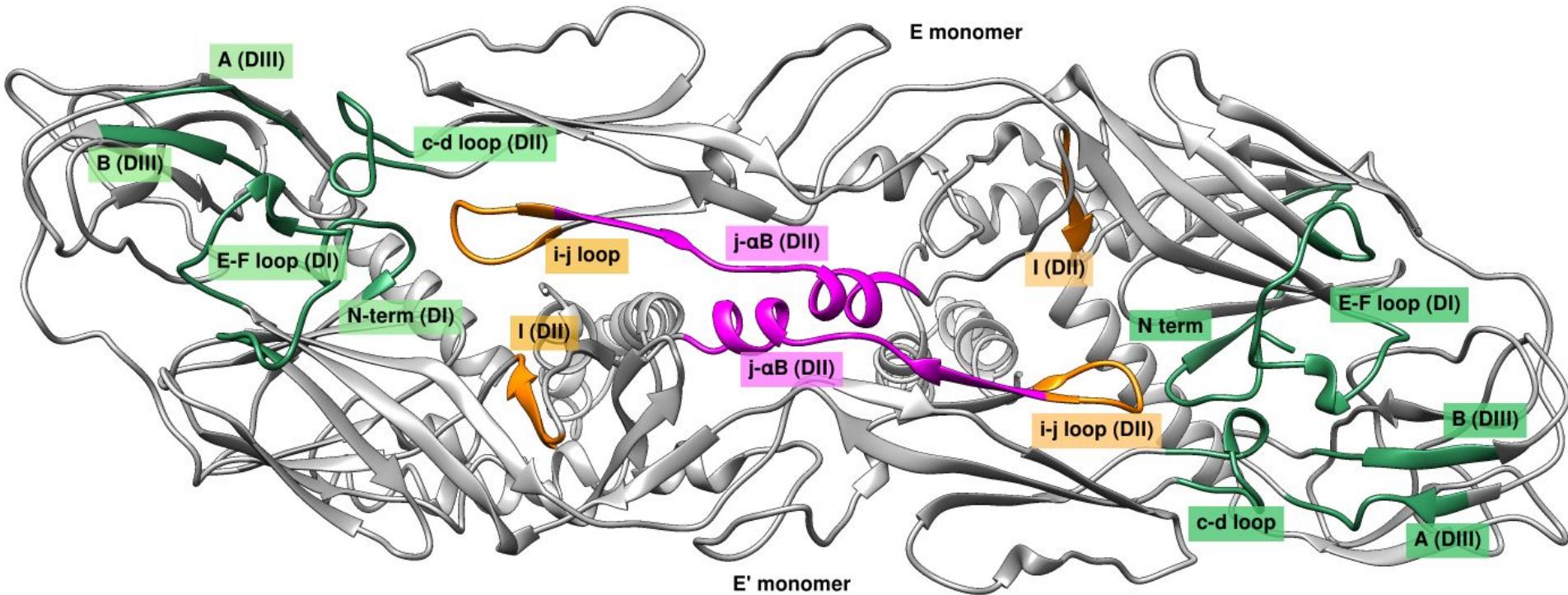


Interactions

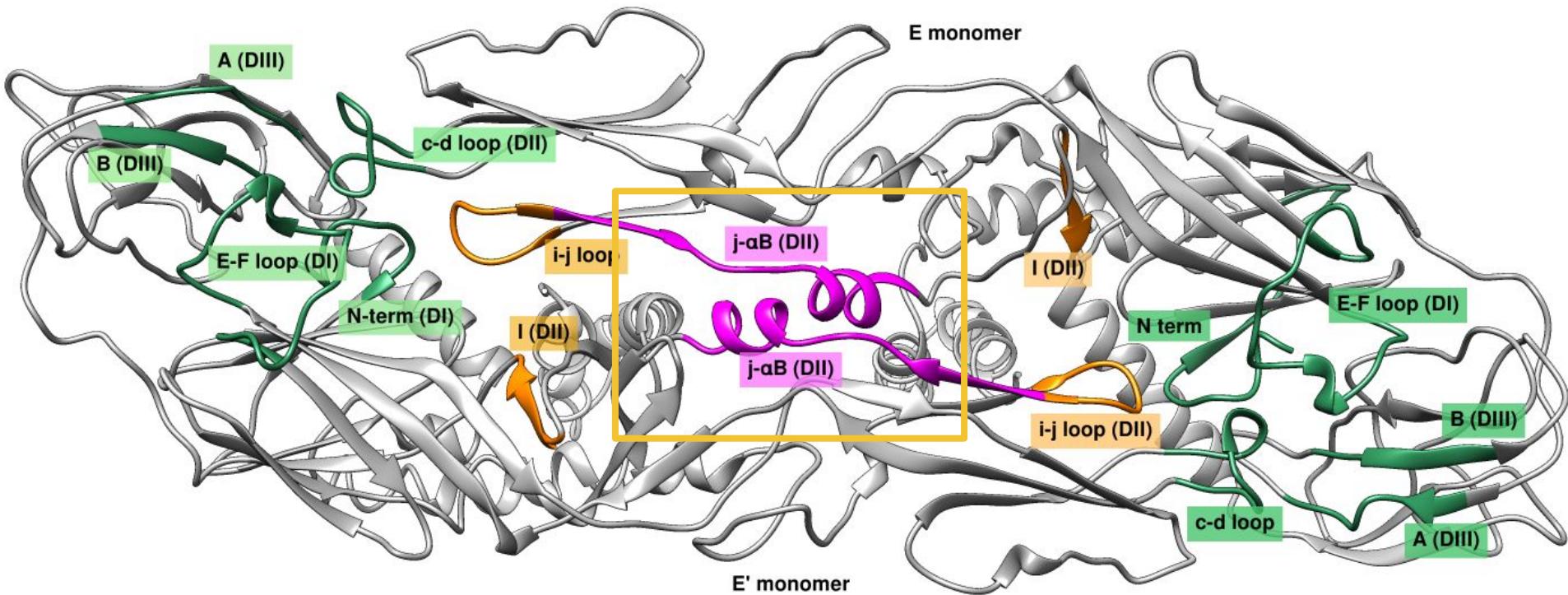
2-fold interface



2-FOLD E PROTEIN AXIS E-E INTERACTIONS



2-FOLD E PROTEIN AXIS E-E POLAR INTERACTIONS



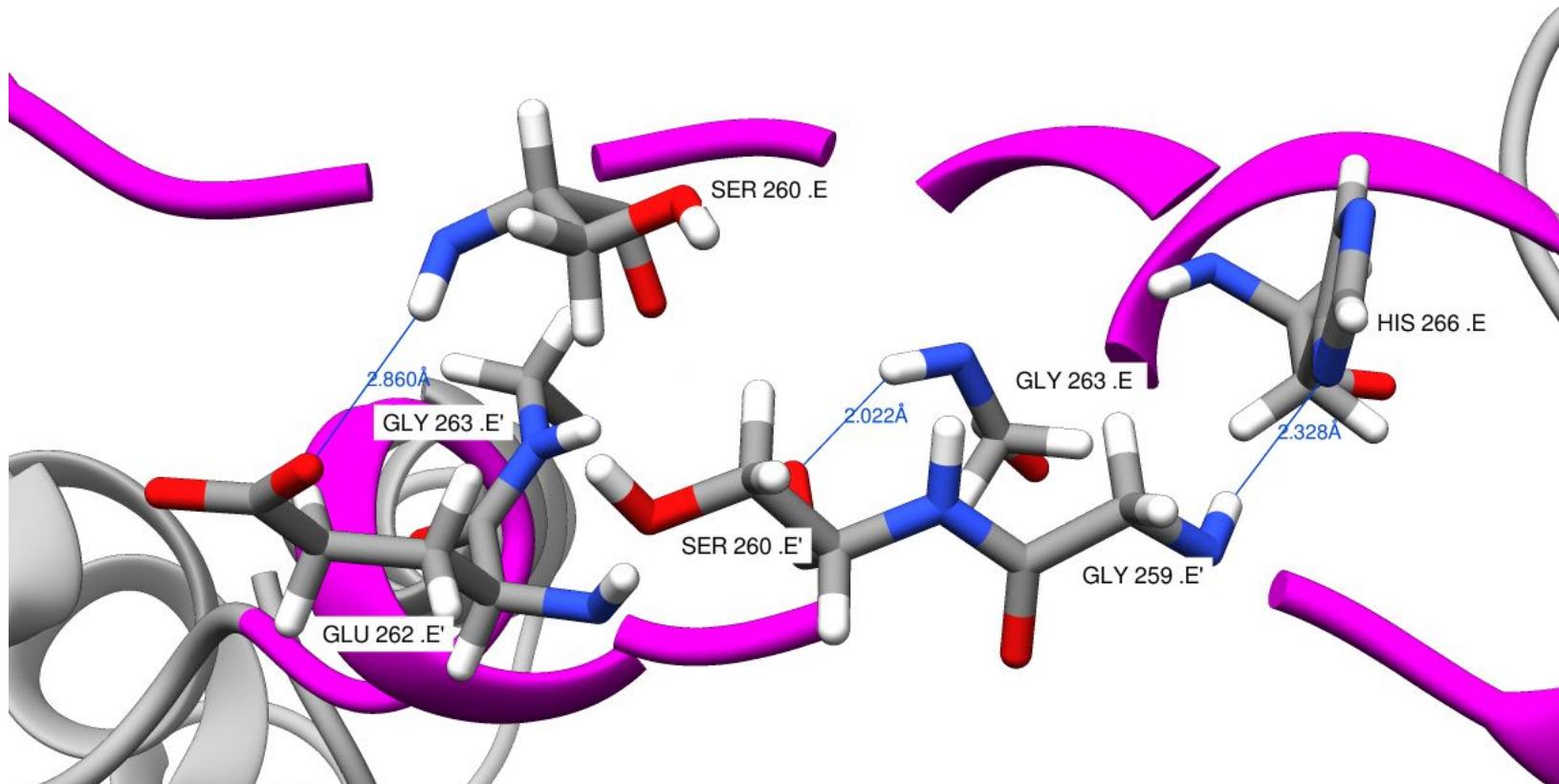
2-FOLD E PROTEIN AXIS E-E POLAR INTERACTIONS

Zika_virus_1/1-504
Zika_virus_2/1-498
Japanese_encephalitis_virus_1/1-500
Japanese_encephalitis_virus_2/1-499
West_Nile_virus_1/1-501
West_Nile_virus_2/1-501
Dengue_virus_4_1/1-495
Dengue_virus_4_2/1-495
Dengue_virus_1_1/1-495
Dengue_virus_1_2/1-495
Dengue_virus_3_1/1-493
Dengue_virus_3_2/1-493
Dengue_virus_2_1/1-495
Dengue_virus_2_2/1-495
Yellow_fever_virus_1/1-493
Yellow_fever_virus_2/1-493

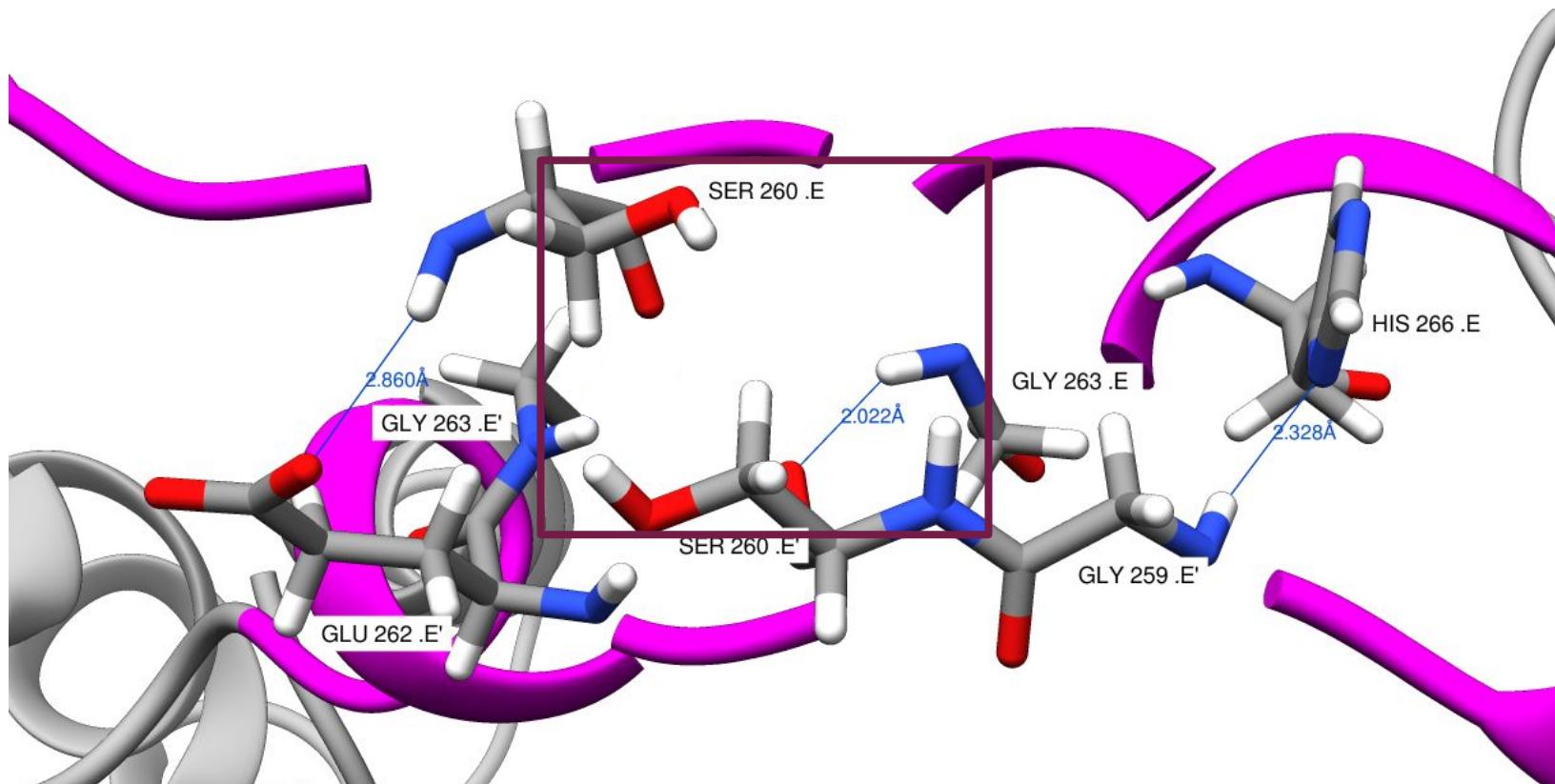
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KRQTVVV	LGSQEGAVHTAL	AGALEAEAMDGA---	KGRLFSGHLKCRLKMDK	291
TKQSVVA	LGSQEGGLHQAL	AGAIVVEYSS---	SVKLTSGHLKCRLKMDK	293
TKQSVVA	LGSQEGSLHQAL	AGAIVVEYSS---	SVKLTSGHLKCRLKMDK	292
TKQSVIA	LGSQEGALHQAL	AGAIPVEFSSN---	TVKLTSGHLKCRVKLEK	294
TKQSVVA	LGSQEGALHQAL	AGAIPVEFSSN---	TVKLTSGHLKCRVKMEK	294
KRQDVT	LGSQEGAMHSAL	AGATEVDSGD---	GNHMFAGHLKCKVRMEK	291
KRQDVT	LGSQEGAMHSAL	AGATEVDSGD---	GNHMFAGHLKCKVRMEK	291
KKQEVVV	LGSQEGAMHTAL	TGATEIQTSG---	TTTIFAGHLKCRLKMDK	291
KKQEVVV	LGSQEGAMHTAL	TGATEIQTSG---	TTTIFAGHLKCRLKMDK	291
KKQEVVV	LGSQEGAMHTAL	TGATEIQTSG---	GTSIFAGHLKCRLKMDK	289
KKQEVVV	LGSQEGAMHTAL	TGATEIQTSG---	GTSIFAGHLKCRLKMDK	289
KKQDVVV	LGSQEGAMHTAL	TGATEIQMSS---	GNLLFTGHLKCRLRMDK	291
KKQDVVV	LGSQEGAMHTAL	TGATEIQMSS---	GNLLFTGHLKCRLRMDK	291
ATIKVLA	LGNQEGSLKTA	TGAMRVTKDTNNSKLYKLHGGHVACRVKLSA	289	
ATIKVLA	LGNQEGSLKTA	TGAMRVTKDTNNSKLYKLHGGHVACRVKLSA	289	

* . **.***. :! **:*** . . : **: *::::.

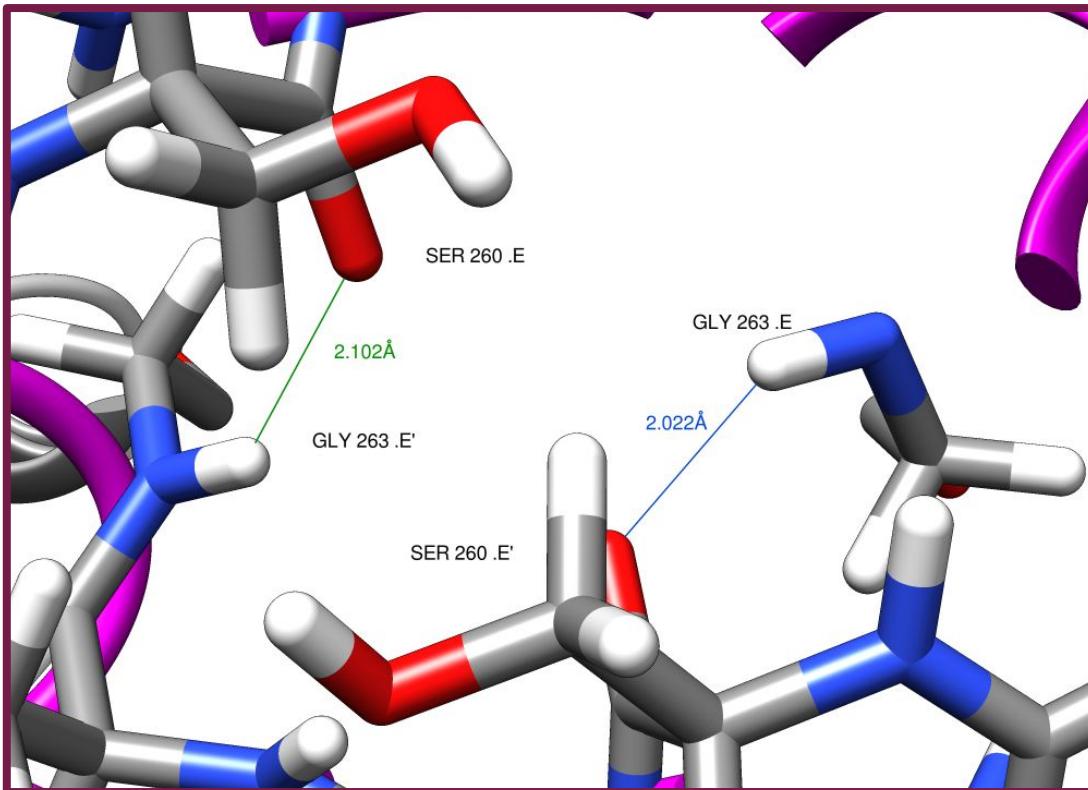
2-FOLD E PROTEIN AXIS E-E POLAR INTERACTIONS



2-FOLD E PROTEIN AXIS E-E POLAR INTERACTIONS

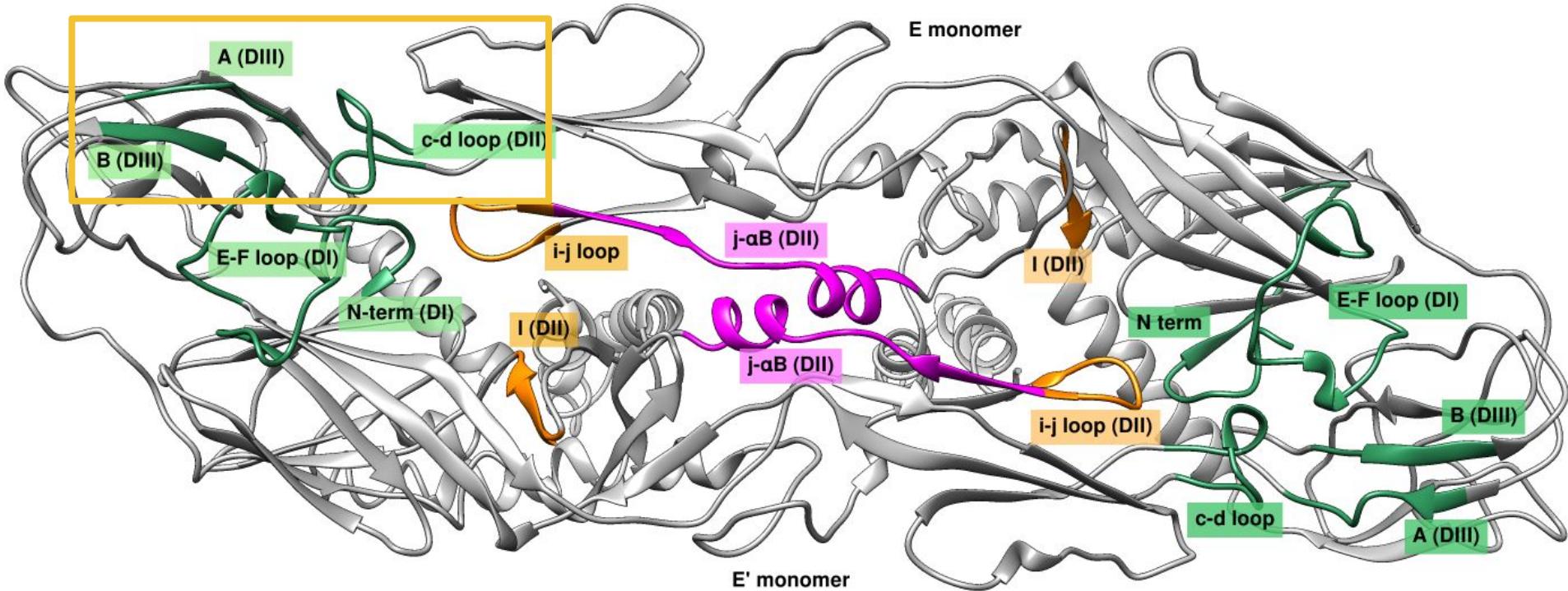


2-FOLD E PROTEIN AXIS E-E POLAR INTERACTIONS

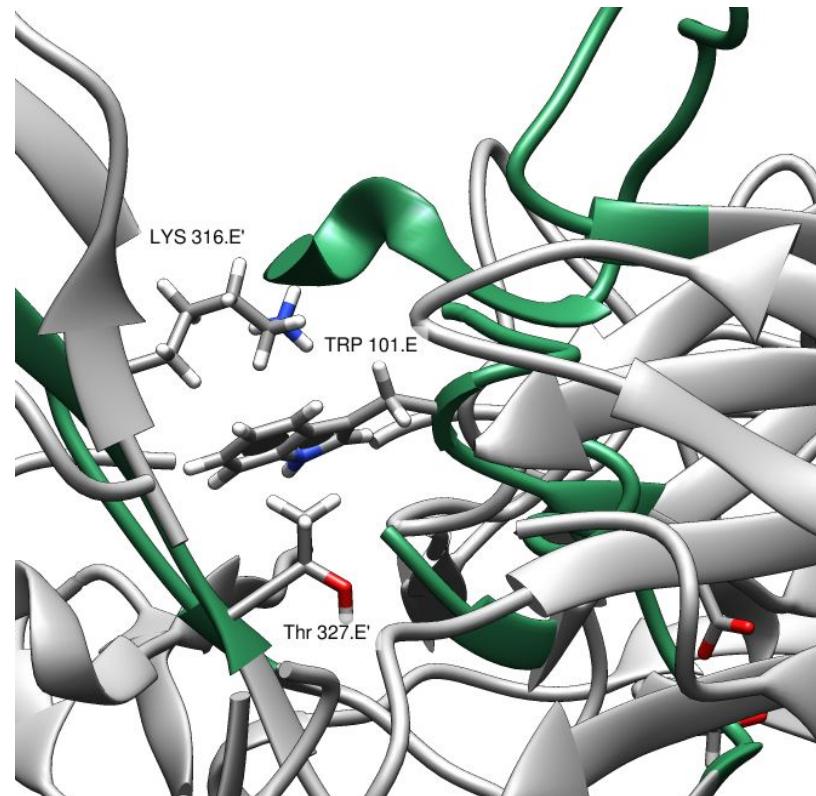
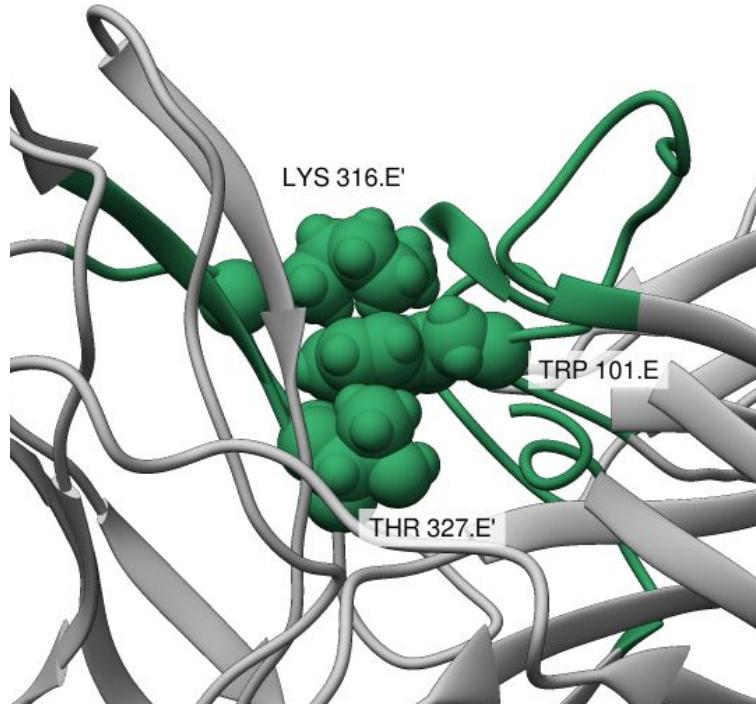


Example
of
Distorted
Hbond

2-FOLD E PROTEIN AXIS E-E HYDROPHOBIC INTERACTIONS

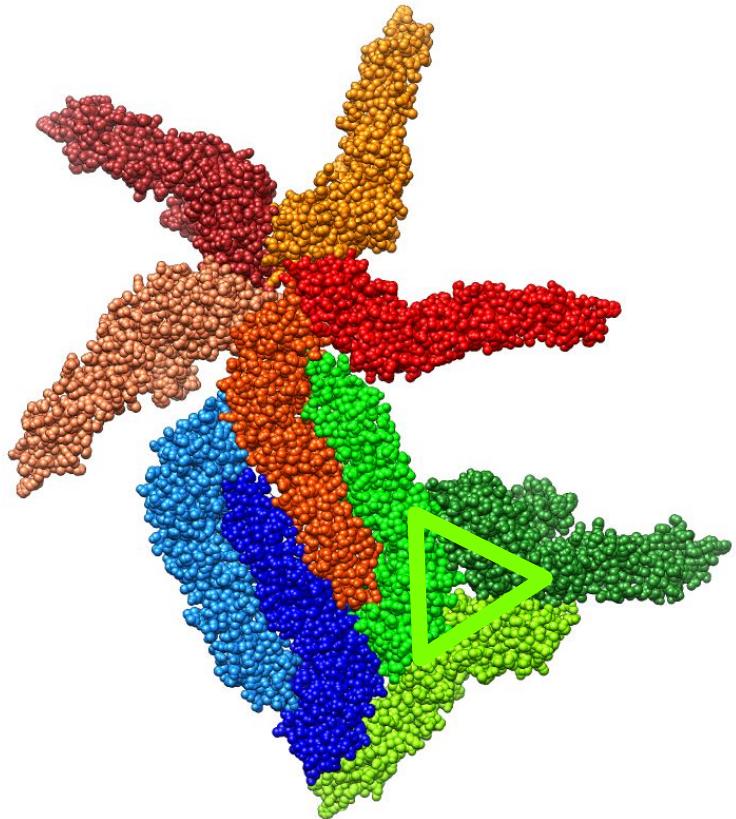


2-FOLD E PROTEIN AXIS E-E HYDROPHOBIC INTERACTIONS

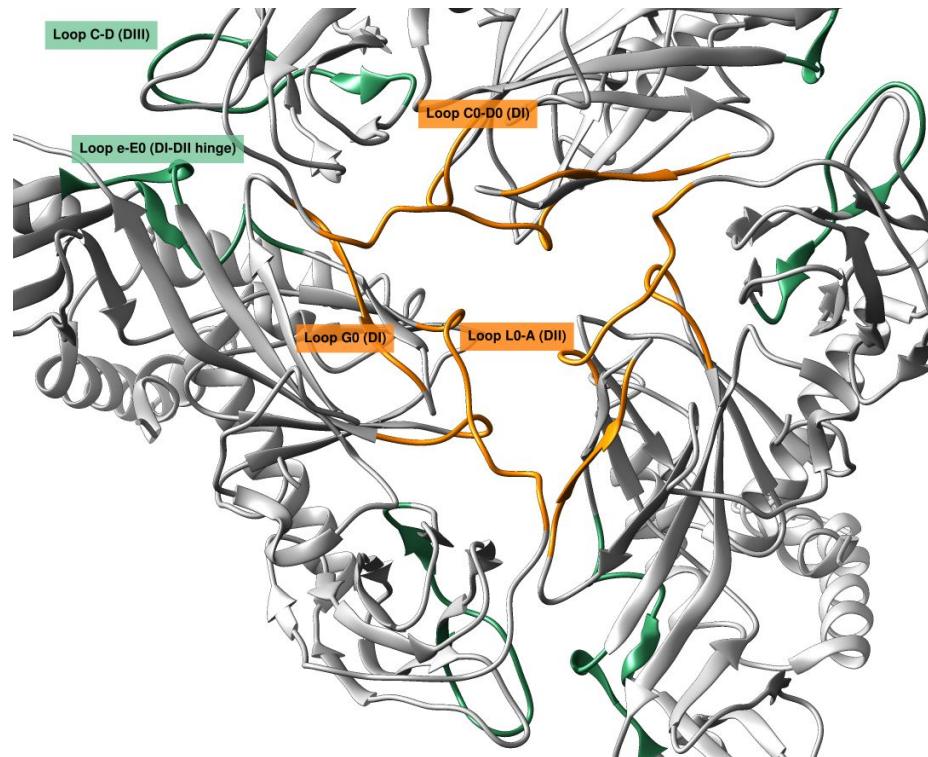
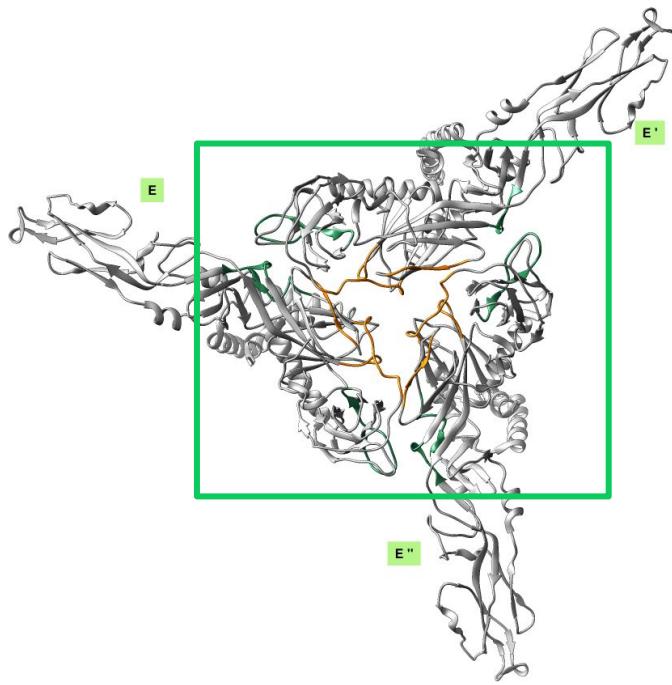


Interactions

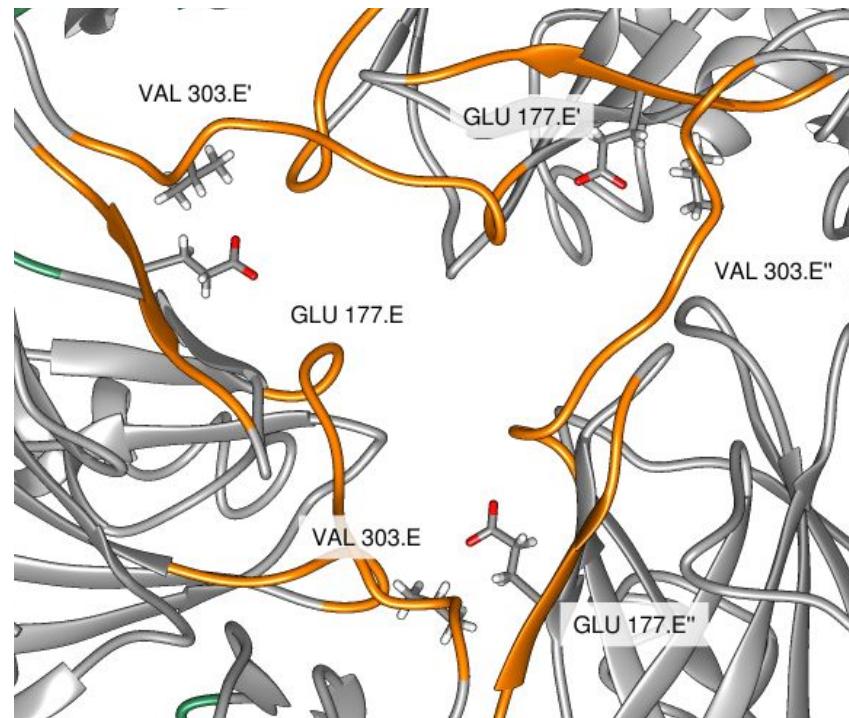
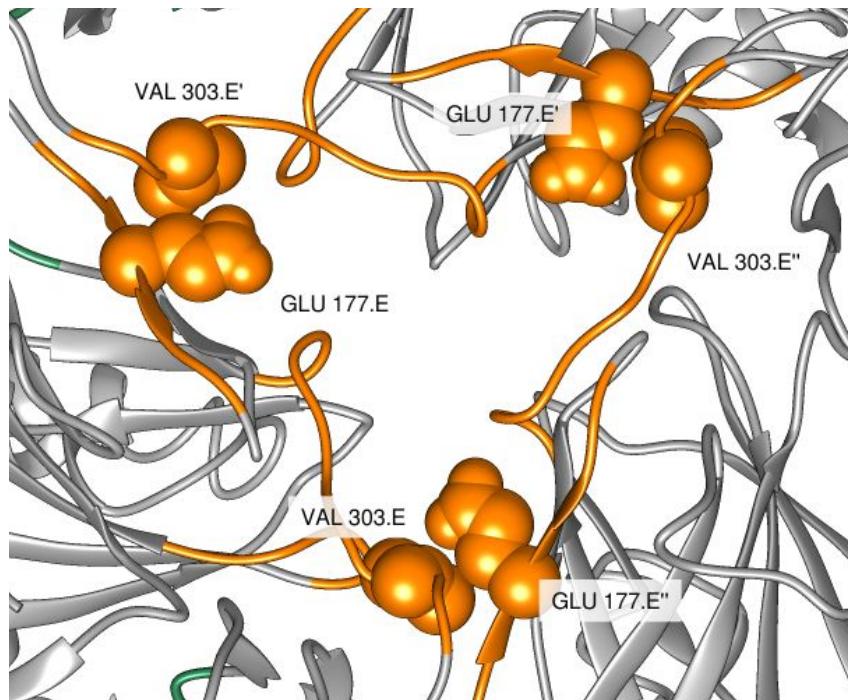
3-fold interface



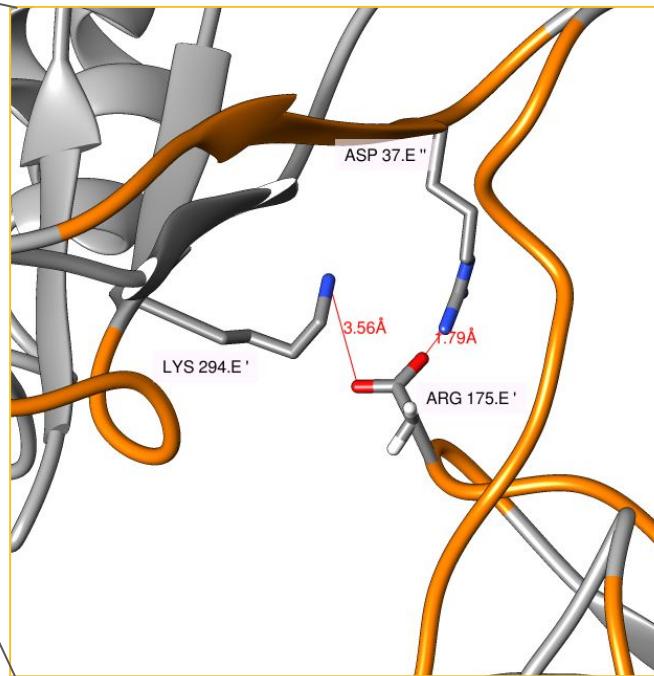
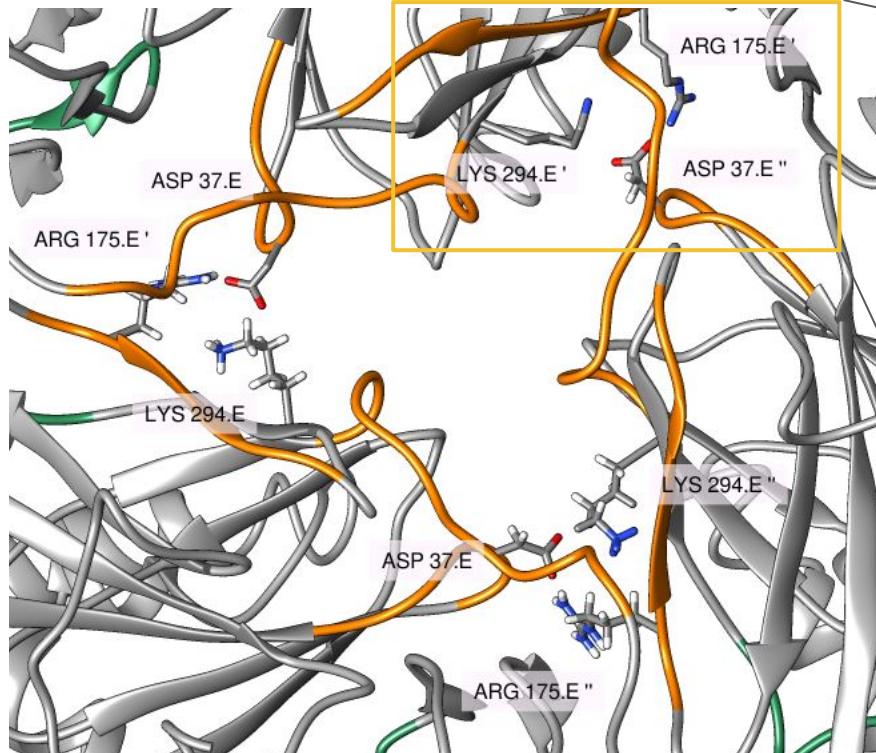
3-FOLD E PROTEIN AXIS E-E INTERACTIONS



3-FOLD E PROTEIN AXIS E-E HYDROPHOBIC INTERACTIONS



3-FOLD E PROTEIN AXIS E-E ELECTROSTATIC INTERACTIONS

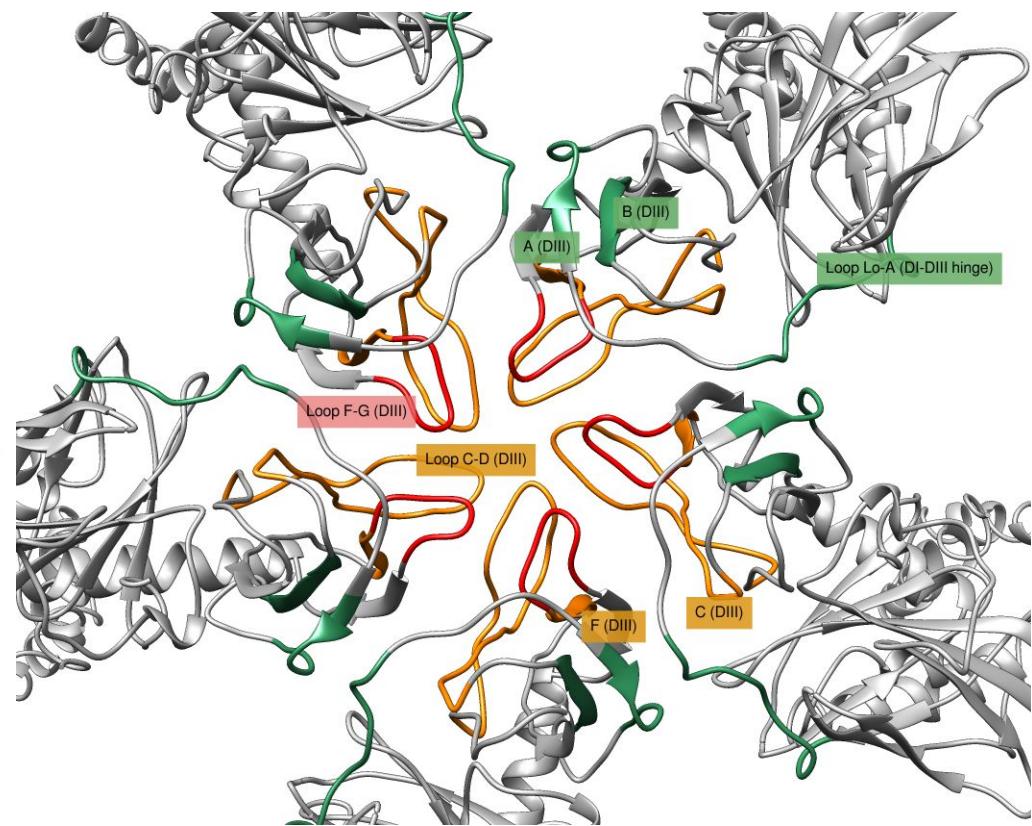
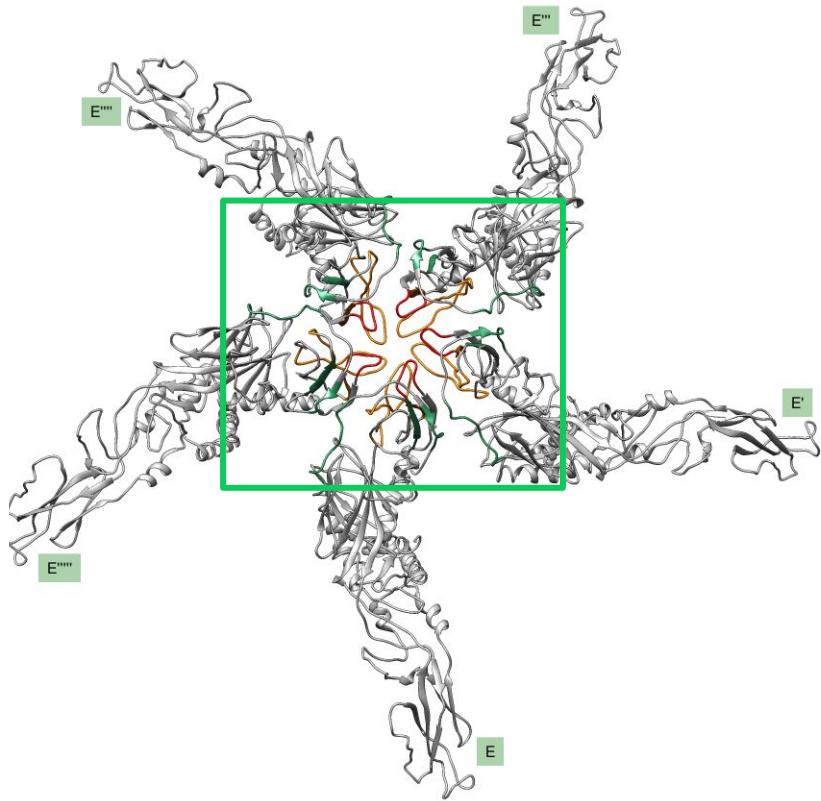


Interactions

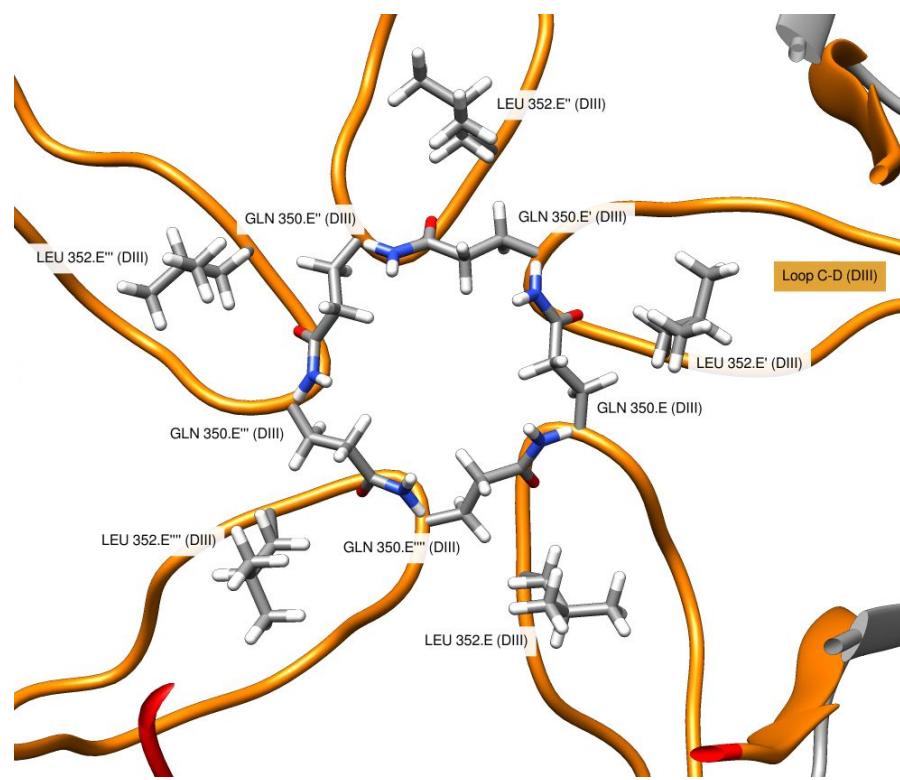
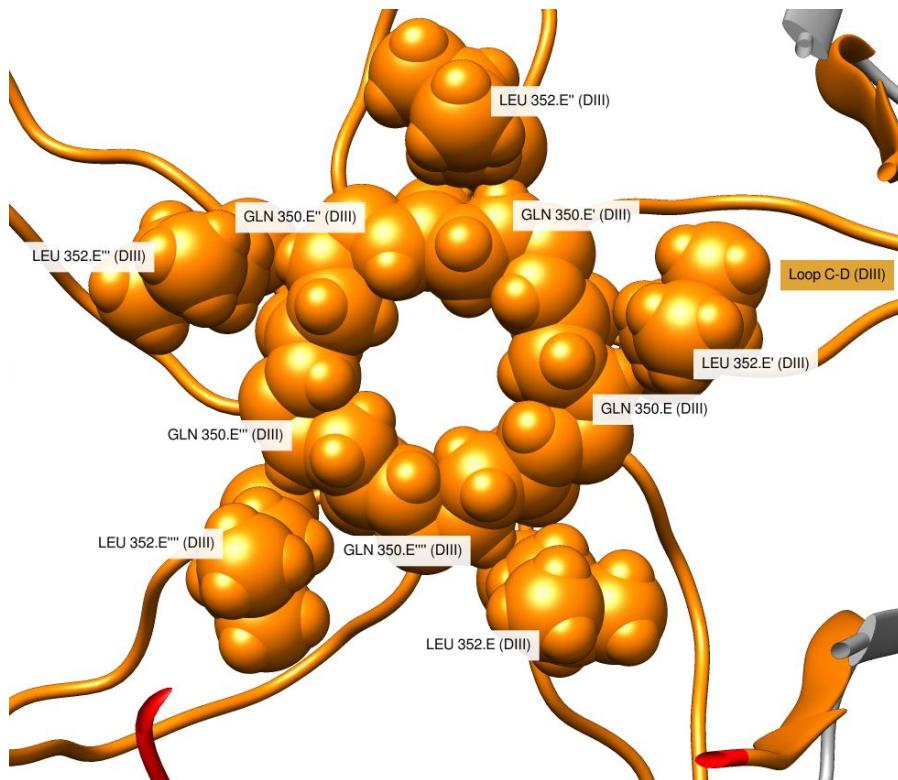
5-fold interface



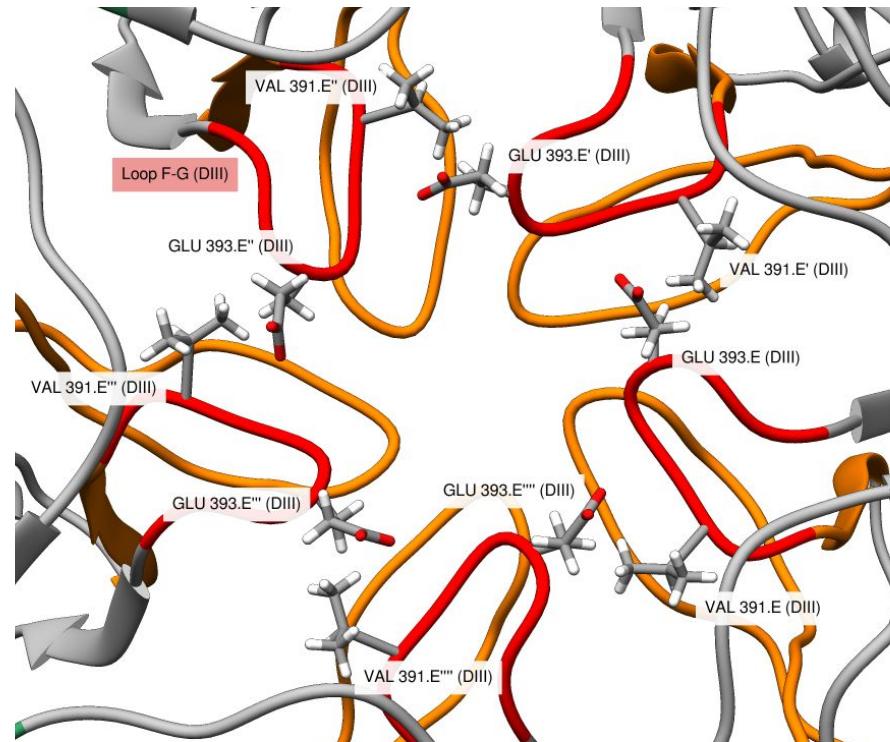
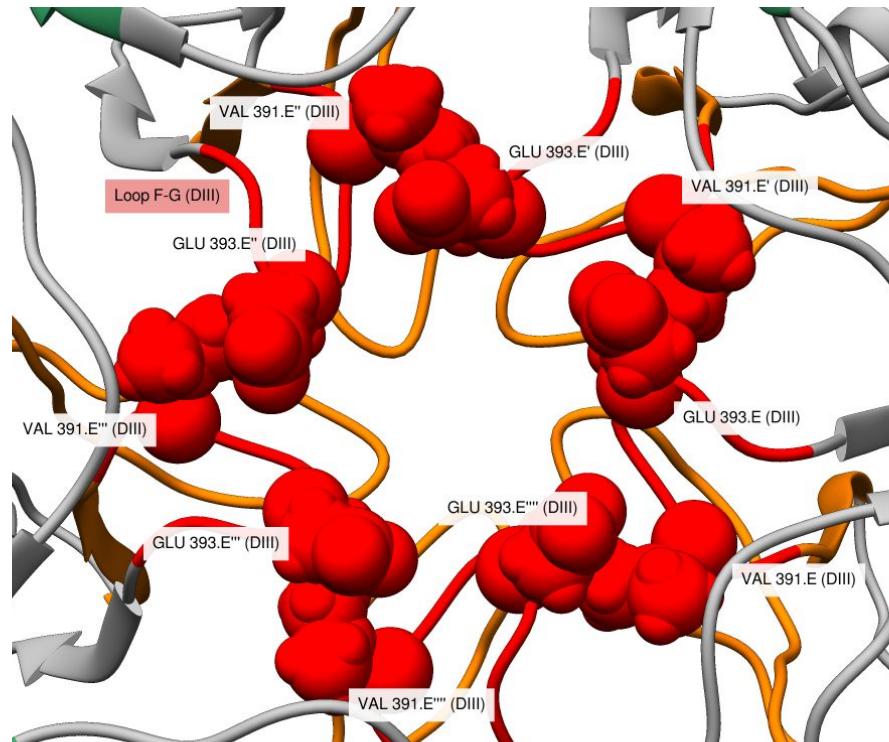
5-FOLD E PROTEIN AXIS E-E INTERACTIONS



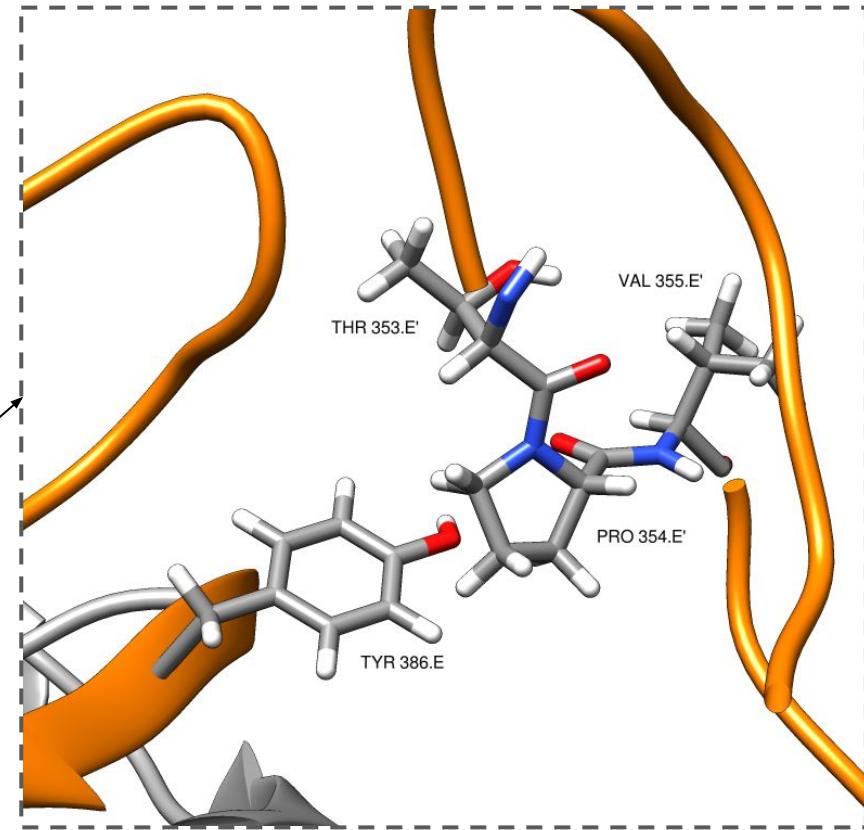
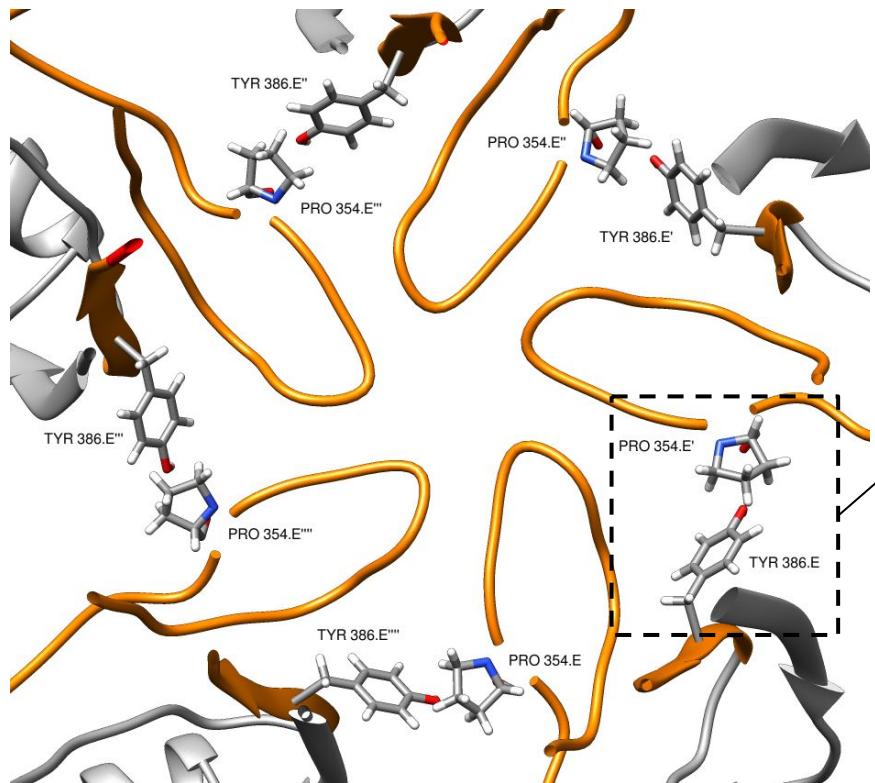
5-FOLD E PROTEIN AXIS E-E HYDROPHOBIC INTERACTIONS (LOOP C-D)



5-FOLD E PROTEIN AXIS E-E HYDROPHOBIC INTERACTIONS (LOOP F-G)

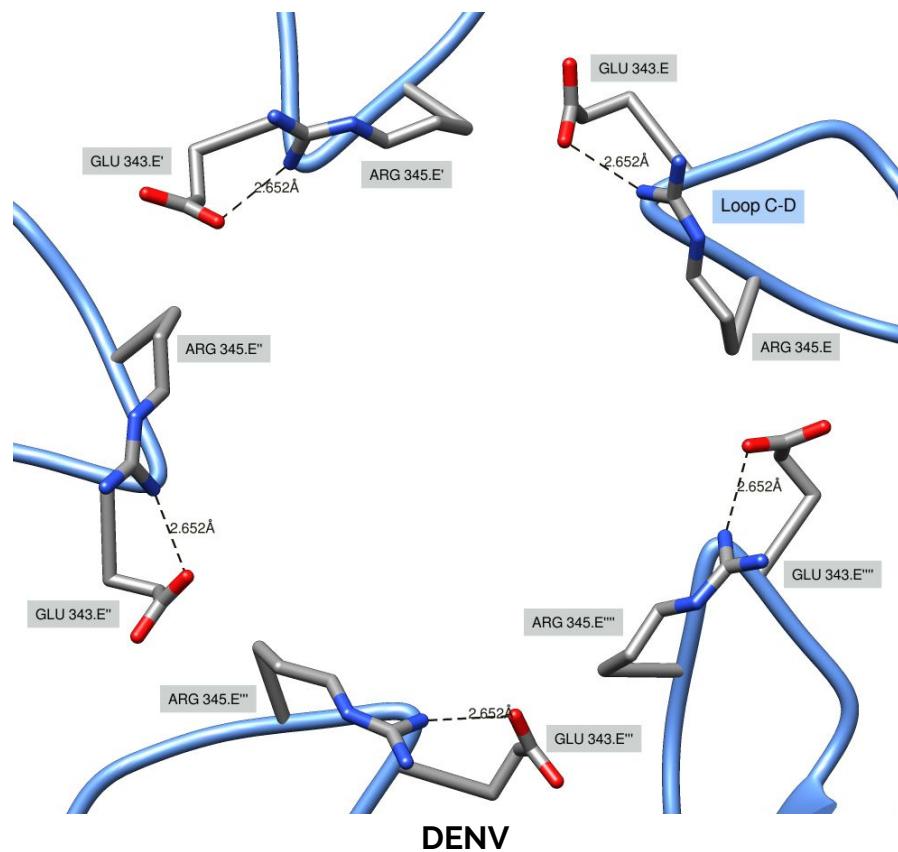
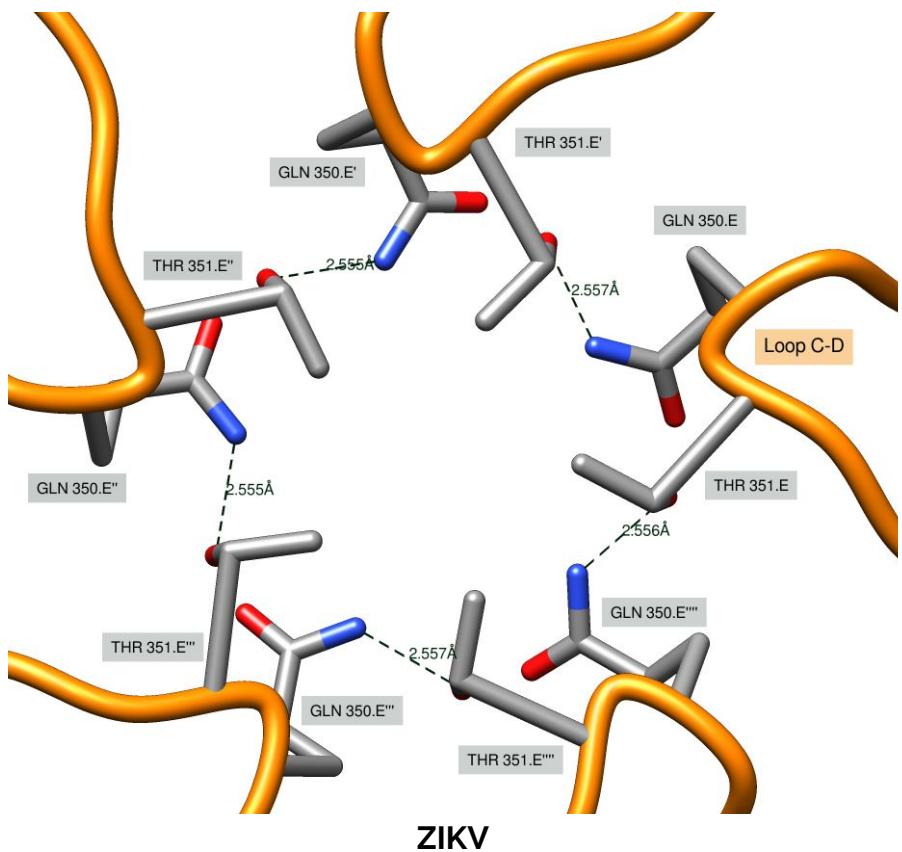


5-FOLD E PROTEIN AXIS E-E POLAR INTERACTIONS (LOOP C-D)



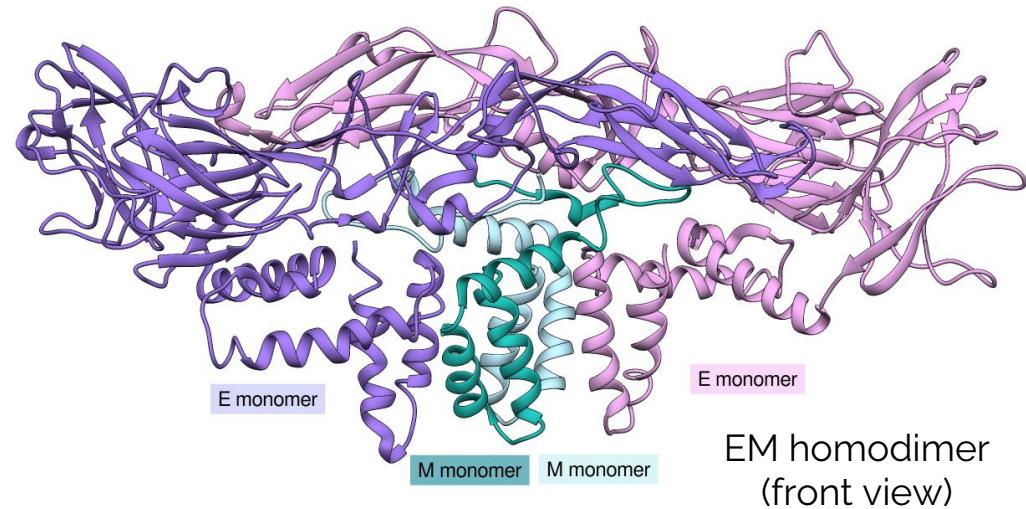
5-FOLD E PROTEIN

AXIS E-E POLAR INTERACTIONS (LOOP C-D): ZIKV AND DENV 5-FOLD VERTEX COMPARISON



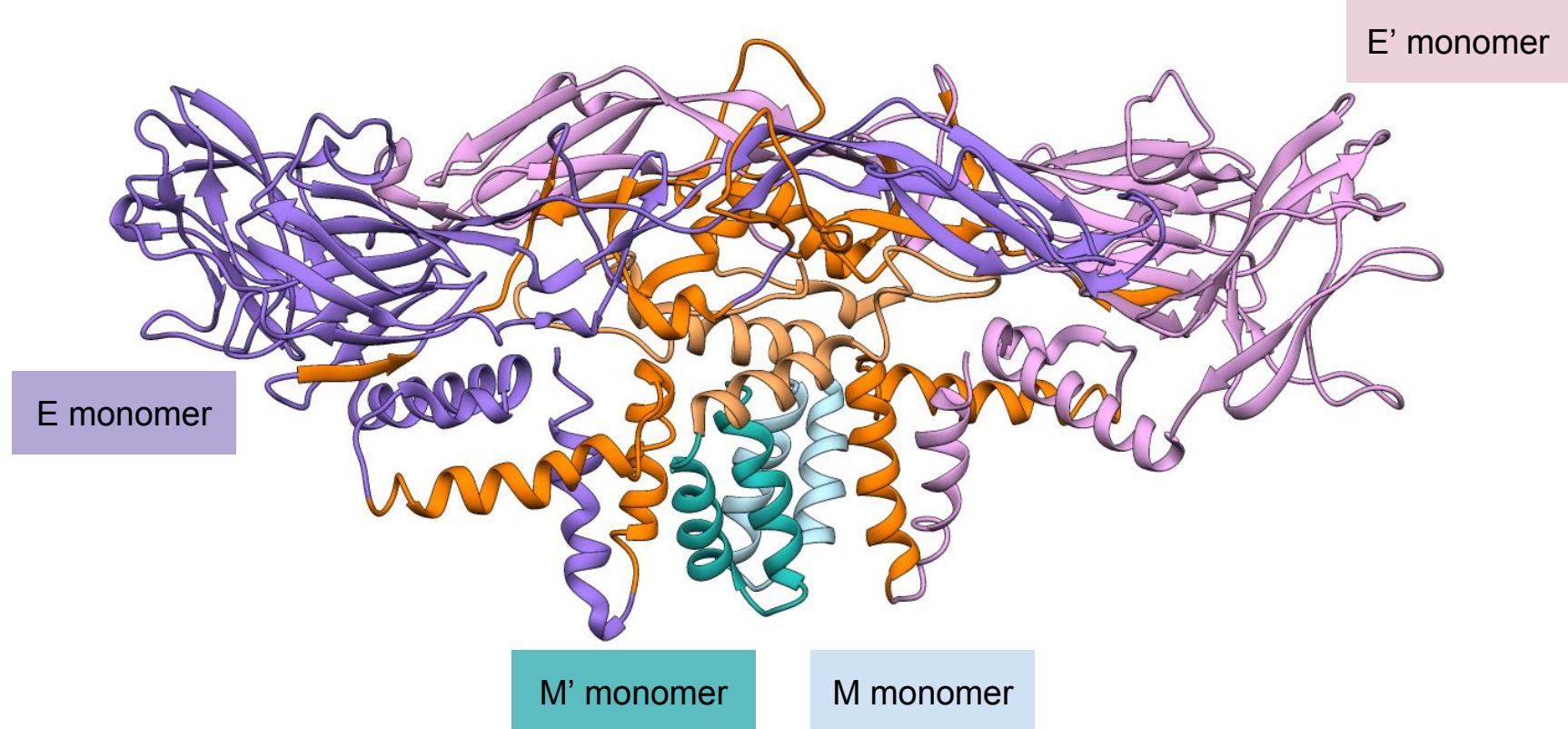
Interactions

E-M interactions



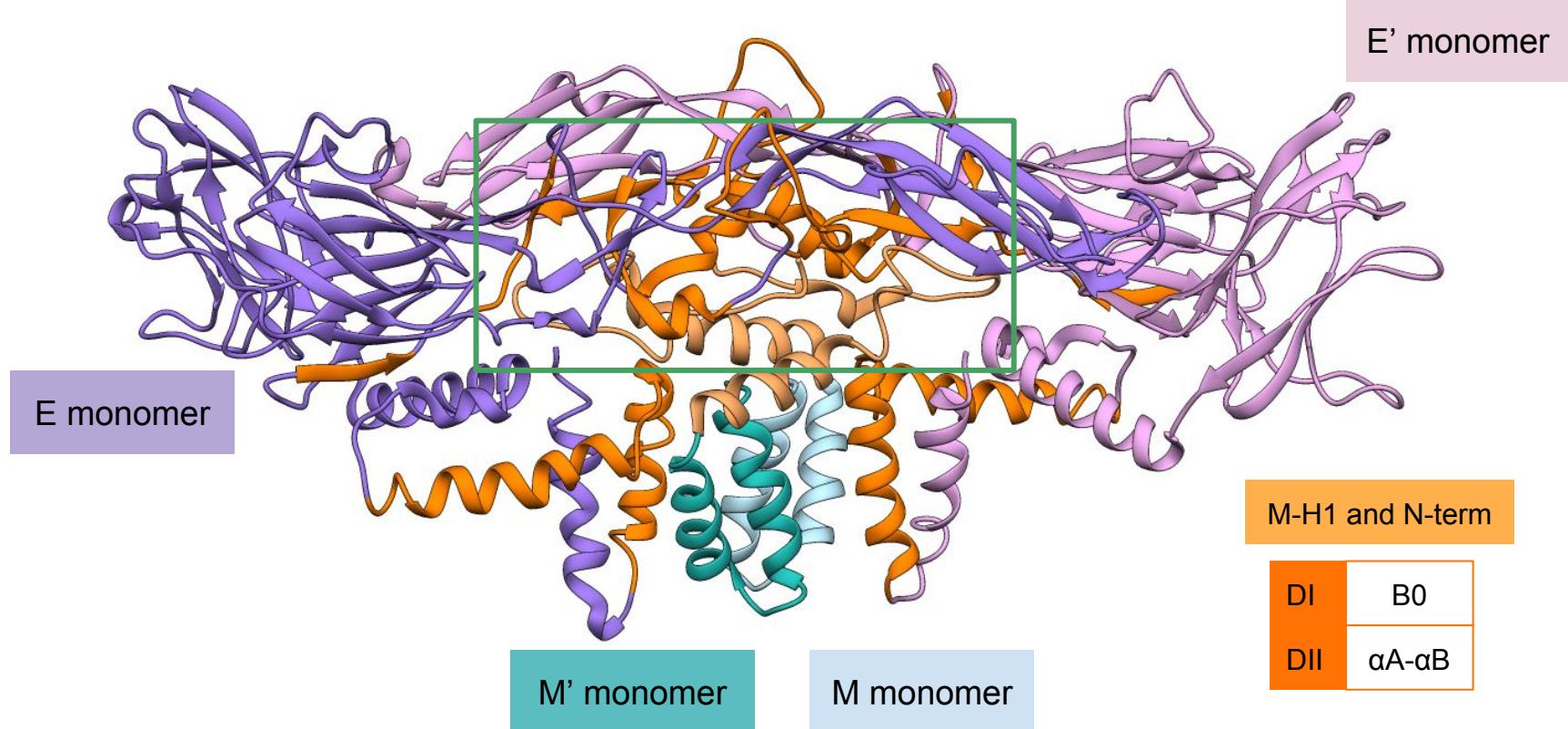
E-M INTERACTIONS

INTERACTION REGIONS



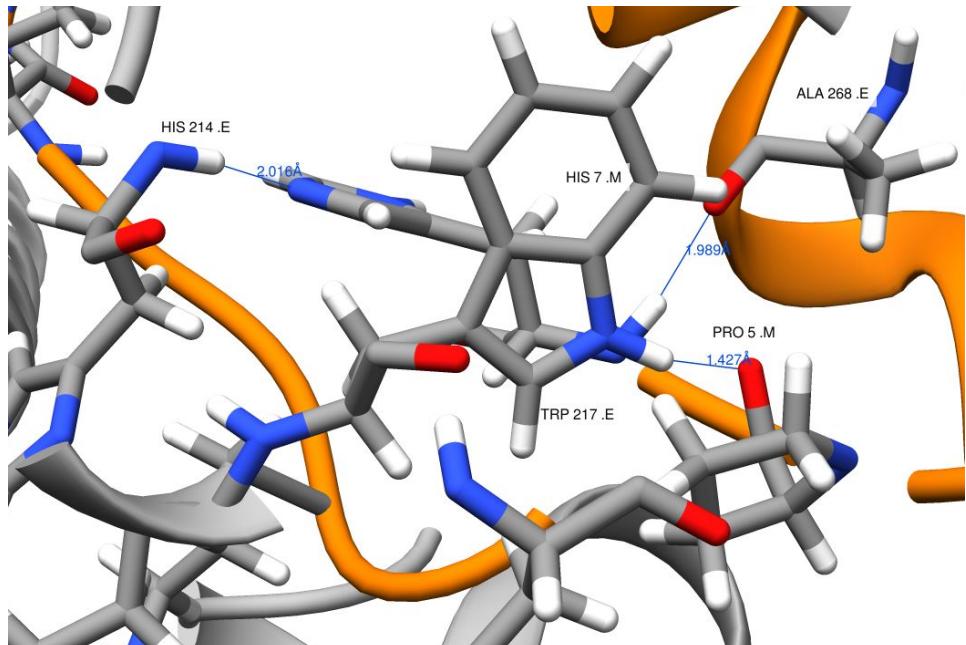
E-M INTERACTIONS

INTERACTION REGIONS

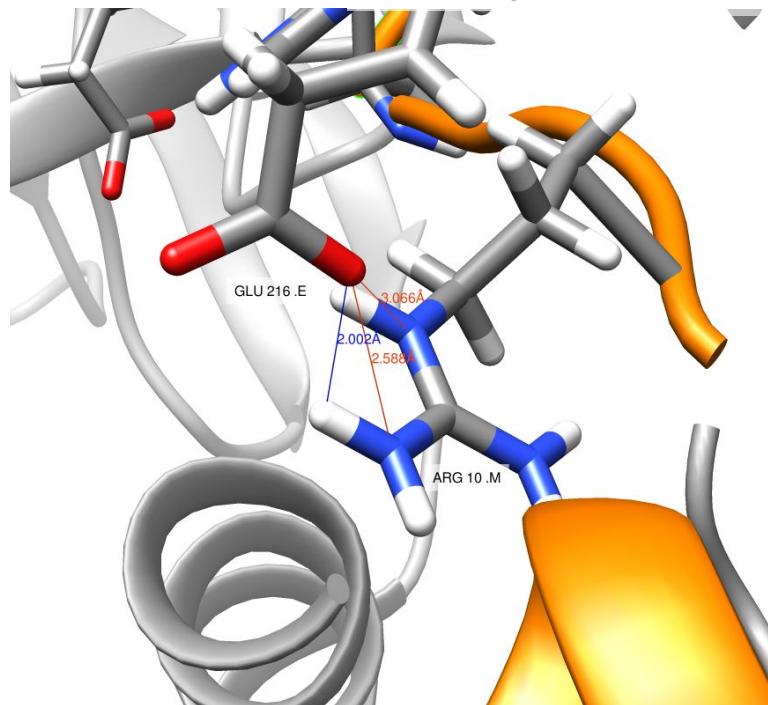


EM PROTEINS

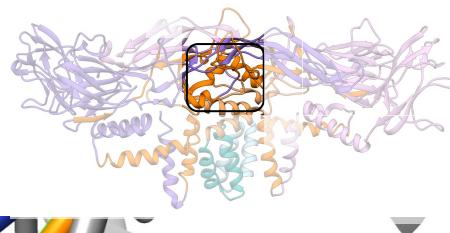
E-M POLAR INTERACTIONS



H-Bonds



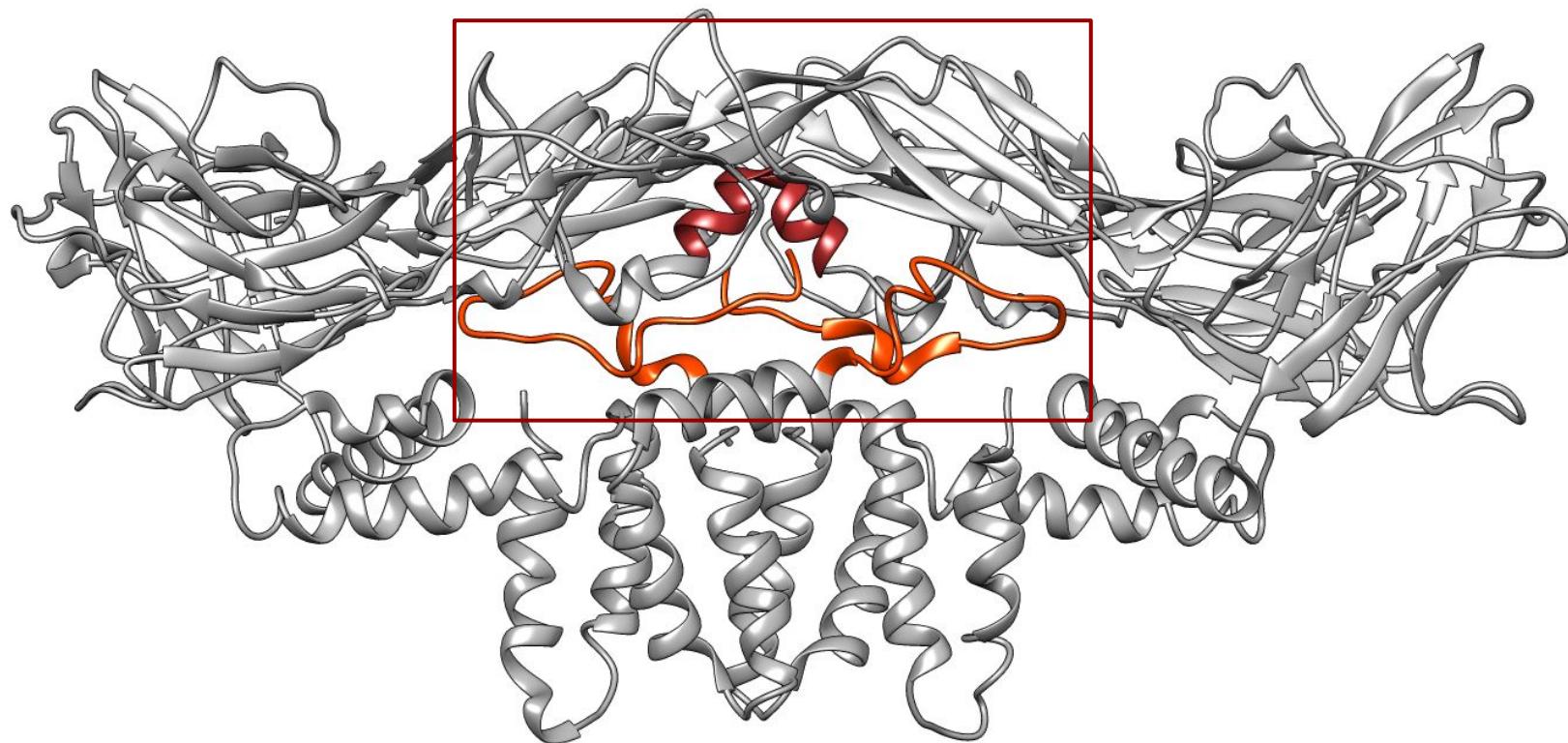
Salt-bridge



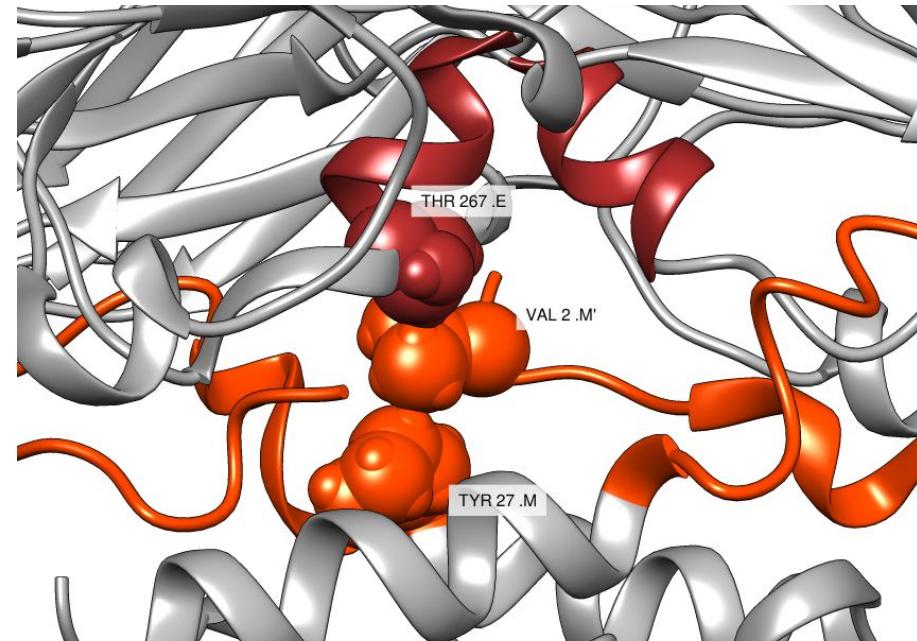
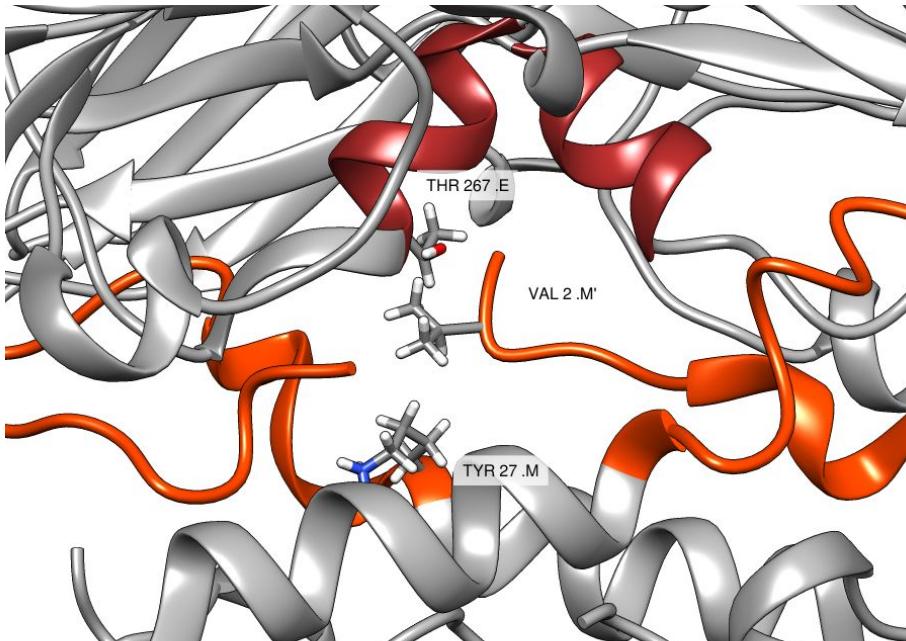
EM PROTEINS

THERMOSTABILITY

α -Helix B

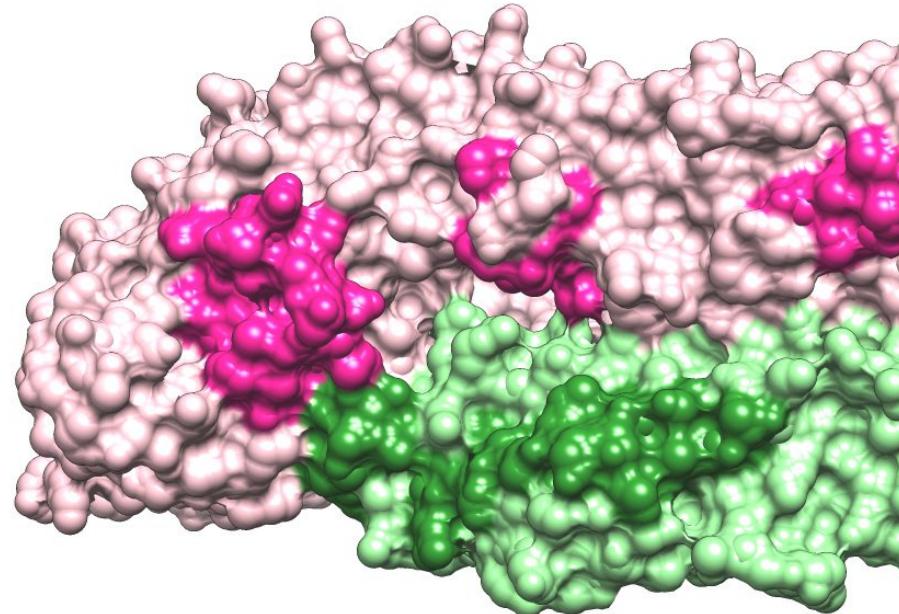


EM PROTEINS THERMOSTABILITY



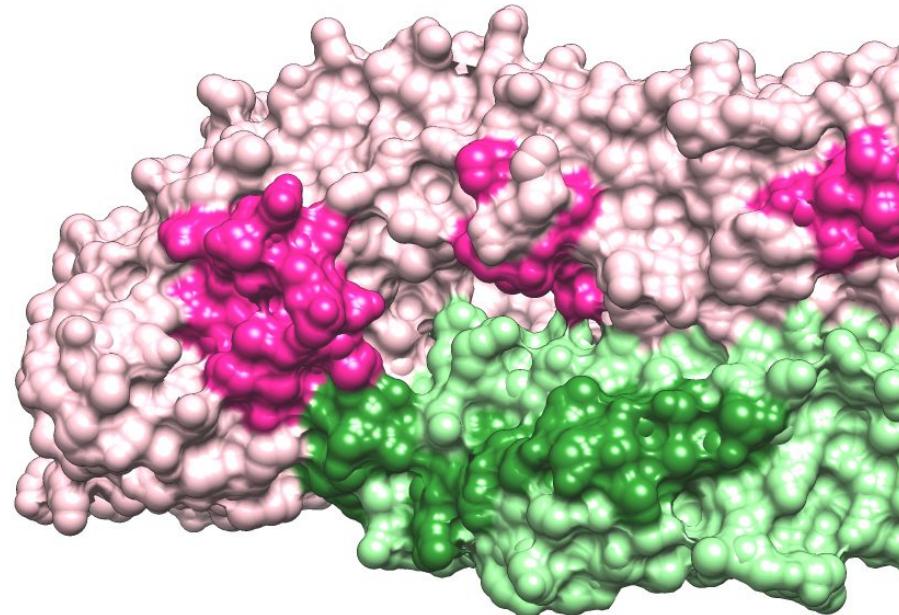
Immunogenicity

Antibodies

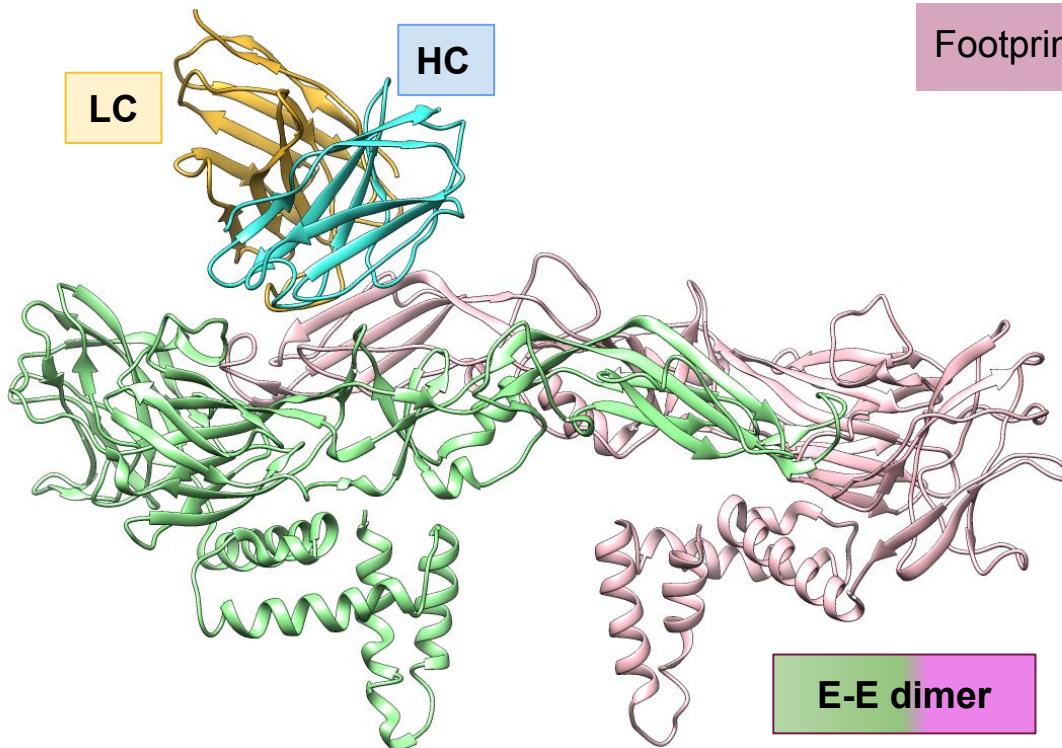


Immunogenicity

Antibodies: ZIKV-195



ZIKV-195: POTENT NEUTRALIZING HUMAN MONOCLONAL ANTIBODY



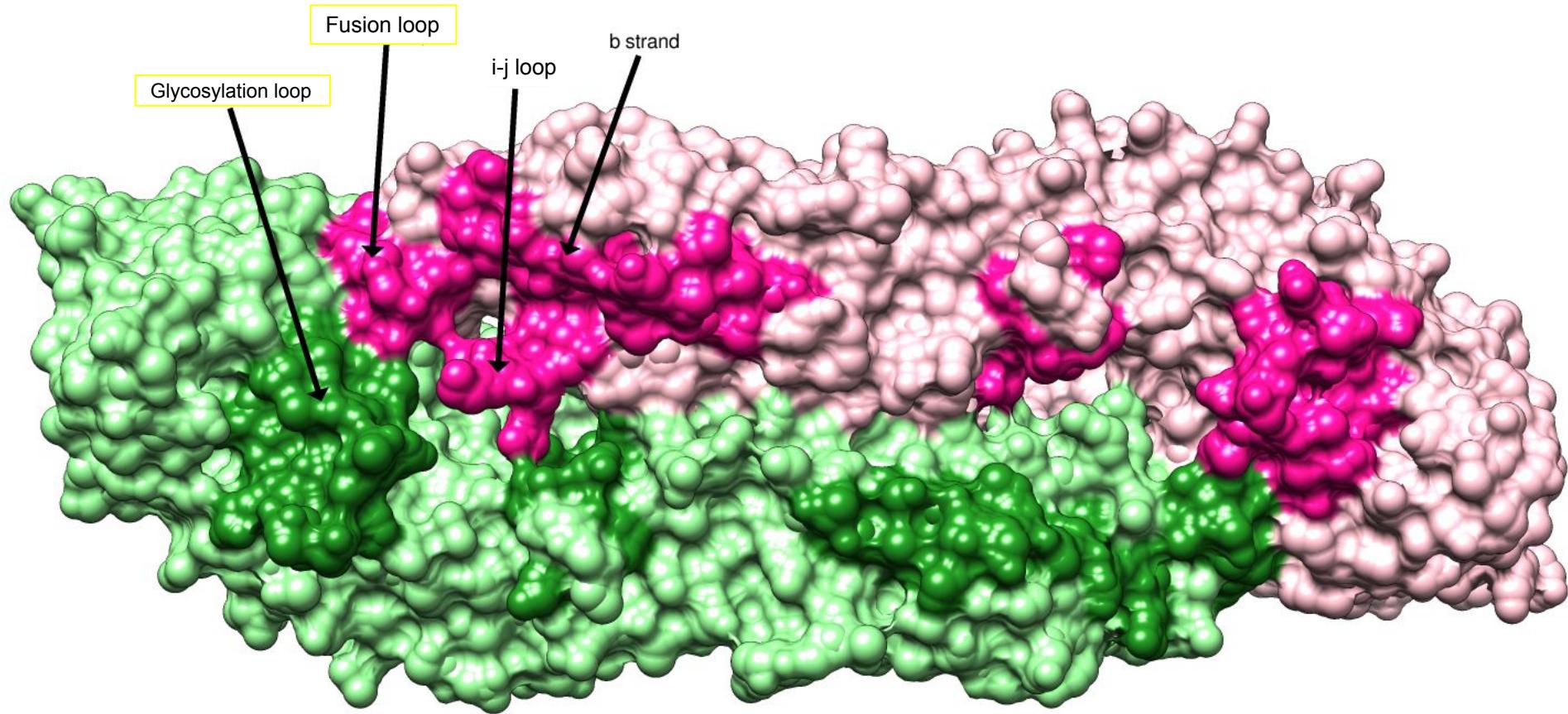
Footprint

Secondary structural elements of DI and DII

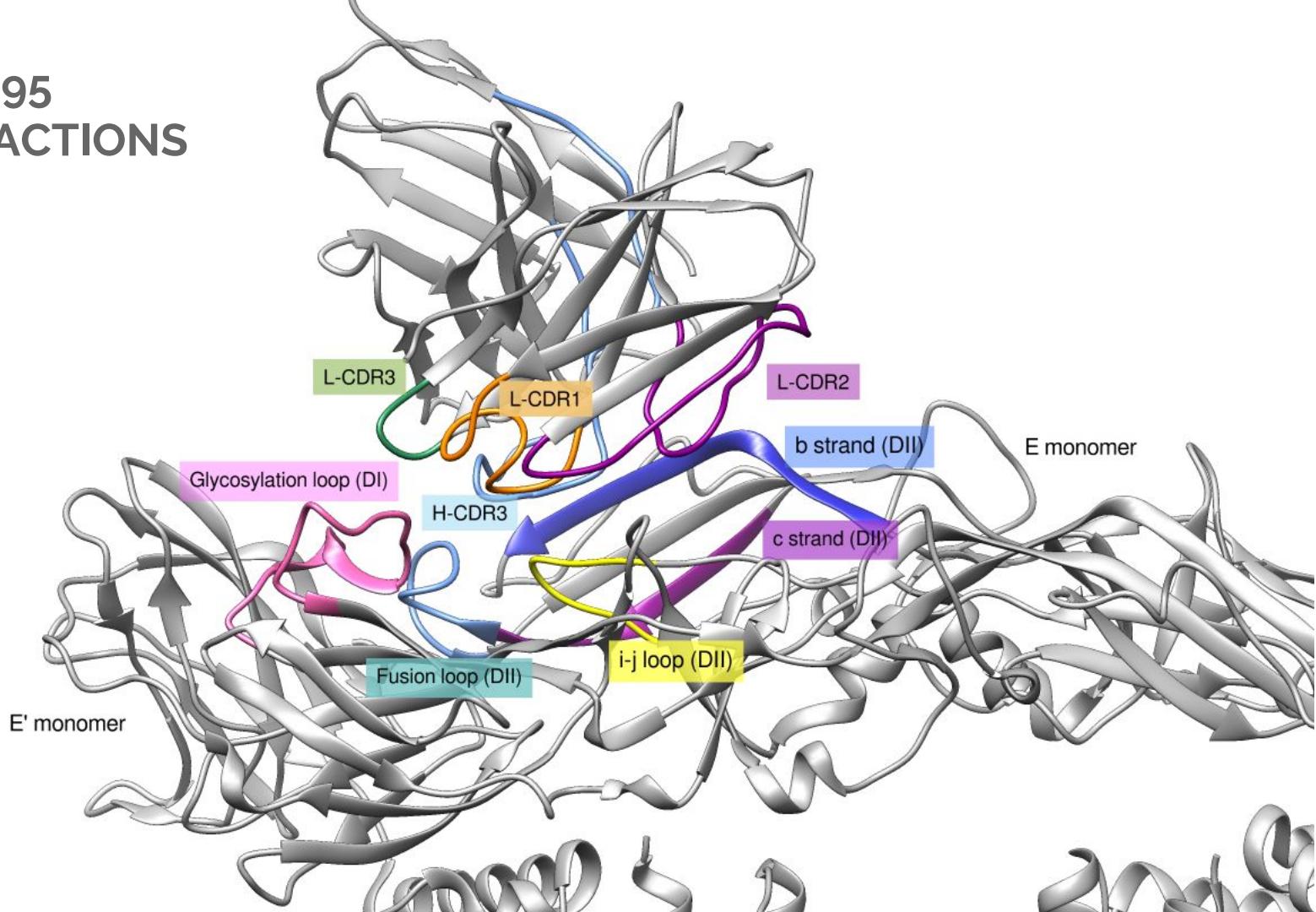
Binds to EE dimers

Specific for ZIKA virus

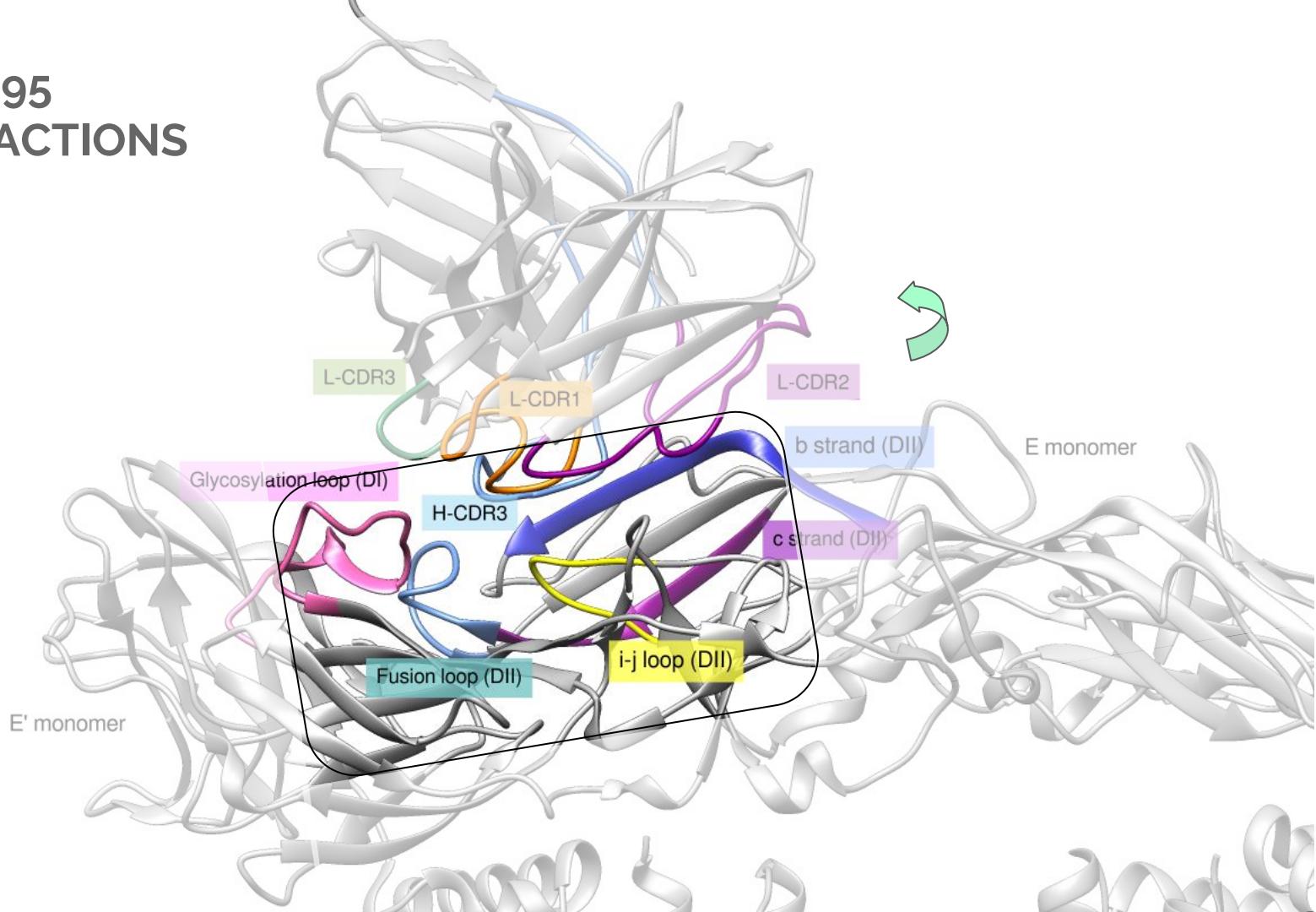
ZIKV-195 VIRAL PATCH



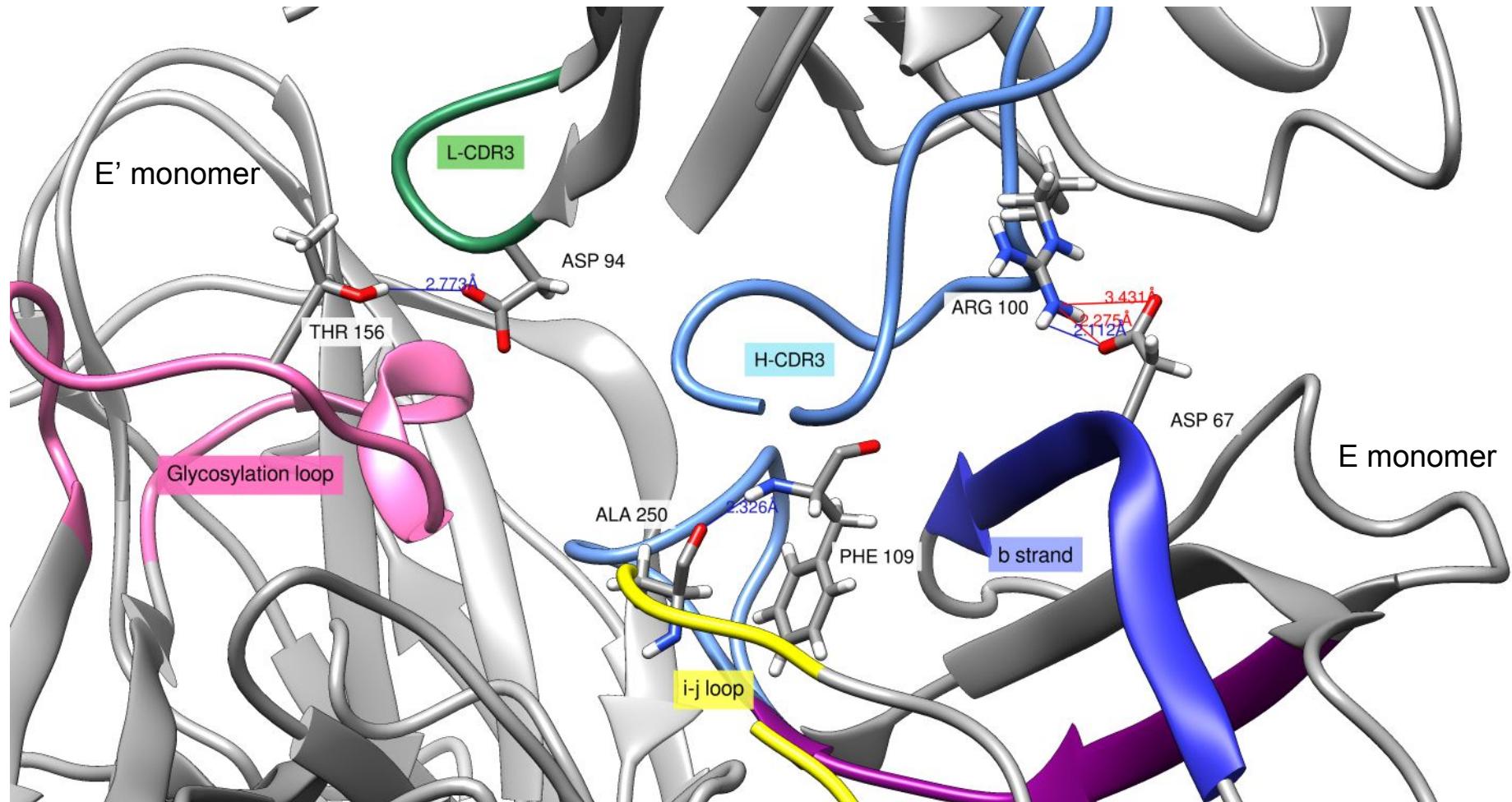
ZIKV-195 INTERACTIONS



ZIKV-195 INTERACTIONS



ZIKV-195 INTERACTIONS



ZIKV-195 SPECIFICITY

b strand

Glycosylation loop

i-j loop

b strand

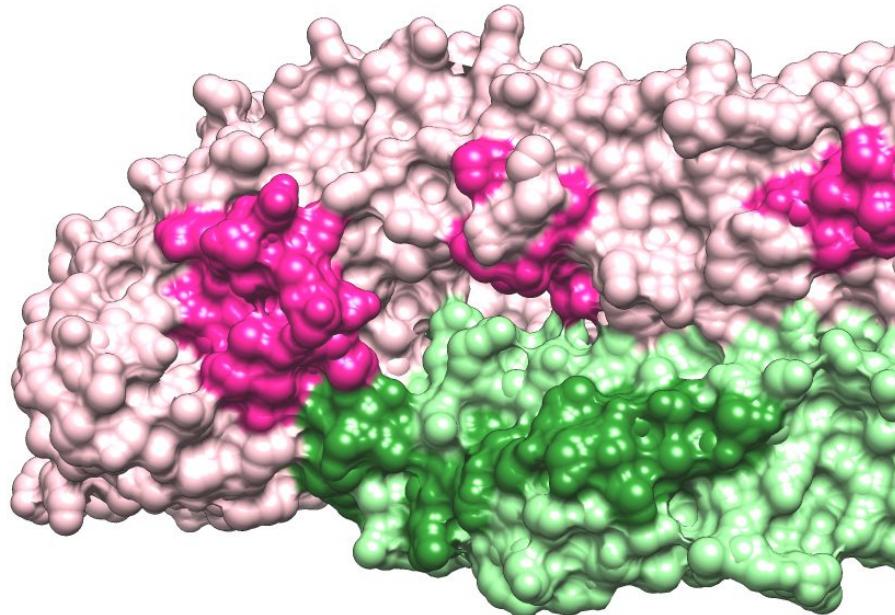
Glycosylation loop

i-j loop

i-i loop

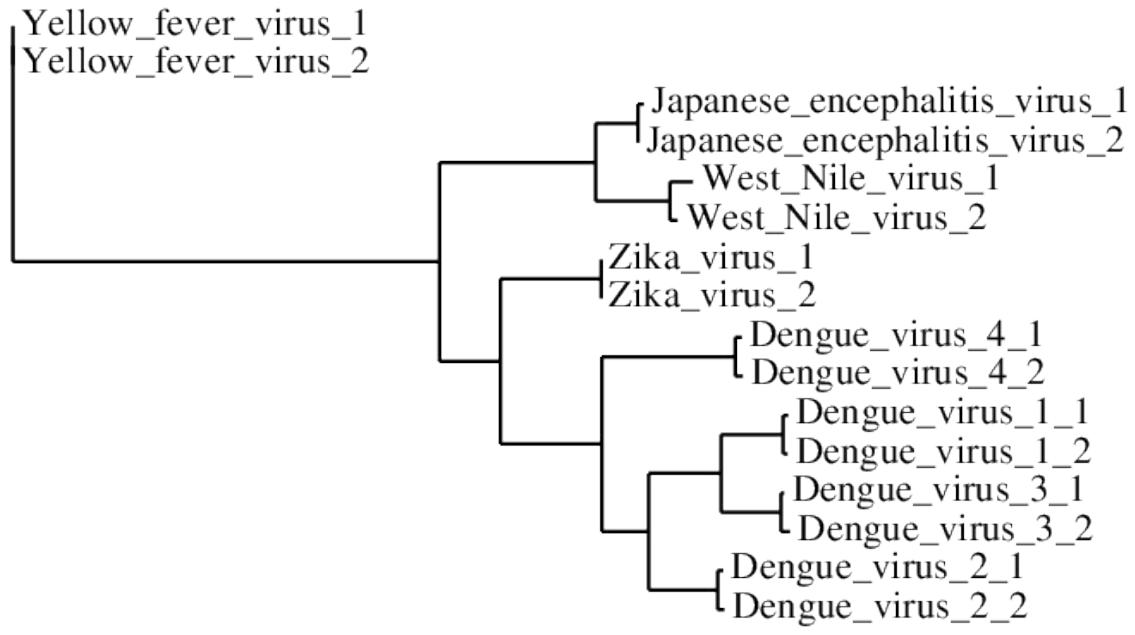
Immunogenicity

Antibodies: A-11

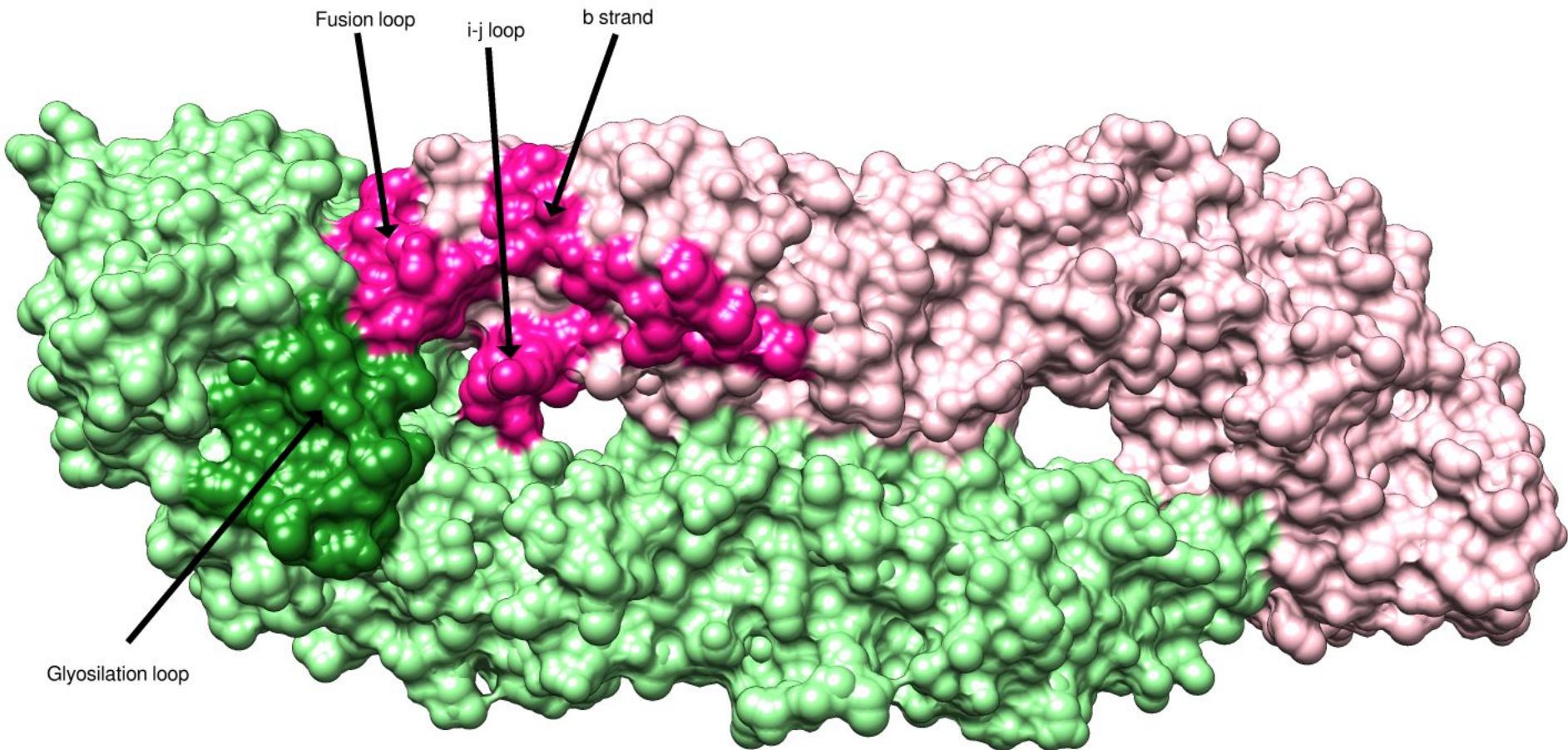


ANTIBODY CROSS-NEUTRALIZATION: A11

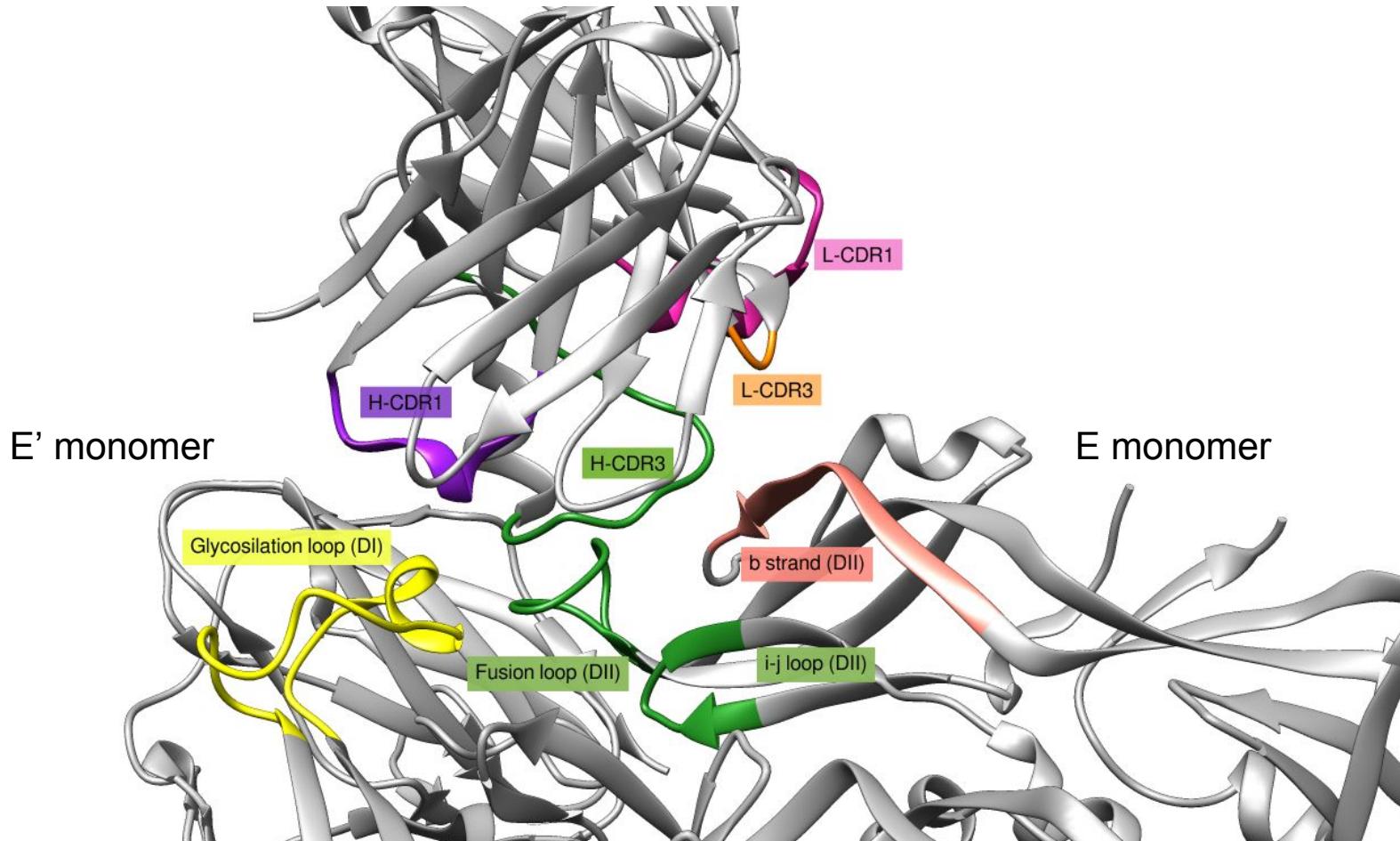
PHYLOGENETIC TREE



ANTIBODY CROSS-NEUTRALIZATION: A11 VIRAL PATCH

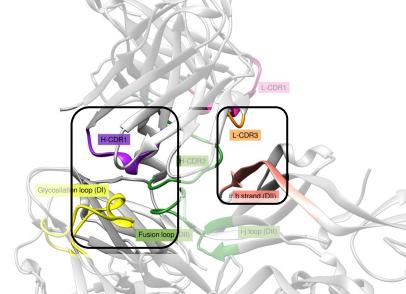
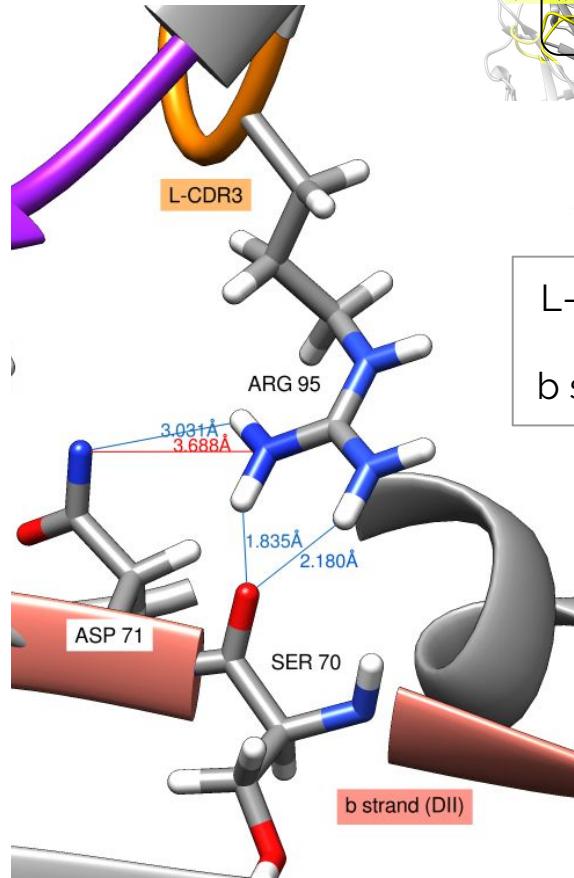
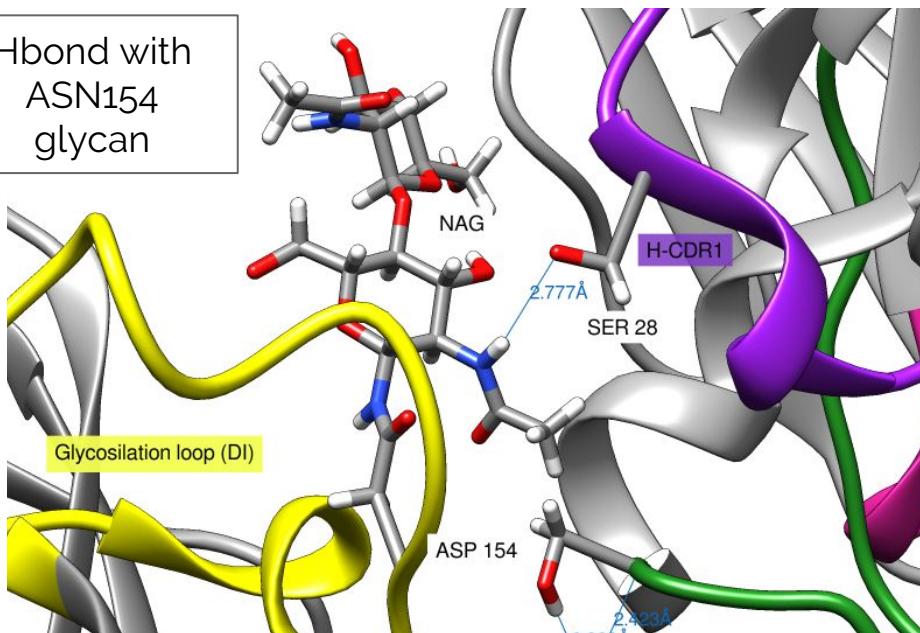


ANTIBODY CROSS-NEUTRALIZATION: A11 BINDING ZONES

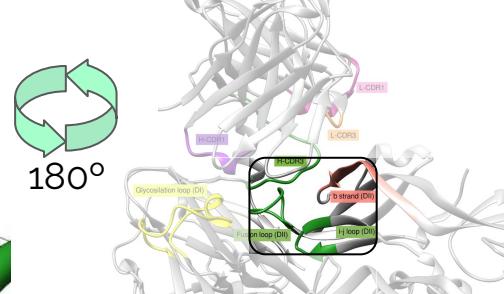
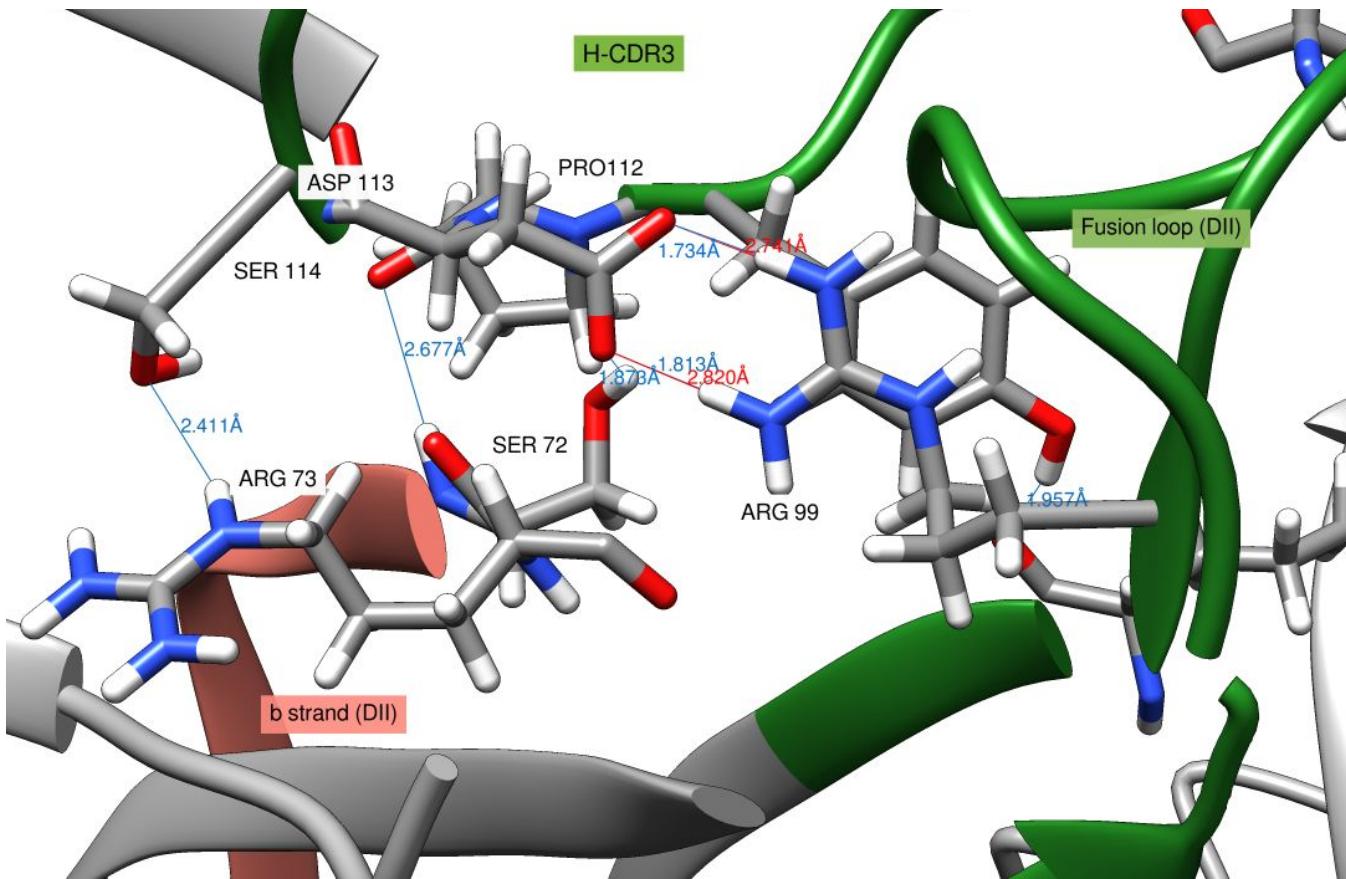


ANTIBODY CROSS-NEUTRALIZATION: A11 INTERACTIONS

Hbond with
ASN154
glycan



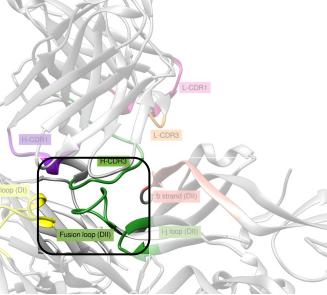
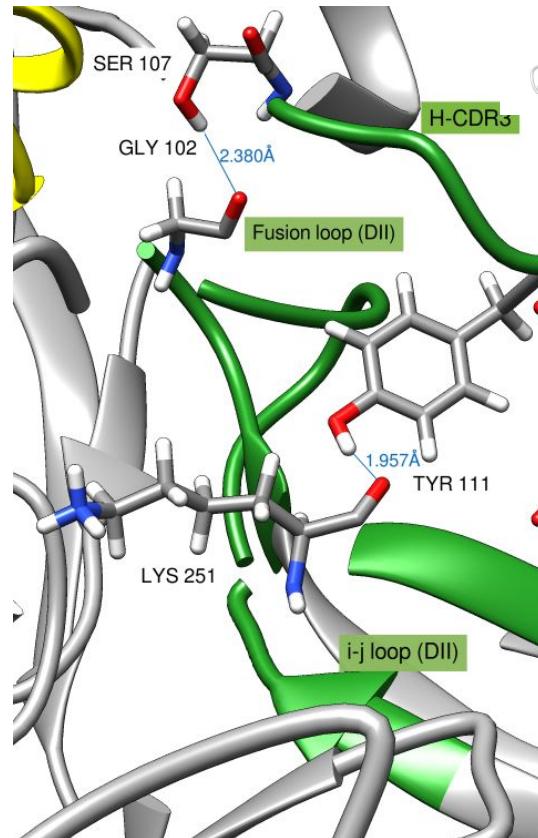
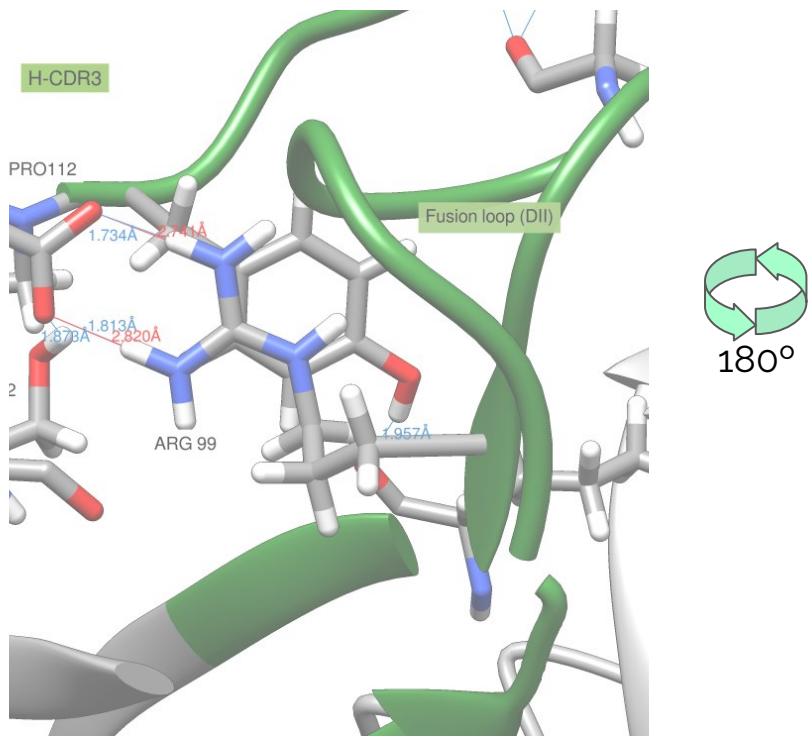
ANTIBODY CROSS-NEUTRALIZATION: A11 INTERACTIONS



H-CDR3
+
b strand and
Fusion loop

Back view

ANTIBODY CROSS-NEUTRALIZATION: A11 INTERACTIONS



H-CDR3
+
Fusion loop
and i-j loop

ANTIBODY CROSS-NEUTRALIZATION: A11

COMPARISON WITH DENV

ZIKV	IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTV	50
DENV_2	MRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEA	50
	.*.*. .***:*** *.:***. .** . *.*: *: .:***:*. : .	
ZIKV	SNMAEVRSYCYEASISDMD	55
DENV_2	SDSRCP	55
	PTQGEAYLDKQSDTQYVCKRTLVD	55
ZIKV	RG 100	100
DENV_2	KQPATLRKYCIEAKLTNTT	100
	TSRCP	100
ZIKV	TSRCP	100
DENV_2	QGEPSLKEE	100
	QDKR	100
ZIKV	DKR	100
DENV_2	VCKHSMV	100
	DG 100	100
ZIKV	WNGCGLFGKGSLVTCAK	150
DENV_2	FACSKKMTGKSIQ	150
	OPENLEYRIMLSVHGSQHSG	150
ZIKV	WNGCGLFGKG	149
DENV_2	GIVTCAMFTCKKNMEGKIV	149
	QOPENLEYTIVVTPHSGEEH-	149
ZIKV	WNGCGLFGKG	149
DENV_2	GIVTCAMFTCKKNMEGKIV	149
	QOPENLEYTIVVTPHSGEEH-	149
ZIKV	MIVNDTG	200
DENV_2	HETDENRAKVEITPNSPRAEATLGGFGSGLGLDCEPRTGLDFSD	200
	AVGNDTG	200
ZIKV	AVGNDTG	200
DENV_2	---KHGKEIKVTPQSSITEAELTG	200
	YGTVTMECS	200
ZIKV	YGTVTMECS	200
DENV_2	RTGLDFNE	200
	---	200
ZIKV	LYYLTMNNKH	250
DENV_2	WLVHK	250
	EWFHD	250
ZIKV	EWFHD	250
DENV_2	IPW	250
	WAGADTG	250
ZIKV	WAGADTG	250
DENV_2	TPH	250
	WNNKEAL	250
ZIKV	WNNKEAL	250
DENV_2	VEFKDAHA	250
	---	250
ZIKV	MVLLQ	245
DENV_2	MENKA	245
	WLVRQW	245
ZIKV	WLVRQW	245
DENV_2	FLDLPL	245
	PWLPGADK	245
ZIKV	PWLPGADK	245
DENV_2	QESNWI	245
	QKETL	245
ZIKV	QKETL	245
DENV_2	LVTFKNP	245
	HA	245
ZIKV	HA	245
DENV_2	KRQTVVVLGSQEGAVHTALAGALEAEMDG	297
	---KGR	297
ZIKV	---KGR	297
DENV_2	SSGHLK	297
	CRLK	297
ZIKV	CRLK	297
DENV_2	MDK	297
	---	297
ZIKV	KKQD	291
DENV_2	VVLGSQEGAMHTALT	291
	GATEIQMSS	291
ZIKV	GATEIQMSS	291
DENV_2	GNLLFTGHL	291
	CRLRMDK	291
ZIKV	CRLRMDK	291
DENV_2	---	291

b strand

Fusion loop

Glycosylation loop

i-j loop

Cross-react binding residues

COMPARISON OF ZIKV-195 AND A11

Sequence alignment of ZIKV and DENV_2 proteins. The alignment shows the following regions and motifs:

- Top Region:** Consists of two lines of amino acid sequence. The first line starts with 'IRCIGVSNRDFVEGMSGGTWVVLEHGGCVTVMAQDKPTV' and the second with 'MRCIGISNRDFVEGVSGGSWDIVLEHGSCVTTMAKNKPTLDFELIKTEA'. Above the alignment are two green diamond-shaped motifs, each containing a yellow 'SDS' sequence.
- Second Region:** Consists of two lines of amino acid sequence. The first line starts with 'SNMAEVRSYCYEASIS' and the second with 'KQPATLRKYCIEAKLTNTT'. Above the alignment are two green diamond-shaped motifs, each containing a yellow 'SDS' sequence. Below the alignment are two purple diamond-shaped motifs, each containing a purple 'ESR' sequence.
- Third Region:** Consists of two lines of amino acid sequence. The first line starts with 'WNGCGLFGKGSLVTCAK' and the second with 'WNGCGLFGKGIVTCAMFTCK'. Above the alignment are two purple diamond-shaped motifs, each containing a purple 'ESR' sequence. Below the alignment is a red double-headed arrow spanning the 'WNGCGL...' and 'WNGCGL...' lines.
- Fourth Region:** Consists of two lines of amino acid sequence. The first line starts with 'MIVNDTGHETDENRAKVEITPNSPRAEATLGGFGSLGLDCEPRTGLDFSD' and the second with 'AVGNDTG----KHGKEIKVTPQSSITEAELTGYGTVTMECSVRTGLDFNE'. Above the alignment is a purple diamond-shaped motif containing a purple 'ESR' sequence. Below the alignment is a red double-headed arrow spanning the 'MIVNDT...' and 'AVGNDTG...' lines.
- Fifth Region:** Consists of two lines of amino acid sequence. The first line starts with 'LYYLTMMINKHWLVHK' and the second with 'MVLLQMEENKAWLVRQWFLDLPLPWLGADKQESNWIQKETLVTFKNPHA'. Above the alignment is a purple diamond-shaped motif containing a purple 'ESR' sequence. Below the alignment is a yellow double-headed arrow spanning the 'LYYLTMM...' and 'MVLLQME...' lines.
- Sixth Region:** Consists of two lines of amino acid sequence. The first line starts with 'KQTVVVLGSQEGAVHTALAGALEAEMDGA' and the second with 'KKQDQVVLGSQEGAMHTALTGATEIQMSS'. Above the alignment is a purple diamond-shaped motif containing a purple 'ESR' sequence. Below the alignment is a yellow double-headed arrow spanning the 'KQTVVVL...' and 'KKQDQVVL...' lines.

b strand

Fusion loop

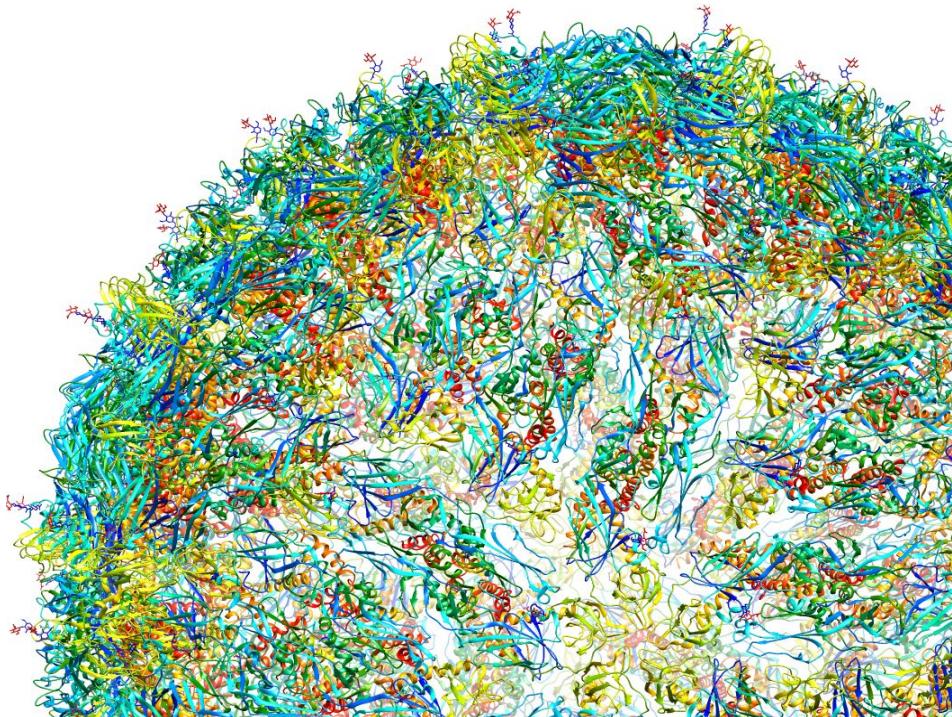
Glycosylation loop

i-j loop

Shared binding residues

Specific binding residues of ZIKV-195

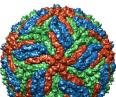
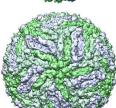
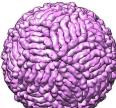
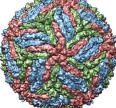
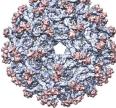
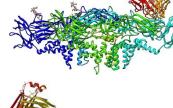
Conclusions



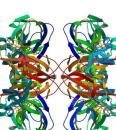
TAKE-HOME MESSAGE

- Simple sources can give rise to complex structures
- Viral variability can be useful to find therapeutic targets
- Recent growth of interest in ZIKA virus
- Refinement of structure resolving techniques are currently improving this study field
- Zika virus is not as structurally studied as other Flaviviruses.

MATERIALS

	<i>PDB code</i>	<i>Protein/Organism</i>	<i>Resolution</i>	<i>Method</i>	<i>Reference (DOI)</i>
	6CO8	Proteins E and M (ZIKV)	3.1 Å	Electron Microscopy	10.1016/j.str.2018.05.006
	3J27	Proteins E and M (DENV2)	3.6 Å	Electron Microscopy	10.1038/nsmb.2463
	5IZ7	Thermally-stable ZIKV	3.7 Å	Electron Microscopy	10.1038/nature17994
	5IRE	Proteins E and M (ZIKV)	3.8 Å	Electron Microscopy	10.1126/science.aaf5316
	5U4W	Proteins E, M and pr domain (ZIKV and DENV2)	9.1 Å	Electron Microscopy	10.1038/nsmb.3352
	6MID	ZIKV-195 + E dimer	4 Å	Electron Microscopy	10.1073/pnas.1815432116
	5LCV	A11 Fab + E dimer	2.64 Å	X-Ray Diffraction	10.1038/nature18938

MATERIALS

	<i>PDB code</i>	<i>Protein/Organism</i>	<i>Resolution</i>	<i>Method</i>	<i>Reference (DOI)</i>
	1UZG	Proteins M and E (DENV3)	3.5 Å	X-Ray Diffraction	10.1128/JVI.79.2.1223-1231.2005
	3UAJ	Proteins M and E (DENV4)	3.2 Å	X-Ray Diffraction	10.1038/emboj.2011.439
	2HG0	Protein E (WNV)	3 Å	X-Ray Diffraction	10.1128/JVI.01125-06
	3P54	Protein E (JEV)	2.097 Å	X-Ray Diffraction	10.1128/JVI.06072-11
	6iW4	Protein E (YEV)	2,801 Å	X-Ray Diffraction	10.1016/j.celrep.2018.12.065

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Questions

- ❖ Which is the **most used** technique to solve viral structures?
 - a) X-ray diffraction
 - b) Cryo-electromicroscopy**
 - c) NMR
 - d) a and b are correct
 - e) all of them are correct
- ❖ Which of the following sentences is correct:
 - a) The Zika virus envelope symmetry consists of one axis of each fold (5, 3 and 2).
 - b) The Zika virus symmetry is icosahedral.**
 - c) Not all the Flaviviruses share the same symmetry.
 - d) The Zika virus has a T=4-like organization of surface.
 - e) The Zika virus envelope is composed by 200 asymmetric units.
- ❖ The asymmetric unit of Zika virus envelope is composed by:
 - a) 60 trimers of E proteins
 - b) The E-M heterodimers trimer**
 - c) A raft of three E homodimers
 - d) 5-fold axis
 - e) None of them are correct
- ❖ Which of the following sentences is false:
 - a) The envelope protein E plays an important role in cell attachment but not in antigenicity.**
 - b) The envelope protein E is formed by three ectodomains (D1, DII, DIII).
 - c) DII and DIII contains the neutralizing epitopes.
 - d) Domains DII and DIII belong to alpha-beta class (CATH classification).
 - e) The envelope protein E is structurally similar among Flaviviruses.

Questions

- ❖ About protein E loops, choose the correct answer:
 - a) There are no variable loop in E protein.
 - b) Zika virus has 10 loops functionally relevant.
 - c) The fusion loop is the most conserved loop of E protein.**
 - d) The DI-DIII hinge is responsible for the viral interaction with the cellular receptor.
 - e) All of them are correct.
- ❖ Related to the Zika virus surface:
 - a) Needs an aqueous environment to survive, that's why the surface of E protein is mainly polar.
 - b) E protein is also anchored on the membrane, so the transmembrane domain has a hydrophobic surface.
 - c) a and b are correct.
 - d) Even though the surface of the ectodomains is polar, there is a hydrophobic pocket.
 - e) All of them are correct.**
- ❖ The interactions between E monomers:
 - a) Are mainly polar.
 - b) Depends on the symmetry axis they adjacent to.
 - c) A and B are correct.**
 - d) Determine the interaction of the M protein with the pr peptide.
 - e) All of the above are correct.
- ❖ M protein:
 - a) Is bigger than E protein.
 - b) Is mainly formed by beta strands.
 - c) In the mature form of the Zika virus is exposed to the solvent.
 - d) Is formed by three alpha helices (H1, H2 and H3)**
 - e) There are no hydrophobic interactions between E and M proteins.

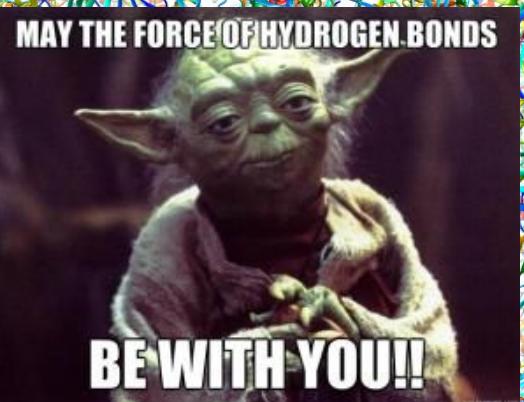
Questions

- ❖ Which of the following sentences is false:
 - a) **T cell epitopes are mainly located in E protein transmembrane domain.**
 - b) ZIKV-195 is a potent human monoclonal antibody that prevents the formation of fusogenic trimers.
 - c) There is cross-neutralization between flavivirus, mainly between Zika and Dengue.
 - d) Some of the Zika virus epitopes are negatively selected.
 - e) The specificity of the antibody ZIKV-195 for the Zika virus is due to the conservation of certain residues among ZIKA virus strains.
- ❖ Select the correct answer:
 1. The k-I Loop of DENV has been associated to the change of conformation of the hydrophobic pocket.
 2. The Histidine 323 is thought to be the molecular sensor for triggering fusion.
 3. The hydrophobic pocket is hiding the fusion loop in neutral pH.
 4. The hydrophobic is hiding the fusion loop in all of the viral conformations.
 - a) 1, 2 and 3
 - b) 1 and 3
 - c) 2 and 4
 - d) 4
 - e) 1, 2, 3 and 4

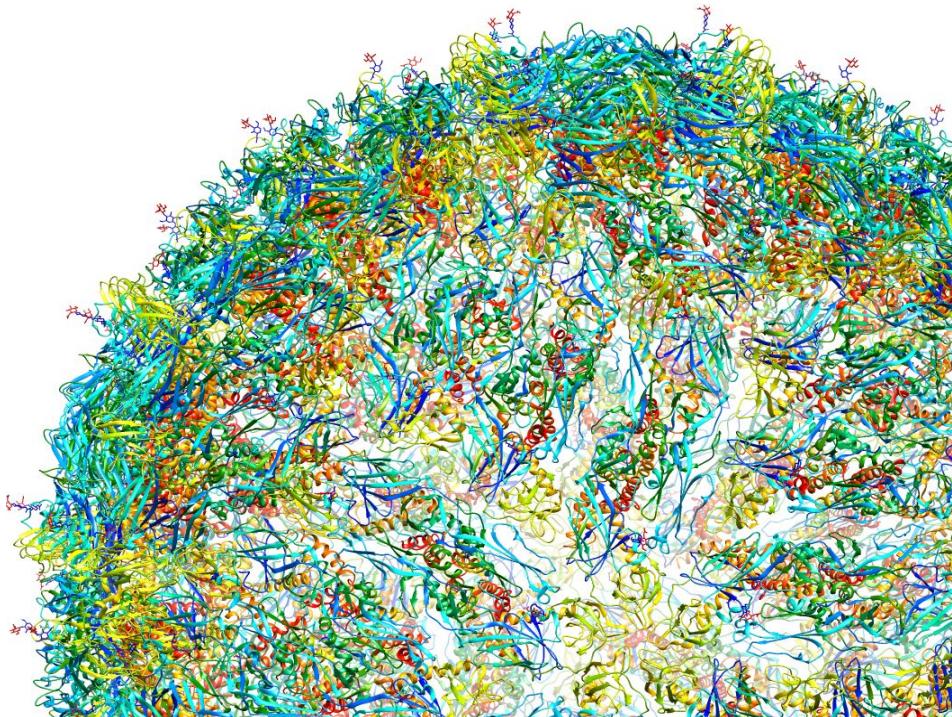
Thank you for your attention

Campos M, Canales A,
Díaz J, Llerena M.

Structural Biology
Human Biology, UPF
2018-2019



Annexes



ANNEX

HMM alignment

Flavivirus glycoprotein, central and dimerisation domains

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

IRCGIVSNRDFVEGMSGGTWDDVLEHGCCVTVMQDKPVTVDIELVTTTV	Zika_virus_1
IRCGIVSNRDFVEGMSGGTWDDVLEHGCCVTVMQDKPVTVDIELVTTTV	Zika_virus_2
IRCGIVSNRDFVEGMSGGTWDDVLEHGCCVTVMQDKPVTVDIELVTTTV	Zika_virus_3
IRCGIVSNRDFVEGMSGGTWDDVLEHGCCVTVMQDKPVTVDIELVTTTV	Zika_virus_4
MRCVGIGSRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILLKTEV	Dengue_virus_1_1
MRCVGIGNRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILLKTEV	Dengue_virus_1_2
MRCVGIGSRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILLKTEV	Dengue_virus_1_3
MRCVGIGSRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILLKTEV	Dengue_virus_1_4
MRCIGISNRDFVEGSGGSWDIVLEHGCCVTMMAKDKPTLDFELIKTEA	Dengue_virus_2_1
MRCIGISNRDFVEGSGGSWDIVLEHGCCVTMMAKDKPTLDFELIKTEA	Dengue_virus_2_2
MRCIGISNRDFVEGSGGSWDIVLEHGCCVTMMAKDKPTLDFELIKTEA	Dengue_virus_2_3
MRCIGISNRDFVEGSGGSWDIVLEHGCCVTMMAKDKPTLDFELIKTEA	Dengue_virus_2_4
MRCVGVNQRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILQKTEA	Dengue_virus_3_1
MRCVGVNQRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILQKTEA	Dengue_virus_3_2
MRCVGVNQRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILQKTEA	Dengue_virus_3_3
MRCVGVNQRDFVEGLSGATWDDVLEHGCCVTMMAKDKPTLDEILQKTEA	Dengue_virus_3_4
MRCVGVNQRDFVEGSGGAWDLVLEHGCCVTMMAQGKPTLDFELTKTA	Dengue_virus_4_1
MRCVGVNQRDFVEGSGGAWDLVLEHGCCVTMMAQGKPTLDFELTKTA	Dengue_virus_4_2
MRCVGVNQRDFVEGSGGAWDLVLEHGCCVTMMAQGKPTLDFELTKTA	Dengue_virus_4_3
MRCVGVNQRDFVEGSGGAWDLVLEHGCCVTMMAQGKPTLDFELTKTA	Dengue_virus_4_4
FNCLGMNSNRDFLEGSGATWDLVLEGDSCLTIMANDKPTLDRVMINIEA	Japanese_encephalitis_virus_1
FNCLGMNSNRDFLEGSGATWDLVLEGDSCLTIMANDKPTLDRVMINIEA	Japanese_encephalitis_virus_2
FNCLGMNSNRDFLEGSGATWDLVLEGDSCLTIMANDKPTLDRVMINIEA	Japanese_encephalitis_virus_3
FNCLGMNSNRDFLEGSGATWDLVLEGDSCLTIMANDKPTLDRVMINIEA	Japanese_encephalitis_virus_4
—	West_Nile_virus_1
—	West_Nile_virus_2
—	West_Nile_virus_3
—	West_Nile_virus_4
AHCIGITDRDFIEVGHGGTWSATLEQDKCVCVTMAPDKPSLDSILETVAI	Yellow_fever_virus_1
AHCIGITDRDFIEVGHGGTWSATLEQDKCVCVTMAPDKPSLDSILETVAI	Yellow_fever_virus_2
AHCIGITDRDFIEVGHGGTWSATLEQDKCVCVTMAPDKPSLDSILETVAI	Yellow_fever_virus_3
AHCIGITDRDFIEVGHGGTWSATLEQDKCVCVTMAPDKPSLDSILETVAI	Yellow_fever_virus_4
XX	#=GC RF

ANNEX

HMM alignment

Flavivirus glycoprotein, central and dimerisation domains

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#GC RF

SGMIV——.NDENRAKVEVTNPNSPRAEATLGGFSGSLGLDCEPRTGLDF
SGMIV——.NDENRAKVEVTNPNSPRAEATLGGFSGSLGLDCEPRTGLDF
SGMIV——.NDENRAKVEVTNPNSPRAEATLGGFSGSLGLDCEPRTGLDF
SGMIV——.NDENRAKVEVTNPNSPRAEATLGGFSGSLGLDCEPRTGLDF
HVGNE——.STEHGTTATITPQAPTSEIQLTDYGALTLCSPRTGLDF
HVGNE——.TTEHGTTATITPQAPTSEIQLTDYGALTLCSPRTGLDF
HVGNE——.STEHGTTATITPQAPTTEIQLTDYGALTLCSPRTGLDF
HVGNE——.STEHGTTATITPQAPTTEIQLTDYGALTLCSPRTGLDF
HAVGND——.TGKHGKEIKVTPQSSITEAELTGYGTVMECSPRTGLDF
HAVGND——.TGKHGKEIKITPOSSITEAELTGYGTVMECSPRTGLDF
HAVGND——.TGKHGKEIKITPOSSITEAELTGYGTVMECSPRTGLDF
HAVGND——.TGKHGKEIKITPOSSITEAELTGYGTVMECSPRTGLDF
HVGQ——.NETQGVTAIEITPOASTVEAILPEYGTGLGLECSPTRGDF
HVGQ——.TQGVTAIEITPQASTVEAILPEYGTGLGLECSPTRGDF
HVGQ——.NETQGVTAIEITPOASTVEAILPEYGTGLGLECSPTRGDF
HVGQ——.NETQGVTAIEITPOASTVEAILPEYGTGLGLECSPTRGDF
HVGQ——.NETQGVTAIEITPOASTVEAILPEYGTGLGLECSPTRGDF
HVGQ——.TSNHGVATITPRSPSVEVLPKLDGYELTLDCERPRSGIDF
HVGQ——.TSNHGVATITPRSPSVEVLPKLDGYELTLDCERPRSGIDF
HVGQ——.TSNHGVATITPRSPSVEVLPKLDGYELTLDCERPRSGIDF
HVGQ——.TSNHGVATITPRSPSVEVLPKLDGYELTLDCERPRSGIDF
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SENHGNYSAQvGASQAQAKFTVTPNAPSITLKLGDYEVTLDCERPRSGLNT
SENHGNYSAQvGASQAQAKFTVTPNAPSITLKLGDYEVTLDCERPRSGLNT
VESHGNYSTQ@GATQAGRFSITPAAPSYTTLKLGEGYEVTVDCERPRSGIDT
VESHGNYSTQ@GATQAGRFSITPAAPSYTTLKLGEGYEVTVDCERPRSGIDT
VESHGNYSTQ@GATQAGRFSITPAAPSYTTLKLGEGYEVTVDCERPRSGIDT
VESHGNYSTQ@GATQAGRFSITPAAPSYTTLKLGEGYEVTVDCERPRSGIDT
VESHGNYSTQ@GATQAGRFSITPAAPSYTTLKLGEGYEVTVDCERPRSGIDT
QEN——.WNTDIKTLFDALSGSQEAFETGYZGRATLECQVQTVADF
QEN——.WNTDIKTLFDALSGSQEAFETGYZGRATLECQVQTVADF
QEN——.WNTDIKTLFDALSGSQEAFETGYZGRATLECQVQTVADF
QEN——.WNTDIKTLFDALSGSQEAEFTGYZGRATLECQVQTVADF
XXXXXXXXXX.XX

ANNEX

HMM alignment

Flavivirus glycoprotein, central and dimerisation domains

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

ANNEX

HMM alignment

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

CRKLMDKLRKGvsy whole line of 100 characters

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis
Japanese_encephalitis
Japanese_encephalitis
Japanese_encephalitis
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus
Yellow_fever_virus
Yellow_fever_virus
Yellow_fever_virus
#GC RF

ANNEX

HMM alignment

Flavivirus glycoprotein, central and dimerisation domains

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#GC RF

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#GC RF

ANNEX

HMM alignment

Zika_virus_1	lggvmiflstavsa
Zika_virus_2	lggvmiflstavsa
Zika_virus_3	lggvmiflstavsa
Zika_virus_4	lggvmiflstavsa
Dengue_virus_1_1	vtlylgvmvqa...
Dengue_virus_1_2	vtlylgvmvqa...
Dengue_virus_1_3	vtlylgvmvqa...
Dengue_virus_1_4	vtlylgvmvqa...
Dengue_virus_2_1	vtlylgvmvqa...
Dengue_virus_2_2	vtlylgamvqa...
Dengue_virus_2_3	vtlylgavvqa...
Dengue_virus_2_4	vtlylgvmvqa...
Dengue_virus_3_1	itlylgavvqa...
Dengue_virus_3_2	itlylgtvvqa...
Dengue_virus_3_3	itlylgavvqa...
Dengue_virus_3_4	itlylgavvqa...
Dengue_virus_4_1	itlflgftvqa...
Dengue_virus_4_2	itlflgftvqa...
Dengue_virus_4_3	itlflgftvqa...
Dengue_virus_4_4	itlflgftvqa...
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2	tggvlvflatnvha
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1	vggvllflsvnvh
West_Nile_virus_2	vggvllflsvnvh
West_Nile_virus_3	vggvllflsvnvh
West_Nile_virus_4	vggvllflsvnvh
Yellow_fever_virus_1	immflslgvga...
Yellow_fever_virus_2	immflslgvga...
Yellow_fever_virus_3	immflslgvga...
Yellow_fever_virus_4	immflslgvga...
#=GC RF

ANNEX

HMM alignment

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

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tevtvpavlrkcieakisnttdsrcptqgeatlveeqdanfvcrrtfv
tevtvpavlrkcieakisnttdsrcptqgeatlveeqdanfvcrrtfv
tevtvpavlrkcieakisnttdsrcptqgeatlveeqdanfvcrrtfv
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teakqpatlrkycieaklntttesrcptqgepslneeqdkrfickhsmv
teakqpatlrkycieaklntttesrcptqgepslneeqdkrfickhsmv
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qkteatqlatrlklicegkitnvttdsrcptqgealpeeqdqnqvckht
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etvaiddgpaearkvcysavlnvkindkcpstgeahleeneqdnackrt
etvaiddgpaearkvcysavlnvkindkcpstgeahleeneqdnackrt
etvaiddgpaearkvcysavlnvkindkcpstgeahleeneqdnackrt

ANNEX

HMM alignment

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
-GC RF

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ltmnkkhwlvhkewfhidplpwhagadtgtphwnnkealvefkdhakrq
ltmnkkhwlvhkewfhidplpwhagadtgtphwnnkealvefkdhakrq
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lqmedkawlvhrqwflndlplpwlpgadttqgsnwiqketlvtfknpahkk
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lmkkkktwlvhkqwflndlplpwtgadttsevhnwkyermvtfkvphakr
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fymvtvgksfvhrewfhdsllpwtssstawnrrellmefeeahatk
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yvmtvgktflvhrewfmdlnlpwssagsttvrnreltmefeeahatkq
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emekeswivdkqwaqdltlpwqsgsggvwremhhlfefepphaatikvl
emekeswivdkqwaqdltlpwqsgsggvwremhhlfefepphaatikvl
emekeswivdkqwaqdltlpwqsgsggvwremhhlfefepphaatikvl

ANNEX

HMM alignment

Zika_virus_1
Zika_virus_2
Zika_virus_3
Zika_virus_4
Dengue_virus_1_1
Dengue_virus_1_2
Dengue_virus_1_3
Dengue_virus_1_4
Dengue_virus_2_1
Dengue_virus_2_2
Dengue_virus_2_3
Dengue_virus_2_4
Dengue_virus_3_1
Dengue_virus_3_2
Dengue_virus_3_3
Dengue_virus_3_4
Dengue_virus_4_1
Dengue_virus_4_2
Dengue_virus_4_3
Dengue_virus_4_4
Japanese_encephalitis_virus_1
Japanese_encephalitis_virus_2
Japanese_encephalitis_virus_3
Japanese_encephalitis_virus_4
West_Nile_virus_1
West_Nile_virus_2
West_Nile_virus_3
West_Nile_virus_4
Yellow_fever_virus_1
Yellow_fever_virus_2
Yellow_fever_virus_3
Yellow_fever_virus_4
#=GC RF

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TPVGRLLITANPVTESTENSKMMLELDPPFGDSYIVIVGVGDKKITHHWR
TPVGRLLITANPVTESTENSKMMLELDPPFGDSYIVIVGVGDKKITHHWR
TPVGRLLITANPVTESTENSKMMLELDPPFGDSYIVIVGVGDKKITHHWR
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TQNGLRLLITANPIVTDK—EKPVNIEAEPFGESYIVIVGAGEKALKLWSFK
TQNGLRLLITANPIVTDK—EKPVNIEAEPFGESYIVIVGAGEKALKLWSFK
YVLGRLLITVNPIVTEK—DSPVNIEAEPFGDSYIIIGVEPQLKLNWFK
HVLGRLLITVNPIVTEK—DSPVNIEAEPFGDSYIIIGVEPQLKLNWFK
HVLGRLLITVNPIVTEK—DSPVNIEAEPFGDSYIIIGVEPQLKLNWFK
HVLGRLLITVNPIVTEK—DSPVNIEAEPFGDSYIIIGVEPQLKLNWFK
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AHNGLRLLITANPVVTKK—EEPVNIEAEPFGESNIVIGIGDKALKLNWYK
AHNGLRLLITANPVVTKK—EEPVNIEAEPFGESNIVIGIGDKALKLNWYK
AHNGLRLLITANPVVTKK—EEPVNIEAEPFGESNIVIGIGDKALKLNWYK
AHNGLRLLITANPVVTKK—EEPVNIEAEPFGESNIIIGIGDKALKLNWYK
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KVGRIVISSIPAENT—NSVTNIELEPPFGDSYIVIVGVGNSALTlhWFR
KVGRIISSTPFAENT—NSVTNIELEPPFGDSYIVIVGVGDSALTlhWFR
KVGRIISSTPFAENT—NSVTNIELEPPFGDSYIVIVGVGDSALTlhWFR
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TPVGRLLITVNPFVSVTANAKVLIELEPPFGDSYIVVGRGEQOQINHHWHK
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VNKGILVTVNPIASTN—DDEVLIEVNPPFGDSYIIVGTGDSRLTYQWHK
VNKGILVTVNPIASTN—DDEVLIEVNPPFGDSYIIVGTGDSRLTYQWHK
VNKGILVTVNPIASTN—DDEVLIEVNPPFGDSYIIVGTGDSRLTYQWHK
XX

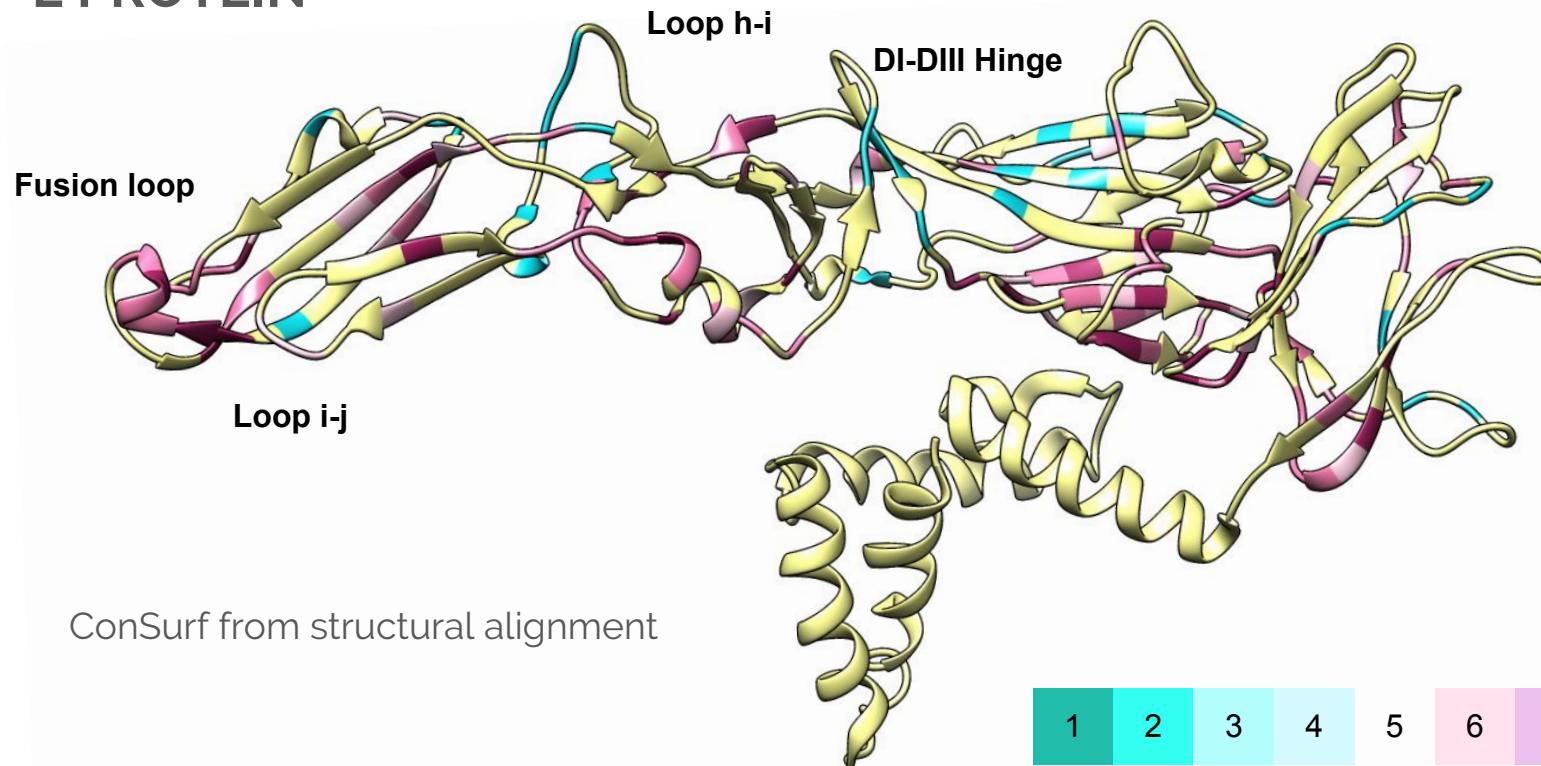
ika_virus_1
ika_virus_2
ika_virus_3
ika_virus_4
dengue_virus_1_1
dengue_virus_1_2
dengue_virus_1_3
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dengue_virus_2_1
dengue_virus_2_2
dengue_virus_2_3
dengue_virus_2_4
dengue_virus_3_1
dengue_virus_3_2
dengue_virus_3_3
dengue_virus_3_4
dengue_virus_4_1
dengue_virus_4_2
dengue_virus_4_3
dengue_virus_4_4
japanese_encephalitis_virus_1
japanese_encephalitis_virus_2
japanese_encephalitis_virus_3
japanese_encephalitis_virus_4
west_Nile_virus_1
west_Nile_virus_2
west_Nile_virus_3
west_Nile_virus_4
yellow_fever_virus_1
yellow_fever_virus_2
yellow_fever_virus_3
yellow_fever_virus_4
=GC RF

ANNEX

HMM alignment

Zika_virus_1	fkslfggmswfsqiligtllvwlglnkngsislclalggvmifl stav	Zika_virus_1	sa
Zika_virus_2	fkslfggmswfsqiligtllvwlglnkngsislclalggvmifl stav	Zika_virus_2	sa
Zika_virus_3	fkslfggmswfsqiligtllvwlglnkngsislclalggvmifl stav	Zika_virus_3	sa
Zika_virus_4	fkslfggmswfsqiligtllvwlglnkngsislclalggvmifl stav	Zika_virus_4	sa
Dengue_virus_1_1	ygvlfgsvshtmkiigivlltwlglnsrstslsmtciavglvtlylgvmv	Dengue_virus_1_1	qa
Dengue_virus_1_2	ygvlfgsvshtmkiigigilltwlglnsrstslsmtciavgmvtlylgvmv	Dengue_virus_1_2	qa
Dengue_virus_1_3	ygvlfgsvshtmkiigivlltwlglnsrstslsmtciavglvtlylgvmv	Dengue_virus_1_3	qa
Dengue_virus_1_4	ygvlfgsvshtmkiigivlltwlglnsrstslsmtciavglvtlylgvmv	Dengue_virus_1_4	qa
Dengue_virus_2_1	ygaafsgvsvtmkiliigviitwigmnsrstslsvslvgivtlylgvmv	Dengue_virus_2_1	qa
Dengue_virus_2_2	ygaafsgvsvtmkiliigviitwigmnsrstslsvslvgivtlylgamv	Dengue_virus_2_2	qa
Dengue_virus_2_3	ygaafsgvsvtmkiliigviitwigmnsrstslsvslvgivtlylgavv	Dengue_virus_2_3	qa
Dengue_virus_2_4	ygaafsgvsvtmkiliigviitwigmnsrstslsvslvgivtlylgvmv	Dengue_virus_2_4	qa
Dengue_virus_3_1	ytalfgsvswimkiigivlltwiglnskntsmsfcivigiitlylgavv	Dengue_virus_3_1	qa
Dengue_virus_3_2	ytalfggvswimkiigivlltwiglnskntsmsfcivigiitlylgtvv	Dengue_virus_3_2	qa
Dengue_virus_3_3	ytalfgsvswimkiigivlltwiglnskntsmsfciaigiitlylgavv	Dengue_virus_3_3	qa
Dengue_virus_3_4	ytalfgsvswimkiigivlltwiglnskntsmsfcivigiitlylgavv	Dengue_virus_3_4	qa
Dengue_virus_4_1	ytmmfggvswimirlgflvlwigtnsrtntsmamtciavggitlflgftv	Dengue_virus_4_1	qa
Dengue_virus_4_2	ytmmfggvswimirlgflvlwigtnsrtntsmamtciavggitlflgftv	Dengue_virus_4_2	qa
Dengue_virus_4_3	ytmmfggvswimirlgflvlwigtnsrtntsmamtciavggitlflgftv	Dengue_virus_4_3	qa
Dengue_virus_4_4	ytmmfggvswimirlgflvlwigtnsrtntsmamtciavggitlflgftv	Dengue_virus_4_4	qa
Japanese_encephalitis_virus_1	Japanese_encephalitis_virus_1	..
Japanese_encephalitis_virus_2	frlfggmswitqqlgallwmgnardrsialaflatggvlfvlatnv	Japanese_encephalitis_virus_2	ha
Japanese_encephalitis_virus_3	Japanese_encephalitis_virus_3	..
Japanese_encephalitis_virus_4	Japanese_encephalitis_virus_4	..
West_Nile_virus_1	frslfggmswitqqlgallwmgnardrsialflavggvllflsvnv	West_Nile_virus_1	ha
West_Nile_virus_2	frslfggmswitqqlgallwmgnardrsiamflavggvllflsvnv	West_Nile_virus_2	ha
West_Nile_virus_3	frslfggmswitqqlgallwmgnardrsialflavggvllflsvnv	West_Nile_virus_3	ha
West_Nile_virus_4	frslfggmswitqqlgallwmgnardrsialflavggvllflsvnv	West_Nile_virus_4	ha
Yellow_fever_virus_1	fqqlfgglswitkvimgvliwvginrnmtnmsmsmilvgvimmflsgv	Yellow_fever_virus_1	ga
Yellow_fever_virus_2	fqqlfgglswitkvimgvliwvginrnmtnmsmsmilvgvimmflsgv	Yellow_fever_virus_2	ga
Yellow_fever_virus_3	fqqlfgglswitkvimgvliwvginrnmtnmsmsmilvgvimmflsgv	Yellow_fever_virus_3	ga
Yellow_fever_virus_4	fqqlfgglswitkvimgvliwvginrnmtnmsmsmilvgvimmflsgv	Yellow_fever_virus_4	ga
#=GC RF	#=GC RF	..
	//		

ANNEX E PROTEIN

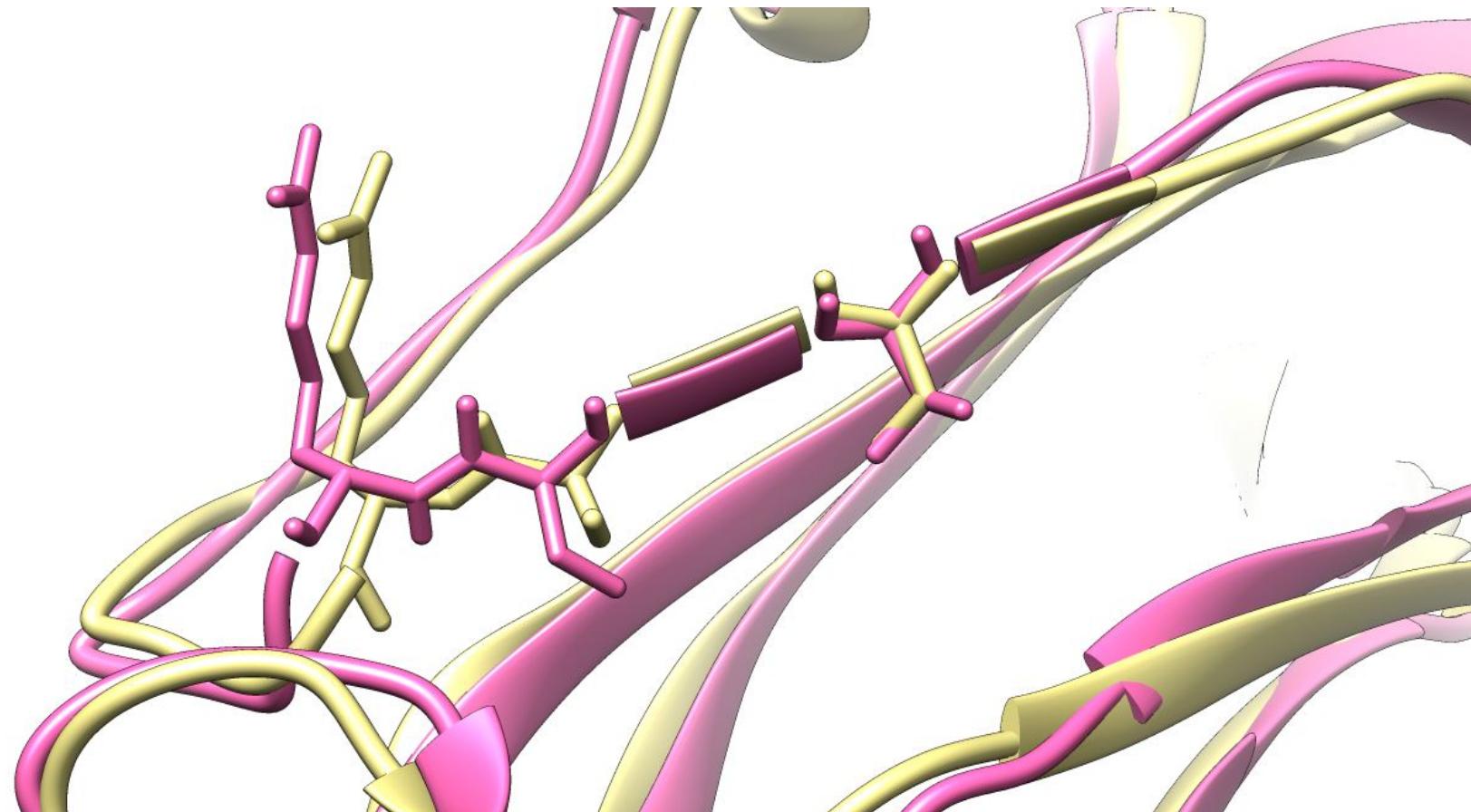


Insufficient data

ANNEX

Cross-neutralizing

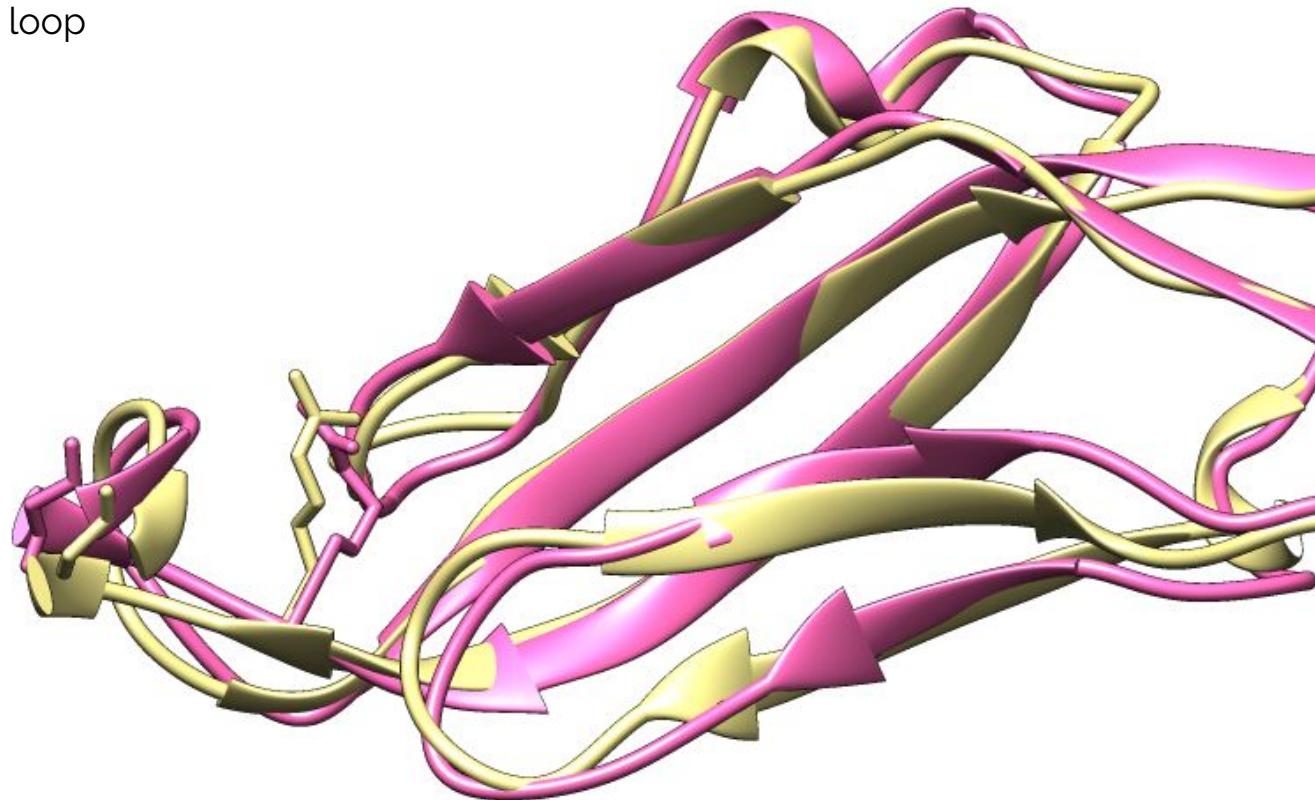
b strand



ANNEX

Cross-neutralizing

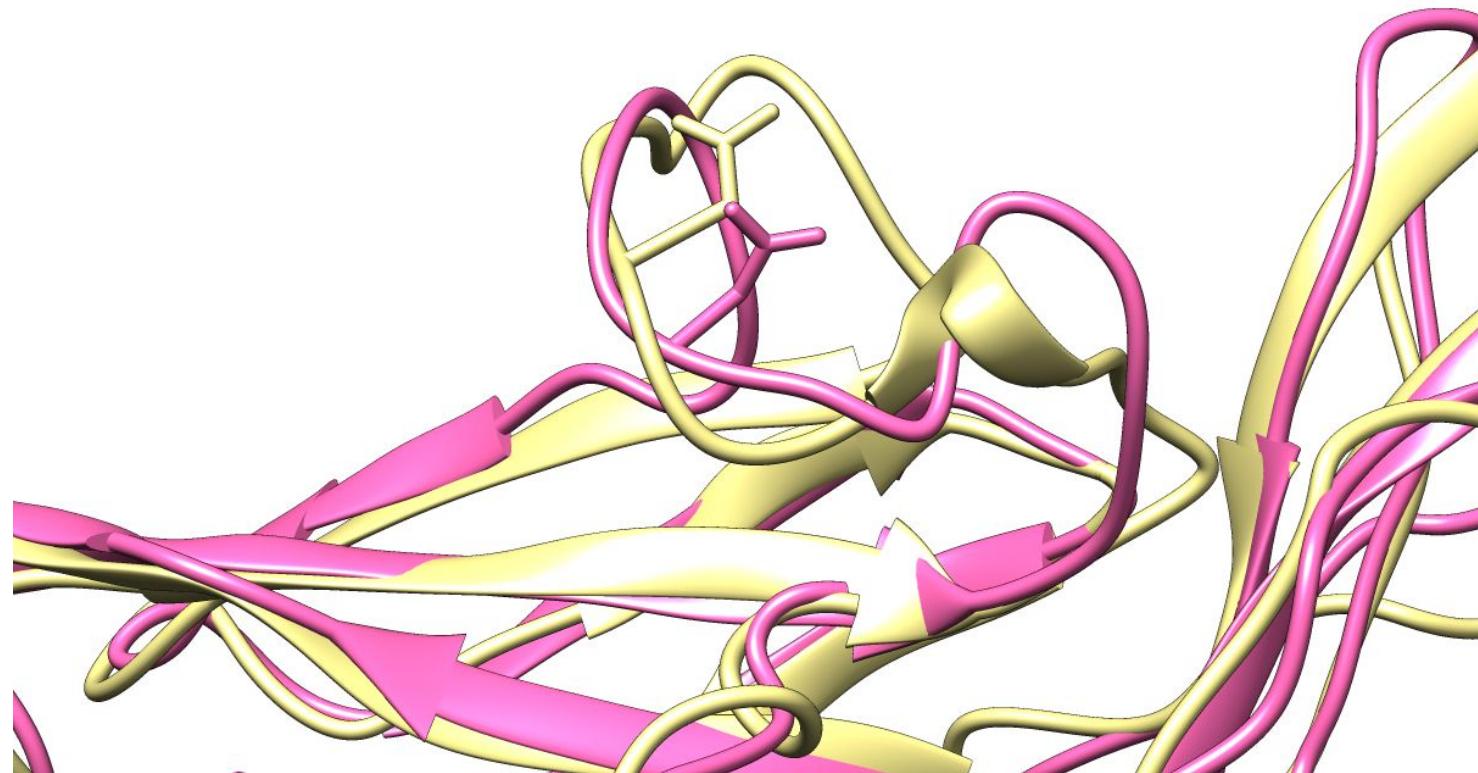
Fusion loop



ANNEX

Cross-neutralizing

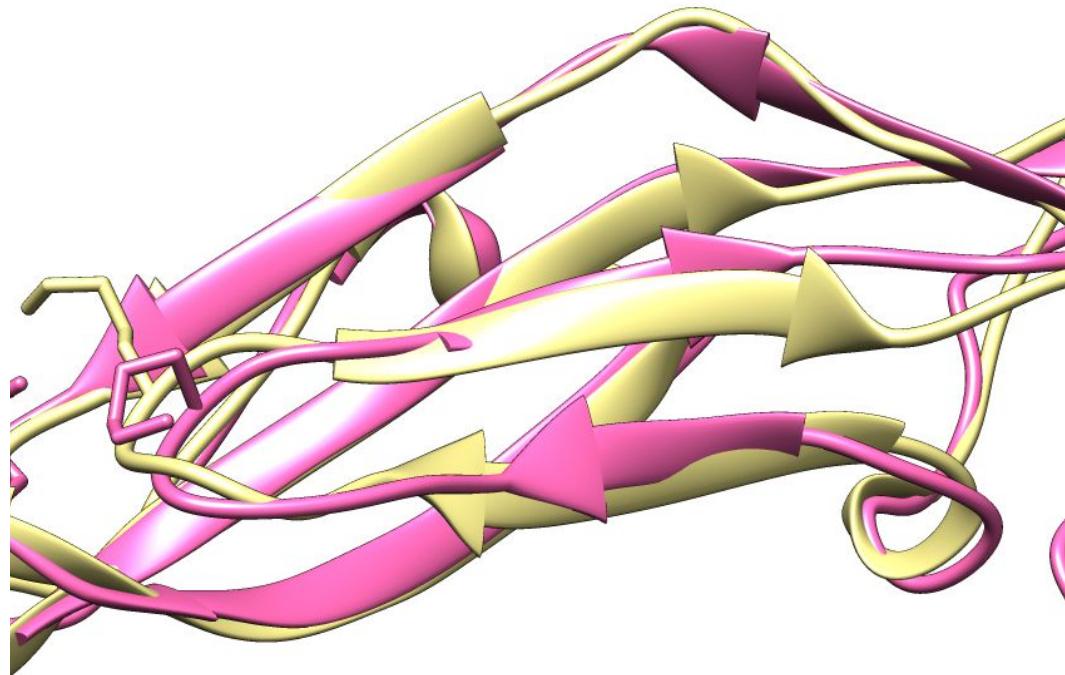
Glycosylation loop



ANNEX

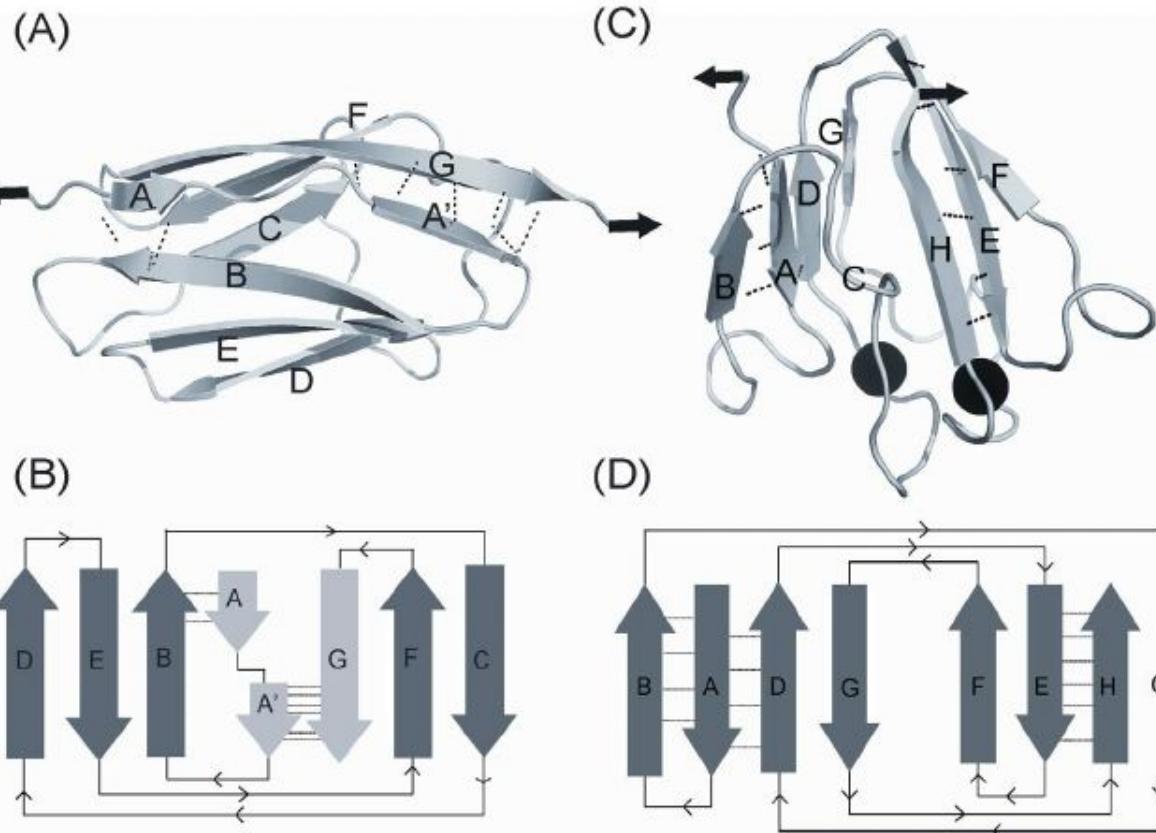
Cross-neutralizing

i-j loop



ANNEX

Beta-sandwich topological diagram



Ramanujam, V., Kotamarthi, H. and Ainavarapu, S. (2014). Ca²⁺ Binding Enhanced Mechanical Stability of an Archaeal Crystallin. *PLoS ONE*, 9(4), p.e94513.