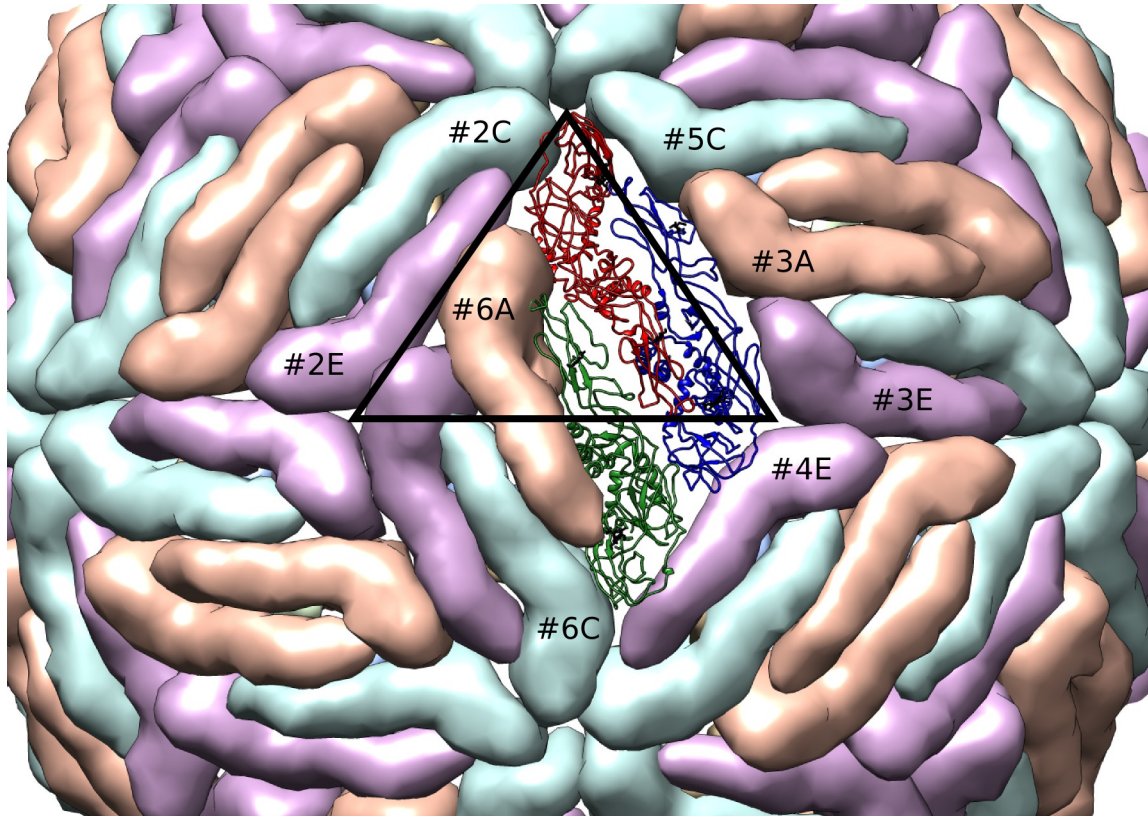


## Supplemental Materials

**List 1.** Residues possibly involved in interaction based on 8Å distance cutoff between C $\alpha$  atoms, below shows list of all residues regardless of its charge and polarity, however main text Table 1 only counts the residues that are charged (Arg, Lys, Asp, Glu, marked “C”) or polar (Asn, Gln, His, marked “H”). Symbol “#” shows the asymmetric unit number with chain ID (refer to below figure), followed by amino acid residue name and its sequence position. Chains A, C, E are E proteins, whereas B, D, F are M proteins. In the figure, the ribbon models show asymmetric unit #0 (chain A – green, chain C – red, chain E - blue), the symmetry-related molecules are shown as clay models. The triangle marks an icosahedral asymmetric unit.



## DENV1 intra-dimeric contacts of two independent dimers in a raft

#0C ARG 2 C  
#0C GLY 5  
#0C ILE 6  
#0C SER 7  
#0C GLY 28  
#0C GLU 62 C  
#0C ARG 99 C  
#0C GLY 100  
#0C TRP 101  
#0C GLY 102  
#0C ASN 103 H  
#0C GLY 104  
#0C GLY 106  
#0C LEU 107  
#0C PHE 108  
#0C GLY 109  
#0C GLN 150 H  
#0C VAL 151  
#0C GLY 152  
#0C ASN 153 H  
#0C GLU 154 C  
#0C HIS 244 H  
#0C ALA 245  
#0C LEU 253  
#0C GLY 254  
#0C SER 255  
#0C GLN 256 H  
#0C GLU 257 C  
#0C GLY 258  
#0C ALA 259  
#0C MET 260  
#0C HIS 261 H  
#0C LYS 310 C  
#0C ALA 313  
#0C GLU 314 C  
#0C THR 315  
#0C GLN 316 H  
#0E VAL 4  
#0E GLY 5  
#0E ILE 6  
#0E GLY 28  
#0E GLU 62 C  
#0E ASP 98 C  
#0E ARG 99 C  
#0E GLY 100  
#0E TRP 101  
#0E GLY 102  
#0E ASN 103 H  
#0E GLY 106  
#0E LEU 107  
#0E PHE 108  
#0E GLY 109  
#0E GLN 150 H  
#0E VAL 151  
#0E GLY 152  
#0E ASN 153 H  
#0E HIS 244 H

#0E LEU 253  
#0E GLY 254  
#0E SER 255  
#0E GLN 256 H  
#0E GLU 257 C  
#0E GLY 258  
#0E ALA 259  
#0E MET 260  
#0E HIS 261 H  
#0E LYS 310 C  
#0E ALA 313  
#0E GLU 314 C  
#0E THR 315  
#0E GLN 316 H  
#0A GLY 5  
#0A ILE 6  
#0A HIS 27 H  
#0A GLY 28  
#0A ASP 98 C  
#0A ARG 99 C  
#0A GLY 100  
#0A TRP 101  
#0A GLY 102  
#0A GLY 106  
#0A LEU 107  
#0A PHE 108  
#0A GLY 109  
#0A VAL 151  
#0A GLY 152  
#0A ASN 153 H  
#0A HIS 244 H  
#0A ALA 245  
#0A LEU 253  
#0A GLY 254  
#0A SER 255  
#0A GLN 256 H  
#0A GLU 257 C  
#0A GLY 258  
#0A ALA 259  
#0A MET 260  
#0A HIS 261 H  
#0A THR 262  
#0A LYS 310 C  
#0A GLU 311 C  
#0A ALA 313  
#0A GLU 314 C  
#0A THR 315  
#0A GLN 316 H  
#6A GLY 5  
#6A ILE 6  
#6A HIS 27 H  
#6A GLY 28  
#6A ASP 98 C  
#6A ARG 99 C  
#6A GLY 100  
#6A TRP 101  
#6A GLY 102  
#6A GLY 106  
#6A LEU 107  
#6A PHE 108  
#6A GLY 109  
#6A VAL 151

#6A GLY 152  
#6A ASN 153 H  
#6A HIS 244 H  
#6A ALA 245  
#6A LEU 253  
#6A GLY 254  
#6A SER 255  
#6A GLN 256 H  
#6A GLU 257 C  
#6A GLY 258  
#6A ALA 259  
#6A MET 260  
#6A HIS 261 H  
#6A THR 262  
#6A LYS 310 C  
#6A GLU 311 C  
#6A ALA 313  
#6A GLU 314 C  
#6A THR 315  
#6A GLN 316 H

**DENV1 inter-dimeric residues that may be involved in contacts in an asymmetric unit (covers half of a raft)**

#0A ALA 54  
#0A ILE 55  
#0A LEU 56  
#0A ARG 57 C  
#0A GLN 77 H  
#0A GLY 78  
#0A GLU 79 C  
#0A THR 81  
#0A LEU 82  
#0A VAL 83  
#0A GLN 86 H  
#0A ASP 87 C  
#0A THR 88  
#0A THR 165  
#0A PRO 166  
#0A GLN 167 H  
#0A ALA 168  
#0A PRO 169  
#0A ASP 184 C  
#0A CYS 185  
#0A SER 186  
#0A PRO 187  
#0A ARG 188 C  
#0A SER 222  
#0A GLY 223  
#0A ALA 224  
#0A SER 225  
#0A GLN 228 H  
#0A THR 230  
#0C ALA 54  
#0C LEU 56  
#0C ARG 57 C  
#0C ARG 73 C  
#0C THR 76  
#0C GLN 77 H  
#0C GLY 78  
#0C GLU 79 C  
#0C ALA 80  
#0C THR 81

#0C VAL 83  
#0C GLN 86 H  
#0C ASP 87 C  
#0C THR 88  
#0C GLU 133 C  
#0C PRO 166  
#0C GLN 167 H  
#0C ALA 168  
#0C PRO 169  
#0C CYS 185  
#0C SER 186  
#0C PRO 187  
#0C ARG 188 C  
#0C THR 189  
#0C SER 222  
#0C GLY 223  
#0C ALA 224  
#0C SER 225  
#0C SER 227  
#0C GLU 229 C  
#0C THR 230  
#0E GLU 342 C  
#0E GLU 375 C  
#0E SER 376  
#0E LEU 387  
#0E LYS 388 C  
#0E LEU 389  
#0E SER 390  
#0E TRP 391  
#6A GLU 311 C  
#6A VAL 312  
#6A ALA 313  
#6A GLU 375 C  
#6A TYR 377  
#6A LEU 387  
#6A LYS 388 C  
#6A LEU 389  
#6A SER 390  
#6A TRP 391  
#6A PHE 392

#### DENV1 residues that may be involved in inter-raft contacts

#0A THR 18  
#0A ASP 37 C  
#0A ASP 290 C  
#0A LYS 291 C  
#0A THR 293  
#0A LEU 294  
#0A LYS 295 C  
#0A GLY 296  
#0A VAL 297  
#0A SER 298  
#0A VAL 300  
#0A MET 301  
#0A LYS 334 C  
#0A ILE 335  
#0A PRO 336  
#0A SER 338  
#0A ALA 382  
#0A GLY 383  
#0C ALA 17

#0C THR 18  
#0C GLY 19  
#0C MET 289  
#0C ASP 290 C  
#0C VAL 297  
#0C SER 298  
#0C TYR 299  
#0C VAL 300  
#0C MET 301  
#0C THR 303  
#0C SER 305  
#0C PHE 306  
#0C LYS 307 C  
#0C LEU 308  
#0C GLU 309 C  
#0C GLU 311 C  
#0C TYR 326  
#0C PRO 336  
#0C GLU 342 C  
#0C LYS 343 C  
#0C GLY 344  
#0C VAL 345  
#0C ILE 346  
#0C GLN 347 H  
#0C ALA 382  
#0C GLY 383  
#0C GLU 384 C  
#0C LYS 385 C  
#0C ALA 386  
#0C LEU 387  
#0E ASP 37 C  
#0E LEU 56  
#0E THR 76  
#0E GLN 77 H  
#0E THR 81  
#0E LEU 82  
#0E VAL 83  
#0E GLU 84 C  
#0E GLN 86 H  
#0E ASP 87 C  
#0E THR 88  
#0E ASN 89 H  
#0E GLN 167 H  
#0E THR 170  
#0E SER 171  
#0E GLU 172 C  
#0E GLN 174 H  
#0E SER 222  
#0E GLY 223  
#0E ALA 224  
#0E THR 226  
#0E SER 227  
#0E GLN 228 H  
#0E GLU 229 C  
#0E THR 230  
#0E VAL 297  
#0E SER 298  
#0E PRO 336  
#0E SER 338  
#3A THR 18  
#3A ASP 37 C  
#3A ASP 290 C

#3A LYS 291 C  
#3A THR 293  
#3A LEU 294  
#3A LYS 295 C  
#3A GLY 296  
#3A VAL 297  
#3A SER 298  
#3A VAL 300  
#3A MET 301  
#3A LYS 334 C  
#3A ILE 335  
#3A PRO 336  
#3A SER 338  
#3A ALA 382  
#3A GLY 383  
#3E ASP 37 C  
#3E VAL 297  
#3E SER 298  
#3E PRO 336  
#3E SER 338  
#5C ALA 17  
#5C THR 18  
#5C GLY 19  
#5C MET 289  
#5C ASP 290 C  
#5C VAL 297  
#5C SER 298  
#5C TYR 299  
#5C VAL 300  
#5C MET 301  
#5C THR 303  
#5C PRO 336  
#5C VAL 345  
#5C ILE 346  
#5C GLN 347 H  
#5C ALA 382  
#5C GLY 383  
#5C GLU 384 C  
#4E LEU 56  
#4E THR 81  
#4E LEU 82  
#4E VAL 83  
#4E GLU 84 C  
#4E GLN 86 H  
#4E ASP 87 C  
#4E THR 88  
#4E ASN 89 H  
#4E GLN 167 H  
#4E THR 170  
#4E SER 171  
#4E GLU 172 C  
#4E GLN 174 H  
#4E SER 222  
#4E GLY 223  
#4E ALA 224  
#4E THR 226  
#4E SER 227  
#4E GLN 228 H  
#4E GLU 229 C  
#4E THR 230  
#2C SER 305  
#2C PHE 306

#2C LYS 307 C  
#2C LEU 308  
#2C GLU 309 C  
#2C GLU 311 C  
#2C TYR 326  
#2C GLU 342 C  
#2C LYS 343 C  
#2C GLY 344  
#2C GLU 384 C  
#2C LYS 385 C  
#2C ALA 386  
#2C LEU 387  
#2E THR 76  
#2E GLN 77 H

**DENV1 residues that may be involved in contacts between E and M proteins in one asymmetric unit (half a raft)**

#0A GLU 26 C  
#0A HIS 27 H  
#0A GLY 28  
#0A LEU 191  
#0A ASP 192 C  
#0A TRP 206  
#0A VAL 208  
#0A HIS 209 H  
#0A TRP 212  
#0A LEU 216  
#0A PRO 217  
#0A LEU 218  
#0A GLN 256 H  
#0A ALA 259  
#0A MET 260  
#0A HIS 261 H  
#0A THR 262  
#0A ALA 263  
#0A LEU 264  
#0A THR 265  
#0A GLY 266  
#0A ALA 267  
#0A THR 268  
#0A GLU 269 C  
#0A ALA 280  
#0A GLY 281  
#0A ILE 414  
#0A LEU 415  
#0A GLY 416  
#0A VAL 446  
#0A LEU 447  
#0A SER 449  
#0A GLY 450  
#0A VAL 451  
#0A SER 452  
#0A THR 454  
#0A GLN 494 H  
#0A ALA 495  
#0C GLU 26 C  
#0C GLY 28  
#0C VAL 208  
#0C HIS 209 H  
#0C TRP 212  
#0C LEU 216  
#0C PRO 217



#0C LEU 218  
#0C GLN 256 H  
#0C ALA 259  
#0C MET 260  
#0C THR 262  
#0C ALA 263  
#0C LEU 264  
#0C THR 265  
#0C GLY 266  
#0C ALA 267  
#0C THR 268  
#0C GLU 269 C  
#0C ALA 280  
#0C GLY 281  
#0C ILE 414  
#0C LEU 415  
#0C GLY 416  
#0C SER 449  
#0C GLY 450  
#0C VAL 451  
#0C SER 452  
#0C TRP 453  
#0C THR 454  
#0C ALA 495  
#0E GLU 26 C  
#0E TRP 206  
#0E VAL 208  
#0E HIS 209 H  
#0E TRP 212  
#0E LEU 216  
#0E PRO 217  
#0E ALA 259  
#0E MET 260  
#0E HIS 261 H  
#0E THR 262  
#0E ALA 263  
#0E LEU 264  
#0E THR 265  
#0E GLY 266  
#0E ALA 267  
#0E THR 268  
#0E GLU 269 C  
#0E ALA 280  
#0E GLY 281  
#0E ARG 411 C  
#0E ILE 414  
#0E LEU 415  
#0E VAL 446  
#0E SER 449  
#0E GLY 450  
#0E VAL 451  
#0E SER 452  
#0E TRP 453  
#0E THR 454  
#0E GLN 494 H  
#0E ALA 495  
#0B SER 1  
#0B VAL 2  
#0B ALA 3  
#0B LEU 4  
#0B ALA 5  
#0B PRO 6

#0B HIS 7 H  
#0B VAL 8  
#0B GLY 9  
#0B LEU 10  
#0B GLY 11  
#0B LEU 12  
#0B GLU 13 C  
#0B THR 14  
#0B ARG 15 C  
#0B THR 16  
#0B GLU 17 C  
#0B THR 18  
#0B TRP 19  
#0B MET 20  
#0B SER 21  
#0B SER 22  
#0B ALA 25  
#0B TRP 26  
#0D SER 1  
#0D VAL 2  
#0D ALA 3  
#0D LEU 4  
#0D ALA 5  
#0D PRO 6  
#0D HIS 7 H  
#0D VAL 8  
#0D GLY 9  
#0D LEU 10  
#0D GLY 11  
#0D LEU 12  
#0D GLU 13 C  
#0D THR 14  
#0D ARG 15 C  
#0D THR 16  
#0D GLU 17 C  
#0D THR 18  
#0D TRP 19  
#0D MET 20  
#0D SER 21  
#0D GLU 23 C  
#0D GLY 24  
#0D ALA 25  
#0F SER 1  
#0F VAL 2  
#0F ALA 3  
#0F LEU 4  
#0F ALA 5  
#0F PRO 6  
#0F HIS 7 H  
#0F VAL 8  
#0F GLY 9  
#0F LEU 10  
#0F GLY 11  
#0F LEU 12  
#0F GLU 13 C  
#0F THR 14  
#0F ARG 15 C  
#0F THR 16  
#0F GLU 17 C  
#0F THR 18  
#0F TRP 19  
#0F MET 20

#OF SER 21  
#OF GLY 24  
#OF ALA 25

## DENV2 intra-dimeric contacts of two independent dimers in a raft

#0C ILE 4  
#0C GLY 5  
#0C ILE 6  
#0C SER 7  
#0C GLY 28  
#0C ASP 98 C  
#0C ARG 99 C  
#0C GLY 100  
#0C TRP 101  
#0C GLY 102  
#0C ASN 103 H  
#0C GLY 106  
#0C LEU 107  
#0C PHE 108  
#0C GLY 109  
#0C LYS 110 C  
#0C VAL 151  
#0C GLY 152  
#0C ASN 153 H  
#0C PRO 243  
#0C HIS 244 H  
#0C ALA 245  
#0C LEU 253  
#0C GLY 254  
#0C SER 255  
#0C GLN 256 H  
#0C GLU 257 C  
#0C GLY 258  
#0C ALA 259  
#0C HIS 261 H  
#0C THR 262  
#0C ALA 313  
#0C GLU 314 C  
#0C THR 315  
#0C GLN 316 H  
#0E ILE 4  
#0E GLY 5  
#0E ILE 6  
#0E SER 7  
#0E HIS 27 H  
#0E GLY 28  
#0E ASP 98 C  
#0E ARG 99 C  
#0E GLY 100  
#0E TRP 101  
#0E GLY 102  
#0E LEU 107  
#0E PHE 108  
#0E GLY 109  
#0E LYS 110 C  
#0E ALA 150  
#0E VAL 151  
#0E GLY 152  
#0E ASN 153 H  
#0E HIS 244 H  
#0E ALA 245  
#0E LEU 253  
#0E GLY 254  
#0E SER 255  
#0E GLN 256 H

#0E GLU 257 C  
#0E GLY 258  
#0E ALA 259  
#0E HIS 261 H  
#0E THR 262  
#0E GLU 269 C  
#0E ALA 313  
#0E GLU 314 C  
#0E THR 315  
#0E GLN 316 H  
#0E HIS 317 H  
#0A GLY 5  
#0A ILE 6  
#0A GLY 28  
#0A ASP 98 C  
#0A GLY 100  
#0A TRP 101  
#0A GLY 102  
#0A ASN 103 H  
#0A LEU 107  
#0A PHE 108  
#0A GLY 109  
#0A ALA 150  
#0A VAL 151  
#0A GLY 152  
#0A ASN 153 H  
#0A PRO 243  
#0A HIS 244 H  
#0A LEU 253  
#0A GLY 254  
#0A SER 255  
#0A GLN 256 H  
#0A GLU 257 C  
#0A GLY 258  
#0A ALA 259  
#0A MET 260  
#0A HIS 261 H  
#0A GLU 269 C  
#0A ALA 313  
#0A GLU 314 C  
#0A THR 315  
#6A GLY 5  
#6A ILE 6  
#6A GLY 28  
#6A ASP 98 C  
#6A GLY 100  
#6A TRP 101  
#6A GLY 102  
#6A ASN 103 H  
#6A LEU 107  
#6A PHE 108  
#6A GLY 109  
#6A ALA 150  
#6A VAL 151  
#6A GLY 152  
#6A ASN 153 H  
#6A PRO 243  
#6A HIS 244 H  
#6A LEU 253  
#6A GLY 254  
#6A SER 255  
#6A GLN 256 H

#6A GLU 257 C  
#6A GLY 258  
#6A ALA 259  
#6A MET 260  
#6A HIS 261 H  
#6A GLU 269 C  
#6A ALA 313  
#6A GLU 314 C  
#6A THR 315

**DENV2 inter-dimeric residues that may be involved in contacts in an asymmetric unit (covers half of a raft)**

#0A ALA 54  
#0A LEU 56  
#0A ARG 57 C  
#0A GLN 77 H  
#0A GLY 78  
#0A GLU 79 C  
#0A PRO 80  
#0A SER 81  
#0A ASN 83 H  
#0A GLN 86 H  
#0A ASP 87 C  
#0A LYS 88 C  
#0A ARG 89 C  
#0A GLU 133 C  
#0A PRO 166  
#0A GLN 167 H  
#0A SER 168  
#0A SER 169  
#0A ILE 170  
#0A SER 186  
#0A PRO 187  
#0A ARG 188 C  
#0A THR 189  
#0A PRO 222  
#0A GLY 223  
#0A ALA 224  
#0A GLY 228  
#0A ASN 230 H  
#0C ALA 54  
#0C THR 55  
#0C LEU 56  
#0C ARG 57 C  
#0C GLN 77 H  
#0C GLY 78  
#0C GLU 79 C  
#0C PRO 80  
#0C SER 81  
#0C ASN 83 H  
#0C GLN 86 H  
#0C ASP 87 C  
#0C LYS 88 C  
#0C ARG 89 C  
#0C VAL 129  
#0C GLU 133 C  
#0C PRO 166  
#0C GLN 167 H  
#0C SER 168  
#0C SER 169  
#0C ILE 170  
#0C GLU 184 C

#0C SER 186  
#0C ARG 188 C  
#0C THR 189  
#0C PRO 222  
#0C GLY 223  
#0C ALA 224  
#0C GLN 227 H  
#0C ASN 230 H  
#0E GLU 311 C  
#0E ASP 375 C  
#0E LEU 387  
#0E LYS 388 C  
#0E LEU 389  
#0E ASN 390 H  
#0E TRP 391  
#0E PHE 392  
#6A GLU 311 C  
#6A GLU 343 C  
#6A LEU 387  
#6A LYS 388 C  
#6A LEU 389  
#6A ASN 390 H  
#6A TRP 391  
#6A PHE 392

#### **DENV2 residues that may be involved in inter-raft contacts**

#0A ASN 37 H  
#0A ASP 290 C  
#0A LYS 291 C  
#0A GLN 293 H  
#0A LEU 294  
#0A MET 297  
#0A SER 298  
#0A SER 300  
#0A MET 301  
#0A PRO 336  
#0A LYS 344 C  
#0A ARG 345 C  
#0A GLY 381  
#0A VAL 382  
#0C GLY 17  
#0C GLY 18  
#0C SER 19  
#0C MET 297  
#0C SER 298  
#0C TYR 299  
#0C SER 300  
#0C MET 301  
#0C THR 303  
#0C LYS 305 C  
#0C PHE 306  
#0C LYS 307 C  
#0C VAL 308  
#0C VAL 309  
#0C LYS 310 C  
#0C GLU 311 C  
#0C VAL 324  
#0C GLN 325 H  
#0C LEU 342  
#0C GLU 343 C  
#0C LYS 344 C

#0C ARG 345 C  
#0C HIS 346 H  
#0C VAL 347  
#0C VAL 382  
#0C GLU 383 C  
#0C PRO 384  
#0C GLY 385  
#0C GLN 386 H  
#0C LEU 387  
#0E THR 76  
#0E GLN 77 H  
#0E GLY 78  
#0E GLU 79 C  
#0E ASN 83 H  
#0E GLN 86 H  
#0E ASP 87 C  
#0E GLN 131 H  
#0E THR 171  
#0E GLU 172 C  
#0E ALA 173  
#0E GLU 174 C  
#0E GLY 223  
#0E ALA 224  
#0E ASP 225 C  
#0E GLN 227 H  
#0E GLY 228  
#0E ASN 230 H  
#0E MET 297  
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#3A LYS 291 C  
#3A GLN 293 H  
#3A LEU 294  
#3A MET 297  
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#3A SER 300  
#3A MET 301  
#3A PRO 336  
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#3A ARG 345 C  
#3A GLY 381  
#3A VAL 382  
#3E MET 297  
#3E SER 298  
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#5C GLY 18  
#5C SER 19  
#5C MET 297  
#5C SER 298  
#5C TYR 299  
#5C SER 300  
#5C MET 301  
#5C THR 303  
#5C ARG 345 C  
#5C HIS 346 H  
#5C VAL 347  
#5C VAL 382  
#5C GLU 383 C  
#4E GLY 78



#4E GLU 79 C  
#4E ASN 83 H  
#4E GLN 86 H  
#4E ASP 87 C  
#4E GLN 131 H  
#4E THR 171  
#4E GLU 172 C  
#4E ALA 173  
#4E GLU 174 C  
#4E GLY 223  
#4E ALA 224  
#4E ASP 225 C  
#4E GLN 227 H  
#4E GLY 228  
#4E ASN 230 H  
#2C LYS 305 C  
#2C PHE 306  
#2C LYS 307 C  
#2C VAL 308  
#2C VAL 309  
#2C LYS 310 C  
#2C GLU 311 C  
#2C VAL 324  
#2C GLN 325 H  
#2C LEU 342  
#2C GLU 343 C  
#2C LYS 344 C  
#2C GLU 383 C  
#2C PRO 384  
#2C GLY 385  
#2C GLN 386 H  
#2C LEU 387  
#2E THR 76  
#2E GLN 77 H

**DENV2 residues that may be involved in contacts between E and M proteins in one asymmetric unit (half a raft)**

#0A GLU 26 C  
#0A HIS 27 H  
#0A GLY 28  
#0A VAL 208  
#0A HIS 209 H  
#0A LEU 216  
#0A PRO 217  
#0A LEU 218  
#0A GLN 256 H  
#0A ALA 259  
#0A MET 260  
#0A HIS 261 H  
#0A THR 262  
#0A ALA 263  
#0A LEU 264  
#0A THR 265  
#0A GLY 266  
#0A ALA 267  
#0A THR 268  
#0A GLU 269 C  
#0A THR 280  
#0A ILE 414  
#0A SER 449  
#0A GLY 450  
#0A VAL 451

#0A SER 452  
#0A TRP 453  
#0A GLN 494 H  
#0A ALA 495  
#0C GLU 26 C  
#0C GLY 28  
#0C VAL 208  
#0C HIS 209 H  
#0C TRP 212  
#0C LEU 216  
#0C PRO 217  
#0C LEU 218  
#0C THR 236  
#0C ALA 259  
#0C MET 260  
#0C THR 262  
#0C ALA 263  
#0C LEU 264  
#0C THR 265  
#0C GLY 266  
#0C ALA 267  
#0C THR 268  
#0C GLU 269 C  
#0C THR 280  
#0C GLY 281  
#0C ILE 414  
#0C SER 449  
#0C GLY 450  
#0C VAL 451  
#0C SER 452  
#0C TRP 453  
#0C ILE 454  
#0C VAL 493  
#0C GLN 494 H  
#0C ALA 495  
#0E GLY 28  
#0E VAL 208  
#0E HIS 209 H  
#0E TRP 212  
#0E LEU 216  
#0E PRO 217  
#0E LEU 218  
#0E GLN 256 H  
#0E ALA 259  
#0E MET 260  
#0E THR 262  
#0E ALA 263  
#0E LEU 264  
#0E THR 265  
#0E GLY 266  
#0E ALA 267  
#0E THR 268  
#0E GLU 269 C  
#0E THR 280  
#0E GLY 281  
#0E ILE 414  
#0E LEU 415  
#0E SER 449  
#0E GLY 450  
#0E VAL 451  
#0E SER 452  
#0E TRP 453

#0E VAL 493  
#0E GLN 494 H  
#0E ALA 495  
#0B SER 1  
#0B VAL 2  
#0B ALA 3  
#0B LEU 4  
#0B VAL 5  
#0B PRO 6  
#0B HIS 7 H  
#0B VAL 8  
#0B GLY 9  
#0B MET 10  
#0B GLY 11  
#0B LEU 12  
#0B GLU 13 C  
#0B THR 14  
#0B ALA 15  
#0B THR 16  
#0B GLU 17 C  
#0B THR 18  
#0B TRP 19  
#0B MET 20  
#0B SER 21  
#0B GLY 24  
#0B ALA 25  
#0D SER 1  
#0D VAL 2  
#0D ALA 3  
#0D LEU 4  
#0D VAL 5  
#0D PRO 6  
#0D HIS 7 H  
#0D VAL 8  
#0D GLY 9  
#0D MET 10  
#0D GLY 11  
#0D LEU 12  
#0D GLU 13 C  
#0D THR 14  
#0D ALA 15  
#0D THR 16  
#0D GLU 17 C  
#0D THR 18  
#0D TRP 19  
#0D MET 20  
#0D SER 21  
#0D GLY 24  
#0D ALA 25  
#0D ALA 29  
#0F SER 1  
#0F VAL 2  
#0F ALA 3  
#0F LEU 4  
#0F VAL 5  
#0F PRO 6  
#0F HIS 7 H  
#0F VAL 8  
#0F GLY 9  
#0F MET 10  
#0F GLY 11  
#0F LEU 12

#0F GLU 13 C  
#0F THR 14  
#0F ALA 15  
#0F THR 16  
#0F GLU 17 C  
#0F THR 18  
#0F TRP 19  
#0F MET 20  
#0F SER 21  
#0F SER 22  
#0F ALA 25

## DENV4 intra-dimeric contacts of two independent dimers in a raft

#0C ARG 2 C  
#0C VAL 4  
#0C GLY 5  
#0C VAL 6  
#0C GLY 7  
#0C GLY 28  
#0C ASP 98 C  
#0C ARG 99 C  
#0C GLY 100  
#0C TRP 101  
#0C GLY 102  
#0C ASN 103 H  
#0C GLY 106  
#0C LEU 107  
#0C PHE 108  
#0C GLY 109  
#0C ALA 150  
#0C VAL 151  
#0C GLY 152  
#0C ASN 153 H  
#0C ASP 154 C  
#0C HIS 244 H  
#0C LEU 253  
#0C GLY 254  
#0C SER 255  
#0C GLN 256 H  
#0C GLU 257 C  
#0C GLY 258  
#0C ALA 259  
#0C MET 260  
#0C HIS 261 H  
#0C SER 262  
#0C ALA 280  
#0C MET 312  
#0C ALA 313  
#0C GLU 314 C  
#0C THR 315  
#0C GLN 316 H  
#0E VAL 4  
#0E VAL 6  
#0E GLY 7  
#0E GLY 28  
#0E ASP 98 C  
#0E ARG 99 C  
#0E GLY 100  
#0E TRP 101  
#0E GLY 102  
#0E ASN 103 H  
#0E GLY 104  
#0E LEU 107  
#0E PHE 108  
#0E GLY 109  
#0E ALA 150  
#0E VAL 151  
#0E GLY 152  
#0E ASN 153 H  
#0E HIS 244 H  
#0E ALA 245  
#0E LEU 253  
#0E GLY 254

#0E SER 255  
#0E GLN 256 H  
#0E GLU 257 C  
#0E GLY 258  
#0E ALA 259  
#0E HIS 261 H  
#0E LYS 310 C  
#0E ALA 313  
#0E GLU 314 C  
#0E THR 315  
#0E GLN 316 H  
#0A GLY 5  
#0A VAL 6  
#0A GLY 28  
#0A ASP 98 C  
#0A GLY 100  
#0A TRP 101  
#0A GLY 102  
#0A ASN 103 H  
#0A GLY 106  
#0A LEU 107  
#0A PHE 108  
#0A GLY 109  
#0A HIS 149 H  
#0A ALA 150  
#0A VAL 151  
#0A GLY 152  
#0A ASN 153 H  
#0A HIS 244 H  
#0A ALA 245  
#0A LEU 253  
#0A GLY 254  
#0A SER 255  
#0A GLN 256 H  
#0A GLU 257 C  
#0A GLY 258  
#0A ALA 259  
#0A MET 260  
#0A HIS 261 H  
#0A MET 312  
#0A ALA 313  
#0A GLU 314 C  
#0A THR 315  
#0A GLN 316 H  
#6A GLY 5  
#6A VAL 6  
#6A GLY 28  
#6A ASP 98 C  
#6A GLY 100  
#6A TRP 101  
#6A GLY 102  
#6A ASN 103 H  
#6A GLY 106  
#6A LEU 107  
#6A PHE 108  
#6A GLY 109  
#6A HIS 149 H  
#6A ALA 150  
#6A VAL 151  
#6A GLY 152  
#6A ASN 153 H  
#6A HIS 244 H

#6A ALA 245  
#6A LEU 253  
#6A GLY 254  
#6A SER 255  
#6A GLN 256 H  
#6A GLU 257 C  
#6A GLY 258  
#6A ALA 259  
#6A MET 260  
#6A HIS 261 H  
#6A MET 312  
#6A ALA 313  
#6A GLU 314 C  
#6A THR 315  
#6A GLN 316 H

**DENV4 inter-dimeric residues that may be involved in contacts in an asymmetric unit (covers half of a raft)**

#0A ALA 54  
#0A LEU 55  
#0A LEU 56  
#0A ARG 57 C  
#0A GLN 77 H  
#0A GLY 78  
#0A PRO 80  
#0A TYR 81  
#0A GLU 85 C  
#0A GLN 86 H  
#0A ASP 87 C  
#0A GLN 88 H  
#0A LEU 129  
#0A PRO 166  
#0A ARG 167 C  
#0A SER 168  
#0A PRO 169  
#0A SER 170  
#0A GLU 186 C  
#0A ARG 188 C  
#0A ALA 222  
#0A GLY 223  
#0A ALA 224  
#0A ASP 225 C  
#0A HIS 230 H  
#0C ALA 54  
#0C LEU 56  
#0C ARG 57 C  
#0C THR 76  
#0C GLN 77 H  
#0C GLY 78  
#0C GLU 79 C  
#0C PRO 80  
#0C TYR 81  
#0C GLU 85 C  
#0C GLN 86 H  
#0C ASP 87 C  
#0C GLN 88 H  
#0C PRO 166  
#0C ARG 167 C  
#0C SER 168  
#0C PRO 169  
#0C SER 170  
#0C ASP 184 C

#0C GLU 186 C  
#0C ARG 188 C  
#0C SER 189  
#0C ALA 222  
#0C GLY 223  
#0C ALA 224  
#0E ASP 375 C  
#0E SER 376  
#0E LEU 387  
#0E THR 388  
#0E LEU 389  
#0E HIS 390 H  
#0E PHE 392  
#6A GLU 311 C  
#6A ASN 343 H  
#6A ASP 375 C  
#6A LEU 387  
#6A THR 388  
#6A LEU 389  
#6A HIS 390 H  
#6A TRP 391  
#6A PHE 392  
#6A ARG 393 C  
#6A LYS 394 C

#### **DENV4 residues that may be involved in inter-raft contacts**

#0A GLY 37  
#0A GLU 290 C  
#0A LYS 291 C  
#0A ARG 293 C  
#0A ILE 294  
#0A LYS 295 C  
#0A MET 297  
#0A SER 298  
#0A THR 300  
#0A MET 301  
#0A SER 303  
#0A LYS 334 C  
#0A PRO 336  
#0A GLY 381  
#0C GLY 17  
#0C GLY 18  
#0C ALA 19  
#0C MET 297  
#0C SER 298  
#0C TYR 299  
#0C THR 300  
#0C MET 301  
#0C SER 303  
#0C LYS 305 C  
#0C PHE 306  
#0C SER 307  
#0C ILE 308  
#0C ASP 309 C  
#0C VAL 324  
#0C LYS 325 C  
#0C PRO 336  
#0C ASN 343 H  
#0C LYS 344 C  
#0C LYS 346 C  
#0C VAL 347



#0C VAL 382  
#0C GLY 383  
#0C GLU 384 C  
#0C SER 385  
#0C ALA 386  
#0C LEU 387  
#0E THR 76  
#0E GLN 77 H  
#0E LYS 83 C  
#0E GLU 84 C  
#0E GLN 86 H  
#0E ASP 87 C  
#0E GLN 88 H  
#0E GLN 89 H  
#0E GLU 133 C  
#0E ARG 167 C  
#0E VAL 171  
#0E GLU 172 C  
#0E VAL 173  
#0E ALA 222  
#0E GLY 223  
#0E ALA 224  
#0E ASP 225 C  
#0E GLU 228 C  
#0E VAL 229  
#0E HIS 230 H  
#0E MET 297  
#0E SER 298  
#0E PRO 336  
#0E GLU 338 C  
#0E GLU 345 C  
#2C LYS 305 C  
#2C PHE 306  
#2C SER 307  
#2C ILE 308  
#2C ASP 309 C  
#2C VAL 324  
#2C LYS 325 C  
#2C ASN 343 H  
#2C LYS 344 C  
#2C GLY 383  
#2C GLU 384 C  
#2C SER 385  
#2C ALA 386  
#2C LEU 387  
#2E THR 76  
#2E GLN 77 H  
#3A GLY 37  
#3A GLU 290 C  
#3A LYS 291 C  
#3A ARG 293 C  
#3A ILE 294  
#3A LYS 295 C  
#3A MET 297  
#3A SER 298  
#3A THR 300  
#3A MET 301  
#3A SER 303  
#3A LYS 334 C  
#3A PRO 336  
#3A GLY 381  
#3E MET 297

#3E SER 298  
#3E PRO 336  
#3E GLU 338 C  
#3E GLU 345 C  
#6E LYS 83 C  
#6E GLU 84 C  
#6E GLN 86 H  
#6E ASP 87 C  
#6E GLN 88 H  
#6E GLN 89 H  
#6E GLU 133 C  
#6E ARG 167 C  
#6E VAL 171  
#6E GLU 172 C  
#6E VAL 173  
#6E ALA 222  
#6E GLY 223  
#6E ALA 224  
#6E ASP 225 C  
#6E GLU 228 C  
#6E VAL 229  
#6E HIS 230 H  
#5C GLY 17  
#5C GLY 18  
#5C ALA 19  
#5C MET 297  
#5C SER 298  
#5C TYR 299  
#5C THR 300  
#5C MET 301  
#5C SER 303  
#5C PRO 336  
#5C LYS 346 C  
#5C VAL 347  
#5C VAL 382  
#5C GLY 383  
#5C GLU 384 C

**DENV4 residues that may be involved in contacts between E and M proteins in one asymmetric unit (half a raft)**

#0A GLU 26 C  
#0A HIS 27 H  
#0A GLY 28  
#0A VAL 208  
#0A HIS 209 H  
#0A TRP 212  
#0A LEU 216  
#0A PRO 217  
#0A LEU 218  
#0A GLN 256 H  
#0A ALA 259  
#0A MET 260  
#0A HIS 261 H  
#0A SER 262  
#0A ALA 263  
#0A LEU 264  
#0A ALA 265  
#0A GLY 266  
#0A ALA 267  
#0A THR 268  
#0A GLU 269 C  
#0A PHE 279

#0A ALA 280  
#0A GLY 281  
#0A ALA 413  
#0A ILE 414  
#0A LEU 415  
#0A THR 446  
#0A GLY 449  
#0A GLY 450  
#0A VAL 451  
#0A SER 452  
#0A TRP 453  
#0A VAL 493  
#0A GLN 494 H  
#0A ALA 495  
#0C GLU 26 C  
#0C HIS 27 H  
#0C GLY 28  
#0C GLY 29  
#0C ASP 192 C  
#0C TRP 206  
#0C VAL 208  
#0C HIS 209 H  
#0C TRP 212  
#0C LEU 216  
#0C PRO 217  
#0C LEU 218  
#0C ALA 259  
#0C MET 260  
#0C SER 262  
#0C ALA 263  
#0C LEU 264  
#0C ALA 265  
#0C GLY 266  
#0C ALA 267  
#0C THR 268  
#0C GLU 269 C  
#0C PHE 279  
#0C ALA 280  
#0C GLY 281  
#0C ALA 413  
#0C ILE 414  
#0C LEU 415  
#0C PHE 448  
#0C GLY 449  
#0C GLY 450  
#0C VAL 451  
#0C SER 452  
#0C TRP 453  
#0C TRP 465  
#0C GLN 494 H  
#0C ALA 495  
#0E GLY 28  
#0E ASP 192 C  
#0E TRP 206  
#0E VAL 208  
#0E HIS 209 H  
#0E TRP 212  
#0E LEU 216  
#0E PRO 217  
#0E LEU 218  
#0E GLN 256 H  
#0E GLY 258

#0E ALA 259  
#0E MET 260  
#0E HIS 261 H  
#0E SER 262  
#0E ALA 263  
#0E LEU 264  
#0E ALA 265  
#0E GLY 266  
#0E ALA 267  
#0E THR 268  
#0E GLU 269 C  
#0E PHE 279  
#0E ALA 280  
#0E GLY 281  
#0E ALA 413  
#0E ILE 414  
#0E THR 446  
#0E GLY 449  
#0E GLY 450  
#0E VAL 451  
#0E SER 452  
#0E TRP 453  
#0E GLN 494 H  
#0E ALA 495  
#0B SER 1  
#0B VAL 2  
#0B ALA 3  
#0B LEU 4  
#0B THR 5  
#0B PRO 6  
#0B HIS 7 H  
#0B SER 8  
#0B GLY 9  
#0B MET 10  
#0B GLY 11  
#0B LEU 12  
#0B GLU 13 C  
#0B THR 14  
#0B ARG 15 C  
#0B ALA 16  
#0B GLU 17 C  
#0B THR 18  
#0B TRP 19  
#0B MET 20  
#0B SER 21  
#0B GLY 24  
#0D SER 1  
#0D VAL 2  
#0D ALA 3  
#0D LEU 4  
#0D THR 5  
#0D PRO 6  
#0D HIS 7 H  
#0D SER 8  
#0D GLY 9  
#0D MET 10  
#0D GLY 11  
#0D LEU 12  
#0D GLU 13 C  
#0D THR 14  
#0D ARG 15 C  
#0D ALA 16

#0D GLU 17 C  
#0D THR 18  
#0D TRP 19  
#0D MET 20  
#0D SER 21  
#0D SER 22  
#0D ALA 25  
#0D ILE 58  
#0F SER 1  
#0F VAL 2  
#0F ALA 3  
#0F LEU 4  
#0F THR 5  
#0F PRO 6  
#0F HIS 7 H  
#0F SER 8  
#0F GLY 9  
#0F MET 10  
#0F GLY 11  
#0F LEU 12  
#0F GLU 13 C  
#0F THR 14  
#0F ARG 15 C  
#0F ALA 16  
#0F GLU 17 C  
#0F THR 18  
#0F TRP 19  
#0F MET 20  
#0F SER 21  
#0F SER 22  
#0F GLY 24  
#0F ALA 25  
#0F TRP 26