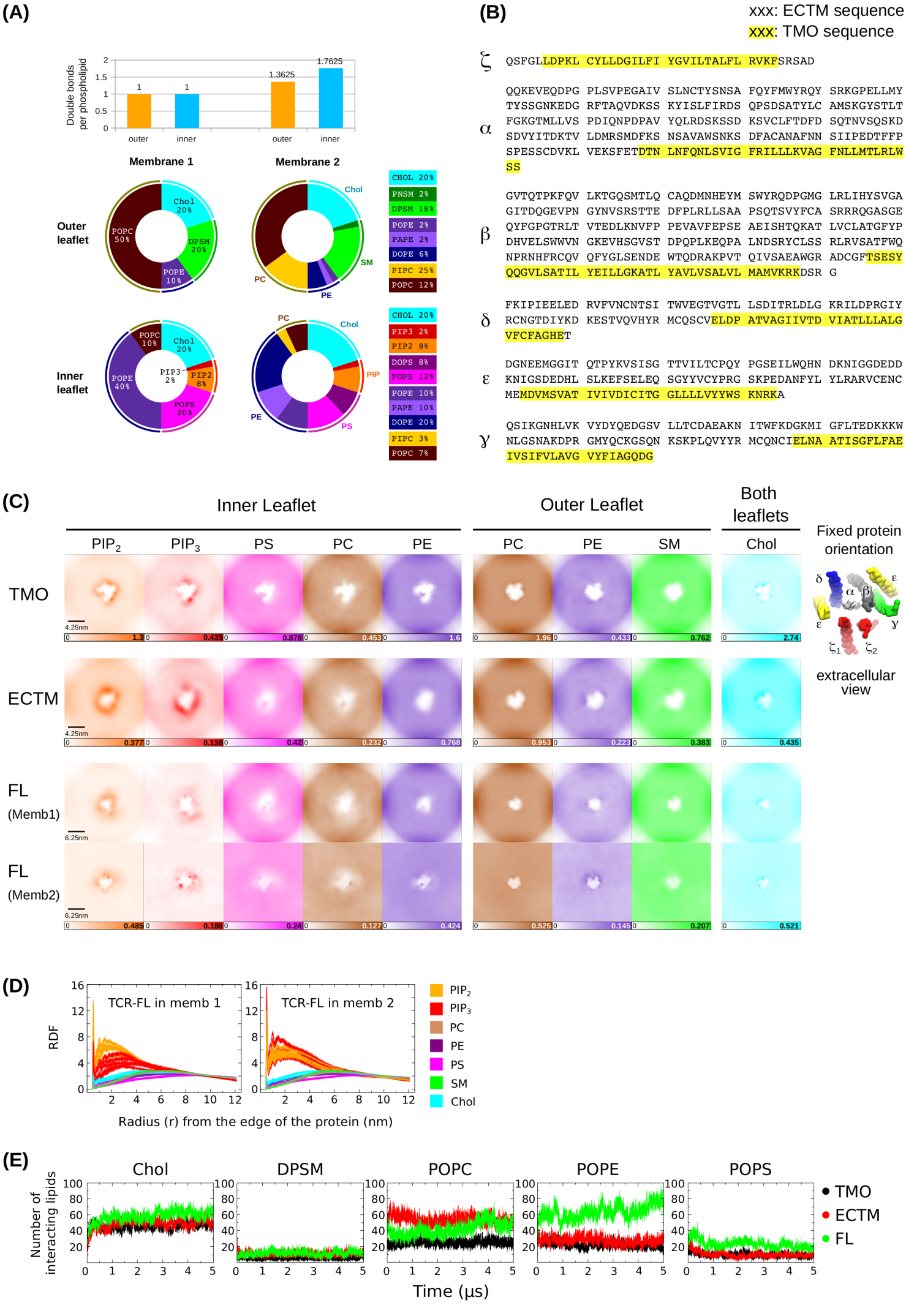
(A)
Double bonds per phospholipid
outer
inner
outer
inner
1
1
1.3625
1.7625
Membrane 1
Membrane 2
Outer leaflet
Inner leaflet
Chol 20%
DPSM 20%
POPE 10%
POPC 50%
Chol
SM
PE
PC
PIP
PS
POPC 10%
PIP3 2%
PIP2 8%
POPS 20%
POPE 40%
CHOL 20%
PNSM 2%
DPSM 18%
POPE 2%
PAPE 2%
DOPE 6%
PIPC 25%
POPC 12%
CHOL 20%
PIP3 2%
PIP2 8%
DOPS 8%
POPS 12%
POPE 10%
PAPE 10%
DOPE 20%
PIPC 3%
POPC 7%
(B)
xxx: ECTM sequence
XXX: TMO sequence
ζ QSFGLLDPKL CYLLDGILFI YGVILTALFL RVKFSRSAD
α QQKEVEQDPG PLSVPEGAIV SLNCTYSNSA FQYFMWYRQY SRKGPELLMY TYSSGNKEDG RFTAQVDKSS KYISLFIRDS QPSDSATYLC AMSKGYSTLT FGKGTMLLVS PDIQNPDPAV YQLRDSKSSD KSVCLFTDFD SQTNVSQSKD SDVYITDKTV LDMRSMDFKS NSAVAWSNKS DFACANAFNN SIIPEDTFFP SPESSCDVKL VEKSFETDTN LNFQNLSVIG FRILLLKVAG FNLLMTLRLW SS
β GVTQTPKFQV LKTGQSMTLQ CAQDMNHEYM SWYRQDPGMG LRLIHYSVGA GITDQGEVPN GYNVSRSTTE DFPLRLLSAA PSQTSVYFCA SRRRQGASGE QYFGPGTRLT VTEDLKNVFP PEVAVFEPSE AEISHTQKAT LVCLATGFYP DHVELSWWVN GKEVHSGVST DPQPLKEQPA LNDSRYCLSS RLRVSATFWQ NPRNHFRCQV QFYGLSENDE WTQDRAKPVT QIVSAEAWGR ADCGFTSESY QQGVLSATIL YEILLGKATL YAVLVSALVL MAMVKRKDSR G
δ FKIPIEELED RVFVNCNTSI TWVEGTVGTL LSDITRLDLG KRILDPRGIY RCNGTDIYKD KESTVQVHYR MCQSCVELDP ATVAGIIVTD VIATLLLALG VFCFAGHET
ε DGNEEMGGIT QTPYKVSISG TTVILTCPQY PGSEILWQHN DKNIGGDEDD KNIGSDEDHL SLKEFSELEQ SGYYVCYPRG SKPEDANFYL YLRARVCENC MEMDVMSVAT IVIVDICITG GLLLLVYYWS KNRKA
γ QSIKGNHLVK VYDYQEDGSV LLTCDAEAKN ITWFKDGKMI GFLTEDKKKW NLGSNAKDPR GMYQCKGSQN KSKPLQVYYR MCQNCIELNA ATISGFLFAE IVSIFVLAVG VYFIAGQDG
(C)
Inner Leaflet
Outer Leaflet
Both leaflets
PIP2
PIP3
PS
PC
PE
PC
PE
SM
Chol
Fixed protein orientation
TMO
ECTM
FL (Memb1)
FL (Memb2)
4.25nm
6.25nm
extracellular view
(D)
TCR-FL in memb 1
TCR-FL in memb 2
RDF
Radius (r) from the edge of the protein (nm)
PIP2
PIP3
PC
PE
PS
SM
Chol
(E)
Chol
DPSM
POPC
POPE
POPS
Number of interacting lipids
Time (μs)
TMO
ECTM
FL