Supporting Information: Development and use of an atomistic CHARMM-based forcefield for peptoid simulation

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PEPTOID FORCEFIELD CHARMM PARAMETER FILE

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!!This file contains lines to be added to an existing CHARMM
!!par_all22_prot.prm parameter file in order to transform it
!!into an MFTOID parameter file for peptoids  DTM
!!Note that the file will need to be modified if both
!!peptoids and peptides are to be used in the same system.
!!To rectify this, one must rename the CA and N atoms of the
!!backbone (along with all references to these atoms) so as
!!to not clash with the peptide backbone carbon alpha and N.

BONDS
CT2  TC    250.000     1.4900 !PEPTOID DTM
CT3  TC    250.000     1.4900 !PEPTOID DTM
NH1  TC    370.000     1.3450 !PEPTOID DTM
O    TC    620.000     1.2300 ! PEPTOID DTM

ANGLES
CT2  NH1  TC     50.000   120.0000 !PEPTOID DTM
CT3  NH1  TC     50.000   120.0000 !PEPTOID DTM
CT3  NH1  CT3    50.000   120.0000 !PEPTOID DTM
CT3  NH1  CT2    50.000   120.0000 !PEPTOID DTM
HA   CT3  TC     33.000    109.50   30.00   2.16300 !PEPTOID DTM
HB   CT2  TC     50.000   109.5000 !PEPTOID DTM
NH1  TC   CT2    80.000   116.5000 !PEPTOID DTM
NH1  TC   CT3    80.000   116.5000 !PEPTOID DTM
NH1  CT2  TC     50.000   107.0000 !PEPTOID DTM
O    TC   CT2    80.000   121.0000 !PEPTOID DTM
O    TC   CT3    80.000   121.0000 !PEPTOID DTM
O    TC   NH1    80.000   122.5000 !PEPTOID DTM
HC   NH1  HC     39.000   106.5000 !DTM trimer
CT2  NH1  CT2    50.000   120.0000 !DTM trimer
HC   NH1  CT2   30.000    109.50   20.00   2.07400 !DTM trimer
CT2  CT2  CA     51.800   107.5000 !DTM trimer



DIHEDRALS
TC   CT2  NH1  CT3      1.8000  1     0.00 !PEPTOID DTM
               ! "di-peptoid" vaccum quantum DTM
TC   CT2  NH1  TC       0.2000  1   180.00 !PEPTOID DTM
CT1  TC   NH1  CT1      0.0000  1     0.00 !DTM  DMA
               ! DMA cis/trans same energy (DTM)
CT1  TC   NH1  CT1      1.8000  2   180.00 !DTM DMA
               ! DMA cis/trans barrier (DTM)
```

```
CT2  TC   NH1  CT3      0.0000  1     0.00 !PEPTOID DTM DMA
CT2  TC   NH1  CT3      1.8000  2   180.00 !PEPTOID DTM DMA
CT2  TC   NH1  CT3      0.0000  1     0.00 !PEPTOID DTM DMA
CT2  TC   NH1  CT3      1.8000  2   180.00 !PEPTOID DTM DMA
O    TC   NH1  CT3      2.5000  2   180.00 ! DMA DTM
O    TC   NH1  CT2      2.5000  2   180.00 ! DMA DTM
CT3  TC   NH1  CT2      0.0000  1     0.00 !PEPTOID DTM DMA
CT3  TC   NH1  CT2      1.8000  2   180.00 !PEPTOID DTM DMA
CT3  TC   NH1  CT3      0.0000  1     0.00 !PEPTOID DTM DMA
CT3  TC   NH1  CT3      1.8000  2   180.00 !PEPTOID DTM DMA
HA   CT3  NH1  TC       0.0000  3     0.00 !PEPTOID DTM
HA   CT3  NH1  CT2      0.0000  3     0.00 !PEPTOID DTM
HA   CT3  NH1  CT3      0.0000  3     0.00 !PEPTOID DTM
HB   CT2  NH1  TC       0.0000  1     0.00 !PEPTOID DTM
HB   CT2  NH1  CT3      0.0000  1     0.00 !PEPTOID DTM
NH1  TC   CT2  HB       0.0000  1     0.00 !PEPTOID DTM
NH1  TC   CT2  NH1      0.6000  1     0.00 !PEPTOID DTM
NH1  TC   CT3  HA       0.0000  3     0.00 !PEPTOID DTM
O    TC   CT2  HB       0.0000  1     0.00 !PEPTOID DTM
O    TC   CT2  NH1      0.0000  1     0.00 !PEPTOID DTM
O    TC   CT3  HA       0.0000  3   180.00 !PEPTOID DTM
O    X    X    TC    120.0000        0      0.0000 !PEPTOID DTM
NH1  X    X    CT3    20.0000        0      0.0000 !PEPTOID DTM
X    CT2  NH1  X        0.1000  3     0.00 !DTM NNER

IMPROPER
NH1  X    X    CT3    20.0000        0      0.0000 !PEPTOID DTM
O    X    X    TC    120.0000        0      0.0000 !PEPTOID DTM

NONBONDED
TC     0.000000  -0.110000     1.700000 !
                ! DMA pure liquid ! DTM
```

PEPTOID FORCEFIELD CHARMM TOPOLOGY FILE

```
!!This file conatines the lines to be added to an existing CHARMM
!!top_all22_prot.rtf topology file in order to transform it
!!into an MFTOID topology file for peptoids. Note there are no CMAP
!!terms specified for any of the peptoid residues here, as the MFTOID
!!forcefield does not use CMAP correstions.  DTM

MASS   122 TC    12.01100 C ! peptoid/DMA carbonyl DTM

DEFA FIRS NNER LAST CTER

RESI TC7         0.00 ! Sarcosine Dipeptoid with/out CMAP term!! DTM
GROUP
ATOM CL   CT3   -0.27  !
ATOM HL1  HA     0.09  !                    HB2
ATOM HL2  HA     0.09  !   HL1      OL     |          OR            HR1
ATOM HL3  HA     0.09  !      \     || HB1-CB-HB3 HA1 ||           /
GROUP                  !       \    ||     |       |   ||          /
ATOM CLP  TC     0.51  !  HL2---CL--CLP----NL----CA--CRP---NR---CR----HR2
ATOM OL   O     -0.51  !       /                  |        |      \
GROUP                  !      /                 HA2  HD1--CD--HD3 \
ATOM NL   NH1   -0.42  !   HL3                             |        HR3
ATOM CA   CT2    0.03  !                                 HD2
ATOM HA1  HB     0.09  !
ATOM HA2  HB     0.09  !
ATOM CB   CT3   -0.06  !
ATOM HB1  HA     0.09  !
ATOM HB2  HA     0.09  !
ATOM HB3  HA     0.09  !
GROUP                  !
ATOM CRP  TC     0.51  !
ATOM OR   O     -0.51  !
GROUP                  !
ATOM NR   NH1   -0.42  !
ATOM CD   CT3   -0.06  !
ATOM HD1  HA     0.09  !
ATOM HD2  HA     0.09  !
ATOM HD3  HA     0.09  !
ATOM CR   CT3   -0.06  !
ATOM HR1  HA     0.09  !
ATOM HR2  HA     0.09  !
ATOM HR3  HA     0.09  !

BOND CL  CLP   CLP NL    NL  CA
```

```
BOND CA  CRP   CRP NR    NR  CR
DOUBLE  CLP OL    CRP OR
BOND NL  CB    NR  CD
BOND CA  HA1   CA  HA2
BOND CL  HL1   CL  HL2   CL  HL3
BOND CB  HB1   CB  HB2   CB  HB3
BOND CD  HD1   CD  HD2   CD  HD3
BOND CR  HR1   CR  HR2   CR  HR3
IMPR CLP CL NL OL    NL CLP CA CB
IMPR CRP CA NR OR    NR CRP CR CD

patch first none last none


RESI FPHE    !!Phenyl sidechain peptoid residue
GROUP
ATOM N    NH1   -0.42
ATOM CA   CT2    0.03
ATOM HA1  HB     0.09
ATOM HA2  HB     0.09
ATOM CB   CT2    0.03
ATOM HB1  HA     0.09
ATOM HB2  HA     0.09
GROUP
ATOM C    TC     0.51
ATOM O    O     -0.51
GROUP
ATOM CG   CA      0.00
GROUP
ATOM CG1  CT2    -0.18
ATOM HG1  HA      0.09
ATOM HG2  HA      0.09
GROUP
ATOM CD1  CA     -0.115
ATOM HD1  HP      0.115
GROUP
ATOM CE1  CA     -0.115
ATOM HE1  HP      0.115
GROUP
ATOM CZ   CA     -0.115
ATOM HZ   HP      0.115
GROUP
ATOM CD2  CA     -0.115
ATOM HD2  HP      0.115
GROUP
```

```
GROUP
ATOM CE2  CA     -0.115
ATOM HE2  HP      0.115

BOND N CA  CA C N CB  C  +N
BOND CA HA1  CA HA2
BOND CB HB1  CB HB2
BOND CG1 CB   CG1 CG CD2 CG  CE1 CD1
BOND CZ  CE2  CG1 HG1 CG1 HG2
BOND CD1 HD1  CD2 HD2  CE1 HE1
BOND CE2 HE2  CZ HZ
DOUBLE  C O CD1 CG  CZ CE1   CE2 CD2

IMPR N -C CA CB  C CA +N O

PRES NNER         1.00 ! standard N-terminus for peptoid
GROUP                  ! use in generate statement
ATOM HT1  HC     0.33
ATOM HT2  HC     0.33
ATOM N    NH1   -0.24
ATOM CA   CT2    0.11
ATOM HA1  HB     0.09
ATOM HA2  HB     0.09
ATOM CB   CT2    0.11
ATOM HB1  HA     0.09
ATOM HB2  HA     0.09
BOND HT1 N HT2 N
DONOR HT1 N
DONOR HT2 N
IC HT1  N    CA   C     0.0000  0.0000  180.0000  0.0000  0.0000
IC HT2  CA   *N   HT1   0.0000  0.0000  120.0000  0.0000  0.0000
```

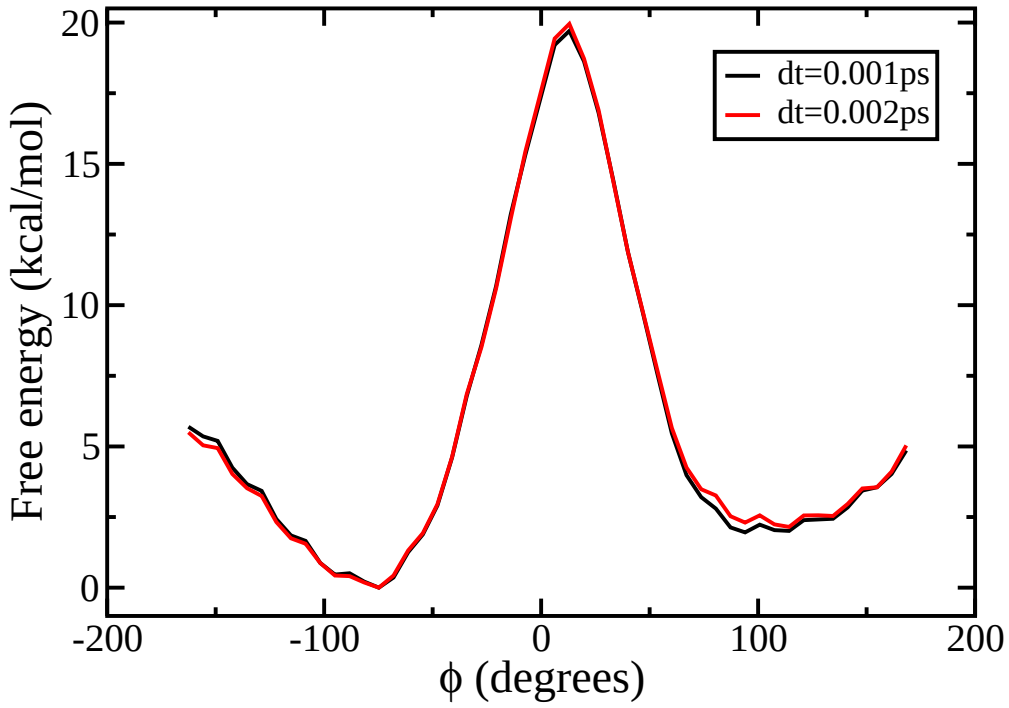

Figure S1: Simulations using both 1 and 2 fs integration timesteps resulted in similar sarcosine dipeptoid free energy profiles over a range of *phi*. These simulations are similar to those shown in Fig. 7a,right (gas phase, $\omega = 180°$ or *trans*), for only one value of ψ (160°). From the two profiles, it is evident that the timestep of 2 fs is acceptable for further simulation studies.

DIPOLE MOMENT

The dipole moment of a single minimized structure of DMA is compared to the experimental gas phase dipole moment. The structures were minimized first with a steepest descent algorithm for 500 steps, followed by an adopted basis Newton Raphson (ABNR) method for 6000 minimization steps. We compare the dipole moment of a minimized structure of DMA using our forcefield to its experimental gas phase value and find a scaling factor that is slightly smaller then that found for DMA described by CGENFF. These scaling factor which are $\mu^{DMA}_{mftoid}/\mu^{DMA}_{exp} = 4.38/3.70 = 1.18$ $\mu^{DMA}_{cgenff}/\mu^{DMA}_{exp} = 4.59/3.70 = 1.24$, represent another way to compare the dipole moments of DMA represented by our forcefield to experiment and to DMA represented by the CGENFF.