

Supporting Information

Development of Potent and Selective Inhibitors for Group VIA Calcium-Independent Phospholipase A₂ Guided by Molecular Dynamics and Structure-Activity Relationships

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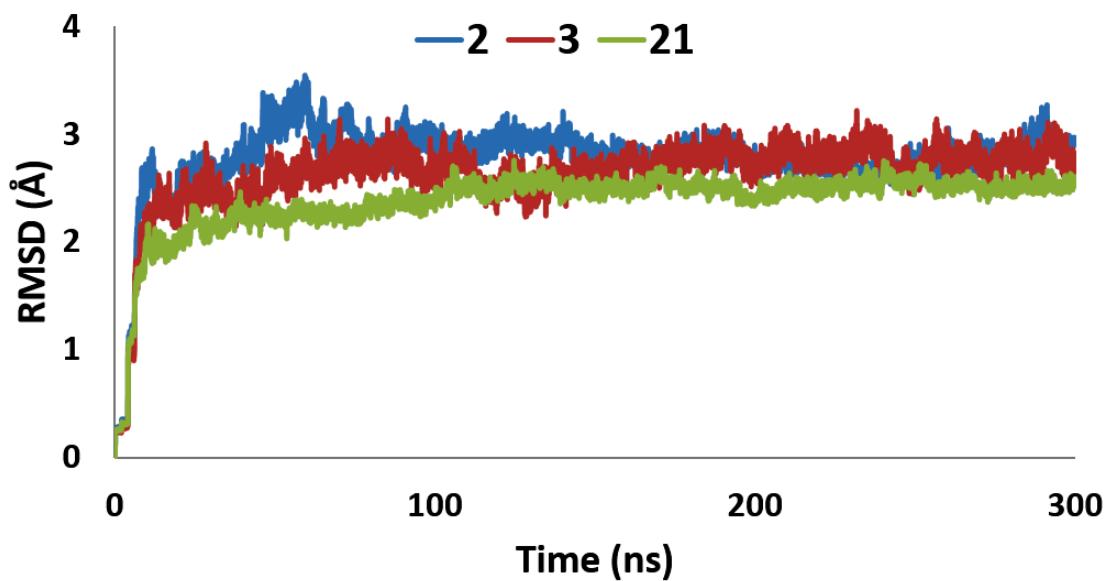


Fig. S1. RMSD of the enzyme backbone atoms over the time course of the MD simulations. Blue and brown curves represent MD simulations on the GVIA iPLA₂-**2** and GVIA iPLA₂-**3** complexes, respectively. The green curve represents a MD simulation on the GIVA cPLA₂-**21** complex.

1. Toppar stream file for compound 2

```
RESI lig      0.000 ! param penalty= 137.000 ; charge penalty= 110.907
GROUP        ! CHARGE CH_PENALTY
ATOM C1    CG302  0.369 ! 85.312
ATOM C2    CG312  0.521 ! 110.907
ATOM C3    CG2O5  0.349 ! 82.596
ATOM C4    CG321 -0.140 ! 4.453
ATOM C5    CG321 -0.181 ! 0.600
ATOM C6    CG321 -0.181 ! 0.000
ATOM C7    CG321 -0.184 ! 0.000
ATOM O8    OG2D3 -0.481 ! 5.758
ATOM C9    CG2R61 0.002 ! 0.000
ATOM C10   CG2R61 -0.117 ! 0.000
ATOM C11   CG2R61 -0.110 ! 0.000
ATOM C12   CG2R61 0.219 ! 0.000
ATOM C13   CG2R61 -0.110 ! 0.000
ATOM C14   CG2R61 -0.117 ! 0.000
ATOM O15   OG301 -0.391 ! 0.000
ATOM C16   CG331 -0.100 ! 0.000
ATOM F17   FGA3 -0.142 ! 6.074
ATOM F18   FGA3 -0.142 ! 6.074
ATOM F19   FGA3 -0.142 ! 6.074
ATOM F20   FGA2 -0.186 ! 16.594
ATOM F21   FGA2 -0.186 ! 16.594
ATOM H22   HGA2  0.090 ! 0.600
ATOM H23   HGA2  0.090 ! 0.600
ATOM H24   HGA2  0.090 ! 0.000
ATOM H25   HGA2  0.090 ! 0.000
ATOM H26   HGA2  0.090 ! 0.000
ATOM H27   HGA2  0.090 ! 0.000
ATOM H28   HGA2  0.090 ! 0.000
ATOM H29   HGA2  0.090 ! 0.000
ATOM H30   HGR61 0.115 ! 0.000
ATOM H31   HGR61 0.115 ! 0.000
ATOM H32   HGR61 0.115 ! 0.000
ATOM H33   HGR61 0.115 ! 0.000
ATOM H34   HGA3  0.090 ! 0.000
```

ATOM H35 HGA3 0.090 ! 0.000
ATOM H36 HGA3 0.090 ! 0.000

BOND C9 C14

BOND C9 C10

BOND C9 C7

BOND C7 H29

BOND C7 H28

BOND C7 C6

BOND C6 H27

BOND C6 H26

BOND C6 C5

BOND C5 H25

BOND C5 H24

BOND C5 C4

BOND C4 H23

BOND C4 H22

BOND C4 C3

BOND C3 O8

BOND C3 C2

BOND C2 F21

BOND C2 F20

BOND C2 C1

BOND C1 F19

BOND C1 F18

BOND C1 F17

BOND C10 H30

BOND C10 C11

BOND C11 H31

BOND C11 C12

BOND C12 O15

BOND C12 C13

BOND C13 H32

BOND C13 C14

BOND C14 H33

BOND O15 C16

BOND C16 H36

BOND C16 H35

BOND C16 H34

IMPR C3 C2 C4 O8

END

BONDS

CG2O5 CG312 330.00 1.5000 ! lig , from CG2O5 CG321, penalty= 55

CG302 CG312 250.00 1.5200 ! lig , from CG302 CG321, penalty= 55

ANGLES

CG312 CG2O5 CG321 35.00 115.60 ! lig , from CG321 CG2O5 CG321, penalty= 12

CG312 CG2O5 OG2D3 75.00 122.20 ! lig , from CG321 CG2O5 OG2D3, penalty= 12

CG312 CG302 FGA3 42.00 112.00 30.00 2.35700 ! lig , from CG321 CG302 FGA3, penalty= 12

CG2O5 CG312 CG302 60.00 113.80 ! lig , from CG2O5 CG321 CG321, penalty= 67

CG2O5 CG312 FGA2 50.00 115.00 30.00 2.35700 ! lig , from CG2R61 CG312 FGA2, penalty= 25

CG302 CG312 FGA2 50.00 112.00 30.00 2.35700 ! lig , from CG331 CG312 FGA2, penalty= 12.9

DIHEDRALS

CG321 CG2O5 CG312 CG302 0.7500 1 0.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 67

CG321 CG2O5 CG312 CG302 0.1800 2 180.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 67

CG321 CG2O5 CG312 CG302 0.0650 3 0.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 67

CG321 CG2O5 CG312 CG302 0.0300 6 0.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 67

CG321 CG2O5 CG312 FGA2 0.7500 1 0.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 98

CG321 CG2O5 CG312 FGA2 0.1800 2 180.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 98

CG321 CG2O5 CG312 FGA2 0.0650 3 0.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 98

CG321 CG2O5 CG312 FGA2 0.0300 6 0.00 ! lig , from CG321 CG2O5 CG321 CG321, penalty= 98

OG2D3 CG2O5 CG312 CG302 0.7500 1 180.00 ! lig , from OG2D3 CG2O5 CG321 CG321, penalty= 67

OG2D3 CG2O5 CG312 CG302 0.1800 2 180.00 ! lig , from OG2D3 CG2O5 CG321
CG321, penalty= 67

OG2D3 CG2O5 CG312 CG302 0.0650 3 180.00 ! lig , from OG2D3 CG2O5 CG321
CG321, penalty= 67

OG2D3 CG2O5 CG312 CG302 0.0300 6 0.00 ! lig , from OG2D3 CG2O5 CG321
CG321, penalty= 67

OG2D3 CG2O5 CG312 FGA2 0.0000 2 0.00 ! lig , from OG2D3 CG2O5 CG311
OG311, penalty= 89

CG312 CG2O5 CG321 CG321 0.7500 1 0.00 ! lig , from CG321 CG2O5 CG321
CG321, penalty= 12

CG312 CG2O5 CG321 CG321 0.1800 2 180.00 ! lig , from CG321 CG2O5 CG321
CG321, penalty= 12

CG312 CG2O5 CG321 CG321 0.0650 3 0.00 ! lig , from CG321 CG2O5 CG321
CG321, penalty= 12

CG312 CG2O5 CG321 CG321 0.0300 6 0.00 ! lig , from CG321 CG2O5 CG321
CG321, penalty= 12

CG312 CG2O5 CG321 HGA2 0.1000 3 0.00 ! lig , from CG321 CG2O5 CG321
HGA2, penalty= 12

FGA3 CG302 CG312 CG2O5 0.2500 3 0.00 ! lig , from FGA3 CG302 CG321 OG311,
penalty= 137

FGA3 CG302 CG312 FGA2 0.2500 3 0.00 ! lig , from FGA3 CG302 CG321 OG311,
penalty= 85

IMPROPERS

CG2O5 CG312 CG321 OG2D3 70.0000 0 0.00 ! lig , from CG2O5 CG321 CG321
OG2D3, penalty= 5.5

END of Toppar stream file for compound 2

2. Toppar stream file for compound 3

```
RESI lig      0.000 ! param penalty= 98.000 ; charge penalty= 81.690
GROUP        ! CHARGE CH_PENALTY
ATOM C1    CG2R61 0.001 ! 0.000
ATOM C2    CG321 -0.184 ! 0.000
ATOM C3    CG321 -0.181 ! 0.000
ATOM C4    CG321 -0.181 ! 0.600
ATOM C5    CG321 -0.140 ! 4.453
ATOM C6    CG2O5  0.349 ! 81.690
ATOM C7    CG3O2  0.422 ! 80.848
ATOM F8    FGA3  -0.110 ! 25.387
ATOM F9    FGA3  -0.110 ! 25.387
ATOM F10   FGA3  -0.110 ! 25.387
ATOM O11   OG2D3 -0.481 ! 5.758
ATOM C12   CG2R61 -0.119 ! 0.000
ATOM C13   CG2R61 0.009 ! 0.000
ATOM C14   CG2R61 -0.116 ! 0.000
ATOM C15   CG2R61 -0.116 ! 0.000
ATOM C16   CG2R61 -0.116 ! 0.000
ATOM C17   CG2R61 -0.116 ! 0.000
ATOM C18   CG2R61 0.004 ! 0.000
ATOM C19   CG2R61 -0.111 ! 0.000
ATOM C20   CG2R61 -0.119 ! 0.000
ATOM H21   HGA2   0.090 ! 0.000
ATOM H22   HGA2   0.090 ! 0.000
ATOM H23   HGA2   0.090 ! 0.000
ATOM H24   HGA2   0.090 ! 0.000
ATOM H25   HGA2   0.090 ! 0.000
ATOM H26   HGA2   0.090 ! 0.000
ATOM H27   HGA2   0.090 ! 0.600
ATOM H28   HGA2   0.090 ! 0.600
ATOM H29   HGR61  0.115 ! 0.000
ATOM H30   HGR61  0.115 ! 0.000
ATOM H31   HGR61  0.115 ! 0.000
ATOM H32   HGR61  0.115 ! 0.000
ATOM H33   HGR61  0.115 ! 0.000
ATOM H34   HGR61  0.115 ! 0.000
```

ATOM H35 HGR61 0.115 ! 0.000

BOND C1 C20

BOND C1 C12

BOND C1 C2

BOND C2 C3

BOND C3 C4

BOND C4 C5

BOND C5 C6

BOND C6 O11

BOND C6 C7

BOND C7 F10

BOND C7 F9

BOND C7 F8

BOND C12 C13

BOND C13 C18

BOND C13 C14

BOND C14 C15

BOND C15 C16

BOND C16 C17

BOND C17 C18

BOND C18 C19

BOND C19 C20

BOND C2 H21

BOND C2 H22

BOND C3 H23

BOND C3 H24

BOND C4 H25

BOND C4 H26

BOND C5 H27

BOND C5 H28

BOND C12 H29

BOND C14 H30

BOND C15 H31

BOND C16 H32

BOND C17 H33

BOND C19 H34

BOND C20 H35

IMPR C6 C7 C5 O11

END

BONDS

CG2O5 CG302 330.00 1.5000 ! lig , from CG2O5 CG321, penalty= 55

ANGLES

CG302 CG2O5 CG321 35.00 115.60 ! lig , from CG321 CG2O5 CG321, penalty= 12

CG302 CG2O5 OG2D3 75.00 122.20 ! lig , from CG321 CG2O5 OG2D3, penalty= 12

CG2O5 CG302 FGA3 50.00 115.00 30.00 2.35700 ! lig , from CG2R61 CG312

FGA2, penalty= 31.1

DIHEDRALS

CG321 CG2O5 CG302 FGA3 0.7500 1 0.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 98

CG321 CG2O5 CG302 FGA3 0.1800 2 180.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 98

CG321 CG2O5 CG302 FGA3 0.0650 3 0.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 98

CG321 CG2O5 CG302 FGA3 0.0300 6 0.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 98

OG2D3 CG2O5 CG302 FGA3 0.0000 2 0.00 ! lig , from OG2D3 CG2O5 CG311

OG311, penalty= 89

CG302 CG2O5 CG321 CG321 0.7500 1 0.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 12

CG302 CG2O5 CG321 CG321 0.1800 2 180.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 12

CG302 CG2O5 CG321 CG321 0.0650 3 0.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 12

CG302 CG2O5 CG321 CG321 0.0300 6 0.00 ! lig , from CG321 CG2O5 CG321

CG321, penalty= 12

CG302 CG2O5 CG321 HGA2 0.1000 3 0.00 ! lig , from CG321 CG2O5 CG321

HGA2, penalty= 12

IMPROBERS

CG2O5 CG302 CG321 OG2D3 70.0000 0 0.00 ! lig , from CG2O5 CG321 CG321

OG2D3, penalty= 5.5

END of Toppar stream file for compound 3

3. Toppar stream file for compound 21

```
RESI Lig      0.000 ! param penalty= 98.000 ; charge penalty= 81.874
GROUP        ! CHARGE CH_PENALTY
ATOM O1    OG2D3 -0.481 ! 5.758
ATOM C2    CG2O5  0.346 ! 81.874
ATOM C3    CG3O2  0.425 ! 80.614
ATOM F4    FGA3  -0.110 ! 25.387
ATOM F5    FGA3  -0.110 ! 25.387
ATOM F6    FGA3  -0.110 ! 25.387
ATOM C7    CG321 -0.140 ! 4.453
ATOM H8    HGA2   0.090 ! 0.600
ATOM H9    HGA2   0.090 ! 0.600
ATOM C10   CG321 -0.181 ! 0.600
ATOM H11   HGA2   0.090 ! 0.000
ATOM H12   HGA2   0.090 ! 0.000
ATOM C13   CG321 -0.181 ! 0.000
ATOM H14   HGA2   0.090 ! 0.000
ATOM H15   HGA2   0.090 ! 0.000
ATOM C16   CG321 -0.182 ! 0.000
ATOM C17   CG2R61 -0.002 ! 0.000
ATOM C18   CG2R61 -0.117 ! 0.000
ATOM H19   HGR61  0.115 ! 0.000
ATOM C20   CG2R61 -0.110 ! 0.000
ATOM H21   HGR61  0.115 ! 0.000
ATOM C22   CG2R67  0.000 ! 0.000
ATOM C23   CG2R67  0.000 ! 0.000
ATOM C24   CG2R61 -0.115 ! 0.000
ATOM H25   HGR61  0.115 ! 0.000
ATOM C26   CG2R61 -0.115 ! 0.000
ATOM H27   HGR61  0.115 ! 0.000
ATOM C28   CG2R61 -0.115 ! 0.000
ATOM H29   HGR61  0.115 ! 0.000
ATOM C30   CG2R61 -0.115 ! 0.000
ATOM H31   HGR61  0.115 ! 0.000
ATOM C32   CG2R61 -0.115 ! 0.000
ATOM H33   HGR61  0.115 ! 0.000
ATOM C34   CG2R61 -0.110 ! 0.000
```

ATOM H35 HGR61 0.115 ! 0.000
ATOM C36 CG2R61 -0.117 ! 0.000
ATOM H37 HGR61 0.115 ! 0.000
ATOM H38 HGA2 0.090 ! 0.000
ATOM H39 HGA2 0.090 ! 0.000

BOND C2 O1

BOND C2 C3

BOND C2 C7

BOND C3 F4

BOND C3 F5

BOND C3 F6

BOND C7 H8

BOND C7 H9

BOND C7 C10

BOND C10 H11

BOND C10 H12

BOND C10 C13

BOND C13 H14

BOND C13 H15

BOND C13 C16

BOND C16 C17

BOND C16 H38

BOND C16 H39

BOND C17 C18

BOND C17 C36

BOND C18 H19

BOND C18 C20

BOND C20 H21

BOND C20 C22

BOND C22 C23

BOND C22 C34

BOND C23 C24

BOND C23 C32

BOND C24 H25

BOND C24 C26

BOND C26 H27

BOND C26 C28

BOND C28 H29
BOND C28 C30
BOND C30 H31
BOND C30 C32
BOND C32 H33
BOND C34 H35
BOND C34 C36
BOND C36 H37
IMPR C2 C3 C7 O1
END

BONDS
CG2O5 CG302 330.00 1.5000 ! Lig , from CG2O5 CG321, penalty= 55

ANGLES
CG302 CG2O5 CG321 35.00 115.60 ! Lig , from CG321 CG2O5 CG321, penalty= 12
CG302 CG2O5 OG2D3 75.00 122.20 ! Lig , from CG321 CG2O5 OG2D3, penalty= 12
CG2O5 CG302 FGA3 50.00 115.00 30.00 2.35700 ! Lig , from CG2R61 CG312
FGA2, penalty= 31.1

DIHEDRALS
CG321 CG2O5 CG302 FGA3 0.7500 1 0.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 98
CG321 CG2O5 CG302 FGA3 0.1800 2 180.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 98
CG321 CG2O5 CG302 FGA3 0.0650 3 0.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 98
CG321 CG2O5 CG302 FGA3 0.0300 6 0.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 98
OG2D3 CG2O5 CG302 FGA3 0.0000 2 0.00 ! Lig , from OG2D3 CG2O5 CG311
OG311, penalty= 89
CG302 CG2O5 CG321 CG321 0.7500 1 0.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 12
CG302 CG2O5 CG321 CG321 0.1800 2 180.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 12
CG302 CG2O5 CG321 CG321 0.0650 3 0.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 12

CG302 CG2O5 CG321 CG321 0.0300 6 0.00 ! Lig , from CG321 CG2O5 CG321
CG321, penalty= 12
CG302 CG2O5 CG321 HGA2 0.1000 3 0.00 ! Lig , from CG321 CG2O5 CG321
HGA2, penalty= 12

IMPROPERs

CG2O5 CG302 CG321 OG2D3 70.0000 0 0.00 ! Lig , from CG2O5 CG321 CG321
OG2D3, penalty= 5.5

END of Toppar stream file for compound 21

4. Toppar stream file for compound 32

```
RESI lig      0.000 ! param penalty= 130.000 ; charge penalty= 68.453
GROUP        ! CHARGE CH_PENALTY
ATOM C1    CG321 -0.179 ! 11.384
ATOM C2    CG321 -0.073 ! 11.655
ATOM S3    SG311 -0.167 ! 15.097
ATOM C4    CG321 -0.110 ! 11.573
ATOM C5    CG2O5  0.365 ! 68.323
ATOM O6    OG2D3 -0.470 ! 5.357
ATOM C7    CG2R53 0.755 ! 68.453
ATOM N8    NG2R50 -0.444 ! 6.250
ATOM O9    OG2R50 -0.139 ! 42.699
ATOM C10   CG2R53 0.462 ! 65.130
ATOM N11   NG2R50 -0.675 ! 15.811
ATOM C12   CG301  0.120 ! 61.857
ATOM C13   CG331 -0.266 ! 19.297
ATOM C14   CG331 -0.266 ! 19.297
ATOM C15   CG331 -0.266 ! 19.297
ATOM C16   CG2R61 0.219 ! 0.000
ATOM C17   CG2R61 -0.108 ! 0.000
ATOM C18   CG2R61 -0.117 ! 0.000
ATOM C19   CG2R61 -0.005 ! 11.384
ATOM C20   CG2R61 -0.117 ! 0.000
ATOM C21   CG2R61 -0.108 ! 0.000
ATOM O22   OG301 -0.391 ! 0.000
ATOM C23   CG331 -0.100 ! 0.000
ATOM H24   HGR61  0.115 ! 0.000
ATOM H25   HGR61  0.115 ! 0.000
ATOM H26   HGR61  0.115 ! 0.000
ATOM H27   HGR61  0.115 ! 0.000
ATOM H28   HGA2   0.090 ! 0.000
ATOM H29   HGA2   0.090 ! 0.000
ATOM H30   HGA2   0.090 ! 0.000
ATOM H31   HGA2   0.090 ! 0.000
ATOM H32   HGA2   0.090 ! 0.425
ATOM H33   HGA2   0.090 ! 0.425
ATOM H34   HGA3   0.090 ! 1.025
```

ATOM H35 HGA3 0.090 ! 1.025
ATOM H36 HGA3 0.090 ! 1.025
ATOM H37 HGA3 0.090 ! 1.025
ATOM H38 HGA3 0.090 ! 1.025
ATOM H39 HGA3 0.090 ! 1.025
ATOM H40 HGA3 0.090 ! 1.025
ATOM H41 HGA3 0.090 ! 1.025
ATOM H42 HGA3 0.090 ! 1.025
ATOM H43 HGA3 0.090 ! 0.000
ATOM H44 HGA3 0.090 ! 0.000
ATOM H45 HGA3 0.090 ! 0.000

BOND C2 C1
BOND C1 C19
BOND C1 H28
BOND C1 H29
BOND C2 H30
BOND C2 H31
BOND C4 C5
BOND C4 H32
BOND C4 H33
BOND C5 O6
BOND C5 C7
BOND C7 N8
BOND C7 N11
BOND N8 O9
BOND C10 O9
BOND N11 C10
BOND C10 C12
BOND C12 C13
BOND C12 C14
BOND C12 C15
BOND C13 H34
BOND C13 H35
BOND C13 H36
BOND C14 H37
BOND C14 H38
BOND C14 H39

BOND C15 H40
BOND C15 H41
BOND C15 H42
BOND C17 C16
BOND C21 C16
BOND C16 O22
BOND C18 C17
BOND C17 H24
BOND C19 C18
BOND C18 H25
BOND C19 C20
BOND C20 C21
BOND C20 H26
BOND C21 H27
BOND O22 C23
BOND C23 H43
BOND C23 H44
BOND C23 H45
BOND S3 C4
BOND C2 S3
IMPR C5 C7 C4 O6
END

BONDS

CG2O5 CG2R53 254.00 1.4600 ! lig , from CG2O5 CG2R61, penalty= 45
CG2R53 CG301 229.63 1.5000 ! lig , from CG2R51 CG321, penalty= 40

ANGLES

CG2R53 CG2O5 CG321 20.00 116.50 ! lig , from CG2R61 CG2O5 CG321, penalty= 8.5
CG2R53 CG2O5 OG2D3 70.00 121.30 ! lig , from CG2R61 CG2O5 OG2D3, penalty= 8.5
CG2O5 CG2R53 NG2R50 65.00 127.80 ! lig , from NG2R53 CG2R53 OG2D1, penalty= 75
CG301 CG2R53 NG2R50 45.80 120.00 ! lig , from CG321 CG2R51 NG2R50, penalty= 29.8
CG301 CG2R53 OG2R50 45.80 124.00 ! lig , from CG321 CG2R51 NG2R51, penalty= 74.8
CG2R53 CG301 CG331 58.35 114.00 ! lig , from CG2R51 CG321 CG331, penalty= 14.5

CG2O5 CG321 SG311 65.00 111.82 ! lig , from CG2O4 CG321 CLGA1, penalty= 16.6

DIHEDRALS

CG321 CG2O5 CG2R53 NG2R50 0.2700 2 180.00 ! lig , from CG321 CG2O5 CG2R61
CG2R61, penalty= 130

OG2D3 CG2O5 CG2R53 NG2R50 1.5850 2 180.00 ! lig , from OG2D3 CG2O5 CG2R61
CG2R61, penalty= 130

CG2R53 CG2O5 CG321 SG311 0.1000 1 0.00 ! lig , from OG2D1 CG2O4 CG321
CLGA1, penalty= 92.1

CG2R53 CG2O5 CG321 SG311 1.0000 2 180.00 ! lig , from OG2D1 CG2O4 CG321
CLGA1, penalty= 92.1

CG2R53 CG2O5 CG321 SG311 0.5500 3 180.00 ! lig , from OG2D1 CG2O4 CG321
CLGA1, penalty= 92.1

CG2R53 CG2O5 CG321 HGA2 0.1000 3 0.00 ! lig , from CG2R61 CG2O5 CG321
HGA2, penalty= 8.5

OG2D3 CG2O5 CG321 SG311 0.1000 1 0.00 ! lig , from OG2D1 CG2O4 CG321
CLGA1, penalty= 36.6

OG2D3 CG2O5 CG321 SG311 1.0000 2 180.00 ! lig , from OG2D1 CG2O4 CG321
CLGA1, penalty= 36.6

OG2D3 CG2O5 CG321 SG311 0.5500 3 180.00 ! lig , from OG2D1 CG2O4 CG321
CLGA1, penalty= 36.6

NG2R50 CG2R53 CG301 CG331 0.1900 3 0.00 ! lig , from NG2R50 CG2R51 CG321
CG311, penalty= 41.5

OG2R50 CG2R53 CG301 CG331 0.1900 3 0.00 ! lig , from NG2R51 CG2R51 CG321
CG331, penalty= 85

CG2O5 CG2R53 NG2R50 CG2R53 12.0000 2 180.00 ! lig , from NG2R51 CG2R53
NG2R50 CG2R53, penalty= 92

CG2O5 CG2R53 NG2R50 OG2R50 12.0000 2 180.00 ! lig , from CG2R51 CG2R52
NG2R50 OG2R50, penalty= 84.5

CG301 CG2R53 NG2R50 CG2R53 3.0000 2 180.00 ! lig , from CG321 CG2R51

NG2R50 CG2R53, penalty= 29.8

CG301 CG2R53 OG2R50 NG2R50 9.0000 2 180.00 ! lig , from NG2R50 CG2R53
OG2R50 NG2R50, penalty= 114.5

CG2R53 CG301 CG331 HGA3 0.1600 3 0.00 ! lig , from CG2R51 CG321 CG331
HGA3, penalty= 14.5

CG2R61 CG321 CG321 SG311 0.2000 3 0.00 ! lig , from CG2O1 CG311 CG321
SG311, penalty= 34

CG2O5 CG321 SG311 CG321 0.2400 1 180.00 ! lig , from CG321 CG321 SG311
CG321, penalty= 71
CG2O5 CG321 SG311 CG321 0.3700 3 0.00 ! lig , from CG321 CG321 SG311
CG321, penalty= 71

IMPROPERs

CG2O5 CG2R53 CG321 OG2D3 72.0000 0 0.00 ! lig , from CG2O5 CG2R61 CG321
OG2D3, penalty= 4.5

END of Toppar stream file for compound 32

5. Toppar stream file for compound 33

```
RESI lig      0.000 ! param penalty= 130.000 ; charge penalty= 68.409
GROUP        ! CHARGE CH_PENALTY
ATOM C1    CG321 -0.180 !  0.000
ATOM C2    CG321 -0.183 !  0.000
ATOM C3    CG321 -0.181 !  0.470
ATOM C4    CG321 -0.166 !  5.824
ATOM C5    CG2O5  0.365 ! 67.969
ATOM O6    OG2D3 -0.470 !  5.247
ATOM C7    CG2R53 0.755 ! 68.409
ATOM N8    NG2R50 -0.444 !  6.250
ATOM O9    OG2R50 -0.139 ! 42.699
ATOM C10   CG2R53 0.462 ! 65.130
ATOM N11   NG2R50 -0.675 ! 15.811
ATOM C12   CG301  0.120 ! 61.857
ATOM C13   CG331 -0.266 ! 19.297
ATOM C14   CG331 -0.266 ! 19.297
ATOM C15   CG331 -0.266 ! 19.297
ATOM C16   CG2R61 0.219 !  0.000
ATOM C17   CG2R61 -0.108 !  0.000
ATOM C18   CG2R61 -0.117 !  0.000
ATOM C19   CG2R61 -0.004 !  0.000
ATOM C20   CG2R61 -0.117 !  0.000
ATOM C21   CG2R61 -0.108 !  0.000
ATOM O22   OG301 -0.391 !  0.000
ATOM C23   CG331 -0.100 !  0.000
ATOM H24   HGR61  0.115 !  0.000
ATOM H25   HGR61  0.115 !  0.000
ATOM H26   HGR61  0.115 !  0.000
ATOM H27   HGR61  0.115 !  0.000
ATOM H28   HGA2   0.090 !  0.000
ATOM H29   HGA2   0.090 !  0.000
ATOM H30   HGA2   0.090 !  0.000
ATOM H31   HGA2   0.090 !  0.000
ATOM H32   HGA2   0.090 !  0.000
ATOM H33   HGA2   0.090 !  0.000
ATOM H34   HGA2   0.090 !  0.425
```

ATOM H35 HGA2 0.090 ! 0.425
ATOM H36 HGA3 0.090 ! 1.025
ATOM H37 HGA3 0.090 ! 1.025
ATOM H38 HGA3 0.090 ! 1.025
ATOM H39 HGA3 0.090 ! 1.025
ATOM H40 HGA3 0.090 ! 1.025
ATOM H41 HGA3 0.090 ! 1.025
ATOM H42 HGA3 0.090 ! 1.025
ATOM H43 HGA3 0.090 ! 1.025
ATOM H44 HGA3 0.090 ! 1.025
ATOM H45 HGA3 0.090 ! 0.000
ATOM H46 HGA3 0.090 ! 0.000
ATOM H47 HGA3 0.090 ! 0.000

BOND C1 C2
BOND C19 C1
BOND C1 H28
BOND C1 H29
BOND C2 C3
BOND C2 H30
BOND C2 H31
BOND C3 C4
BOND C3 H32
BOND C3 H33
BOND C4 C5
BOND C4 H34
BOND C4 H35
BOND C5 O6
BOND C5 C7
BOND C7 N8
BOND C7 N11
BOND N8 O9
BOND C10 O9
BOND N11 C10
BOND C10 C12
BOND C12 C13
BOND C12 C14
BOND C12 C15

BOND C13 H36
BOND C13 H37
BOND C13 H38
BOND C14 H39
BOND C14 H40
BOND C14 H41
BOND C15 H42
BOND C15 H43
BOND C15 H44
BOND C16 C17
BOND C16 C21
BOND O22 C16
BOND C17 C18
BOND C17 H24
BOND C18 C19
BOND C18 H25
BOND C20 C19
BOND C21 C20
BOND C20 H26
BOND C21 H27
BOND C23 O22
BOND C23 H45
BOND C23 H46
BOND H47 C23
IMPR C5 C7 C4 O6
END

BONDS

CG2O5 CG2R53 254.00 1.4600 ! lig , from CG2O5 CG2R61, penalty= 45
CG2R53 CG301 229.63 1.5000 ! lig , from CG2R51 CG321, penalty= 40

ANGLES

CG2R53 CG2O5 CG321 20.00 116.50 ! lig , from CG2R61 CG2O5 CG321, penalty= 8.5
CG2R53 CG2O5 OG2D3 70.00 121.30 ! lig , from CG2R61 CG2O5 OG2D3, penalty= 8.5
CG2O5 CG2R53 NG2R50 65.00 127.80 ! lig , from NG2R53 CG2R53 OG2D1, penalty= 75

CG301 CG2R53 NG2R50 45.80 120.00 ! lig , from CG321 CG2R51 NG2R50, penalty= 29.8
 CG301 CG2R53 OG2R50 45.80 124.00 ! lig , from CG321 CG2R51 NG2R51, penalty= 74.8
 CG2R53 CG301 CG331 58.35 114.00 ! lig , from CG2R51 CG321 CG331, penalty= 14.5

DIHEDRALS

CG321 CG2O5 CG2R53 NG2R50 0.2700 2 180.00 ! lig , from CG321 CG2O5 CG2R61 CG2R61, penalty= 130
 OG2D3 CG2O5 CG2R53 NG2R50 1.5850 2 180.00 ! lig , from OG2D3 CG2O5 CG2R61 CG2R61, penalty= 130
 CG2R53 CG2O5 CG321 CG321 0.4000 1 0.00 ! lig , from CG2R61 CG2O5 CG321 CG331, penalty= 9.4
 CG2R53 CG2O5 CG321 CG321 0.1700 2 180.00 ! lig , from CG2R61 CG2O5 CG321 CG331, penalty= 9.4
 CG2R53 CG2O5 CG321 CG321 0.1300 3 180.00 ! lig , from CG2R61 CG2O5 CG321 CG331, penalty= 9.4
 CG2R53 CG2O5 CG321 CG321 0.1000 6 180.00 ! lig , from CG2R61 CG2O5 CG321 CG331, penalty= 9.4
 CG2R53 CG2O5 CG321 HGA2 0.1000 3 0.00 ! lig , from CG2R61 CG2O5 CG321 HGA2, penalty= 8.5
 NG2R50 CG2R53 CG301 CG331 0.1900 3 0.00 ! lig , from NG2R50 CG2R51 CG321 CG311, penalty= 41.5
 OG2R50 CG2R53 CG301 CG331 0.1900 3 0.00 ! lig , from NG2R51 CG2R51 CG321 CG331, penalty= 85
 CG2O5 CG2R53 NG2R50 CG2R53 12.0000 2 180.00 ! lig , from NG2R51 CG2R53 NG2R50 CG2R53, penalty= 92
 CG2O5 CG2R53 NG2R50 OG2R50 12.0000 2 180.00 ! lig , from CG2R51 CG2R52 NG2R50 OG2R50, penalty= 84.5
 CG301 CG2R53 NG2R50 CG2R53 3.0000 2 180.00 ! lig , from CG321 CG2R51 NG2R50 CG2R53, penalty= 29.8
 CG301 CG2R53 OG2R50 NG2R50 9.0000 2 180.00 ! lig , from NG2R50 CG2R53 OG2R50 NG2R50, penalty= 114.5
 CG2R53 CG301 CG331 HGA3 0.1600 3 0.00 ! lig , from CG2R51 CG321 CG331 HGA3, penalty= 14.5

IMPROBERS

CG2O5 CG2R53 CG321 OG2D3 72.0000 0 0.00 ! lig , from CG2O5 CG2R61 CG321
OG2D3, penalty= 4.5

END of Toppar stream file for compound 33

