

```
* Stream file for dehydro-amino residues
* If using these parameters please cite:
* Turpin, ER, Mulholland, S, Bonev, BB & Hirst, JD, RSC Adv., 2014, DOI:
10.1039/c4ra09897h
* eleanor.turpin@nottingham.ac.uk SEPTEMBER 2014
*****
* Initial toppar stream file generated by
* CHARMM General Force Field (CGenFF) program version 0.9.6 beta
* For use with CGenFF version 2b7
*
```

```
read rtf card append
* Initial topology guesses generated by
* CHARMM General Force Field (CGenFF) program version 0.9.6 beta
*
```

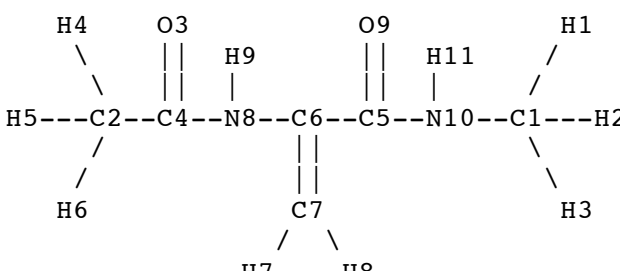
36 1

```
DECL -C
DECL +N
DEFA FIRS NTER LAST CTER
```

```
! Dehydroalanine dipetide
! Initial guess of parameters created by ParamChem website
! ERT Feb 2013
```

```
RESI DHAD          0.000 !
GROUP              !
ATOM C2            CG331 -0.270 !
ATOM H4            HGA3  0.090 !
ATOM H5            HGA3  0.090 !
ATOM H6            HGA3  0.090 !
GROUP              !
ATOM C4            CG201  0.400 !
ATOM O3            OG2D1 -0.400 !
GROUP              !
ATOM N8            NG2S1 -0.670 !
ATOM H9            HGP1   0.360 !
ATOM C6            CG2D10 0.310 !
GROUP              !
ATOM C7            CG2DC3 -0.420 !
ATOM H7            HGA5   0.210 !
ATOM H8            HGA5   0.210 !
GROUP              !
ATOM C5            CG201  0.635 !
ATOM O9            OG2D1 -0.635 !
GROUP              !
ATOM N10           NG2S1 -0.500 !
ATOM H11           HGP1   0.335 !
ATOM C1            CG331 -0.105 !
ATOM H1            HGA3   0.090 !
ATOM H2            HGA3   0.090 !
ATOM H3            HGA3   0.090 !

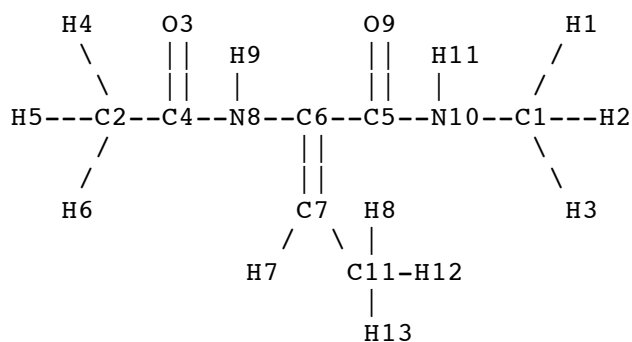
DOUBLE C6      C7
BOND C6      N8
BOND C5      C6
BOND C5      O9
BOND C4      N8
BOND O3      C4
BOND C2      C4
```



BOND C5 N10
 BOND C1 N10
 BOND C1 H1
 BOND C1 H2
 BOND C1 H3
 BOND C2 H4
 BOND C2 H5
 BOND C2 H6
 BOND C7 H7
 BOND C7 H8
 BOND N8 H9
 BOND N10 H11
 IMPR C4 C2 N8 O3
 IMPR C5 C6 N10 O9
 IMPR C6 C7 C5 N8

! Dehydrobutyrine dipetide
 ! Based on DHAD residue
 ! ERT Aug 2013

RESI DHBD 0.000 !
 GROUP !
 ATOM C2 CG331 -0.270 !
 ATOM H4 HGA3 0.090 !
 ATOM H5 HGA3 0.090 !
 ATOM H6 HGA3 0.090 !
 GROUP !
 ATOM C4 CG201 0.400 !
 ATOM O3 OG2D1 -0.400 !
 GROUP !
 ATOM N8 NG2S1 -0.670 !
 ATOM H9 HGP1 0.360 !
 ATOM C6 CG2D1O 0.310 !
 GROUP !
 ATOM C7 CG2DC1 -0.150 !
 ATOM H7 HGA4 0.150 !
 GROUP !
 ATOM C11 CG331 -0.270 !
 ATOM H8 HGA3 0.090 !
 ATOM H12 HGA3 0.090 !
 ATOM H13 HGA3 0.090 !
 GROUP !
 ATOM C5 CG201 0.635 !
 ATOM O9 OG2D1 -0.635 !
 GROUP !
 ATOM N10 NG2S1 -0.500 !
 ATOM H11 HGP1 0.335 !
 ATOM C1 CG331 -0.105 !
 ATOM H1 HGA3 0.090 !
 ATOM H2 HGA3 0.090 !
 ATOM H3 HGA3 0.090 !



DOUBLE C6 C7
 BOND C6 N8
 BOND C5 C6
 BOND C5 O9
 BOND C4 N8
 BOND O3 C4
 BOND C2 C4
 BOND C5 N10

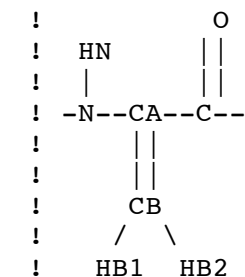
```

BOND C1 N10
BOND C1 H1
BOND C1 H2
BOND C1 H3
BOND C2 H4
BOND C2 H5
BOND C2 H6
BOND C7 H7
BOND N8 H9
BOND N10 H11
BOND C7 C11
BOND C11 H8
BOND C11 H12
BOND C11 H13
IMPR C4 C2 N8 O3
IMPR C5 C6 N10 O9
IMPR C6 C7 C5 N8

```

! Dehydroalanine residue

```
RESI DHAR 0.000 !
```



```

GROUP
ATOM N      NG2S1  -0.670 !
ATOM HN     HGP1   0.360 !
ATOM CA     CG2D10 0.310 !
GROUP
ATOM CB     CG2DC3 -0.420 !
ATOM HB1    HGA5   0.210 !
ATOM HB2    HGA5   0.210 !
GROUP
ATOM C      CG2O1  0.635 !
ATOM O      OG2D1 -0.635 !

```

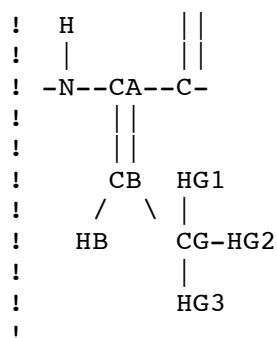
```

DOUBLE CA  CB
BOND CA  N
BOND CA  C
BOND C   O
BOND C   +N
BOND N   HN
BOND CB HB1 CB HB2
IMPR CA CB C N
IMPR C  CA +N O
DONOR HN N
ACCEPTOR O C

```

! Dehydrobutyrine residue
! Based on DHAD residue
! ERT Aug 2013

```
RESI DHBR 0.000 !
!
```



```

GROUP
ATOM N      NG2S1  -0.670 !
ATOM HN     HGP1   0.360 !
ATOM CA     CG2D10 0.310 !
GROUP
ATOM CB     CG2DC1 -0.150 !
ATOM HB     HGA4   0.150 !
GROUP
ATOM CG     CG331  -0.270 !
ATOM HG1    HGA3   0.090 !
ATOM HG2    HGA3   0.090 !
ATOM HG3    HGA3   0.090 !
GROUP
ATOM C      CG2O1  0.635 !
ATOM O      OG2D1 -0.635 !

```

```

BOND N HN N CA CA CB CA C C O C +N
BOND CB HB CB CG CG HG1 CG HG2 CG HG3
IMPR C      CA      +N      O
IMPR CA     CB      C      N
DONOR HN N
ACCEPTOR O C

```

```

! alpha-aminobutyric acid, needed for nisin
! built by analogy

```

```

RESI ABU          0.00 !
GROUP
ATOM N      NH1    -0.47 !
ATOM HN     H      0.31 !
ATOM CA     CT1    0.07 !
ATOM HA     HB1    0.09 !
GROUP
ATOM CB     CT2    -0.18 !
ATOM HB1    HA2    0.09 !
ATOM HB2    HA2    0.09 !
GROUP
ATOM CG     CT3    -0.27 !
ATOM HG1    HA3    0.09 !
ATOM HG2    HA3    0.09 !
ATOM HG3    HA3    0.09 !
GROUP
ATOM C      C      0.51 !
ATOM O      O     -0.51 !

```

```

BOND CB CA N HN N CA
BOND C CA C +N CA HA CB HB1 CB HB2
BOND CB CG CG HG1 CG HG2 CG HG2 CG HG3
DOUBLE O C

```

```
IMPR N -C CA HN C CA +N O
CMAP -C N CA C N CA C +N
DONOR HN N
ACCEPTOR O C
```

```
!Patch to change charge on C+
```

```
PRES DHCC 0.00
```

```
GROUP
```

```
ATOM C C 0.635
```

```
ATOM O O -0.635
```

```
!Patch to connect thioether rings, where first res is ALA
```

```
PRES THIA 0.00
```

```
DELETE ATOM 1HB1
```

```
DELETE ATOM 2HG1
```

```
GROUP
```

```
ATOM 1CB CT2 -0.135
```

```
ATOM 1HB2 HA2 0.09
```

```
ATOM 1HB3 HA2 0.09
```

```
ATOM 2SG S -0.09
```

```
ATOM 2CB CT2 -0.135
```

```
ATOM 2HB1 HA2 0.09
```

```
ATOM 2HB2 HA2 0.09
```

```
BOND 1CB 2SG
```

```
!Patch to connect thioether rings, where first res is ABU
```

```
PRES THIB 0.00
```

```
DELETE ATOM 1HB1
```

```
DELETE ATOM 2HG1
```

```
GROUP
```

```
ATOM 1CB CT2 -0.09
```

```
ATOM 1HB2 HA2 0.09
```

```
ATOM 2SG S -0.09
```

```
ATOM 2CB CT2 -0.09
```

```
ATOM 2HB1 HA2 0.09
```

```
ATOM 2HB2 HA2 0.09
```

```
BOND 1CB 2SG
```

```
END
```

```
read param card flex append
```

```
* Initial parameter guess generated by analogy by
```

```
* CHARMM General Force Field (CGenFF) program version 0.9.6 beta
```

```
*
```

```
BONDS
```

```
CG2D10 CG2DC3 440.00 1.3400 ! Molecule , from CG2D20 CG2DC2,
```

```
CG2D10 CG2O1 440.00 1.4890 ! Molecule , from CG2DC1 CG2O1,
```

```
CG2D10 NG2S1 370.00 1.390 ! edited by ERT
```

```
CG2D10 CG2DC2 440.00 1.3400 ! Molecule , from CG2D20 CG2DC2,
```

```
C NG2S1 370.000 1.3450 ! joining protein & cgenff sets
```

```
CG2O1 NH1 370.000 1.3450 ! joining protein & cgenff sets
```

```
ANGLES
```

```
CG2DC3 CG2D10 CG2O1 60.00 120.00 ! Molecule , from CG2DC3 CG2DC1 CG2O4,
```

```
CG2DC3 CG2D10 NG2S1 80.00 128.00 ! Molecule , from CG2D2 CG2D10 NG321,
```

```
CG2O1 CG2D10 NG2S1 80.00 110.00 ! ERT
```

```
CG2D10 CG2DC3 HGA5 45.00 120.50 ! Molecule , from CG2DC1 CG2DC3 HGA5,
```

```
CG2D10 CG2O1 NG2S1 80.00 116.50 ! Molecule , from CG2DC1 CG2O1 NG2S1,
```

CG2D10	CG2O1	OG2D1	80.00	122.50	!	Molecule	,	from	CG2DC1	CG2O1	OG2D1,
CG2D10	NG2S1	CG2O1	50.00	120.00	!	Molecule	,	from	CG2O1	NG2S1	CG2R61,
CG2D10	NG2S1	HGP1	34.00	117.00	!	Molecule	,	from	CG2R61	NG2S1	HGP1,
CG2DC1	CG2D10	NG2S1	80.00	128.00	!	Molecule	,	from	CG2D2	CG2D10	NG321,
CG2DC1	CG2D10	CG2O1	60.00	120.00	!	Molecule	,	from	CG2DC3	CG2DC1	CG2O4,
CG2D10	CG2DC1	CG331	43.50	126.50	!	ERT	from	CG2D10	CG2DC1	CG321	

! For linking protein and CGenFF parameter sets; analogy w/ prot set

CT1	C	NG2S1	80.000	116.5000							
O	C	NG2S1	80.000	122.5000							
C	NG2S1	HGP1	34.000	123.0000							
C	NG2S1	CG2D10	50.00	120.00							
CG2D10	CG2O1	NH1	80.00	116.50							
OG2D1	CG2O1	NH1	80.000	122.5000							
CG2O1	NH1	H	34.000	123.0000							
CG2O1	NH1	CT1	50.00	120.00							
CG2O1	NH1	CTD1	50.00	120.00							

CT2	S	CT2	34.000	95.0000	!	from	MET	CT3	S	CT2	
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DIHEDRALS

CG2O1	CG2D10	CG2DC3	HGA5	3.2000	2	180.00	!	Molecule	,	from	CG2O4
CG2DC1	CG2DC3	HGA5,									
NG2S1	CG2D10	CG2DC3	HGA5	5.0000	2	180.00	!	Molecule	,	from	CG2DC2
CG2DC1	CG2DC3	HGA5,									
CG2DC3	CG2D10	NG2S1	HGP1	2.5000	2	180.00	!	Molecule	,	from	CG2DC1
CG2O1	NG2S1	HGP1,									
CG2O1	CG2D10	NG2S1	HGP1	2.5000	2	180.00	!	Molecule	,	from	CG2R61
CG2O1	NG2S1	HGP1,									
CG2D10	CG2O1	NG2S1	HGP1	2.5000	2	180.00	!	Molecule	,	from	CG2DC1
CG2O1	NG2S1	HGP1,									

CG2DC1	CG2D10	NG2S1	CG2O1	0.50	1	180.0					
CG2DC1	CG2D10	NG2S1	CG2O1	0.50	2	0.0					
CG2DC1	CG2D10	NG2S1	CG2O1	0.20	3	180.0					

NG2S1	CG2D10	CG2DC1	HGA4	3.0000	2	180.00	!	dhb			
NG2S1	CG2D10	CG2DC1	CG331	3.5000	2	180.00	!	dhb		c11c7c6n8	
NG2S1	CG2D10	CG2DC1	CG331	1.700	1	180.00					
NG2S1	CG2D10	CG2DC1	CG331	0.500	3	180.00					
HGP1	NG2S1	CG2D10	CG2DC1	2.5000	2	180.00	!	dhb			
CG2D10	CG2DC1	CG331	HGA3	0.3000	3	180.00	!	dhb			
CG2DC1	CG2D10	CG2O1	OG2D1	0.57	1	0.0	!	dhb			
CG2DC1	CG2D10	CG2O1	OG2D1	0.59	2	0.0	!	dhb			
CG2DC1	CG2D10	CG2O1	OG2D1	2.96	3	0.0	!	dhb			
CG2DC1	CG2D10	CG2O1	NG2S1	2.10	1	180.0	!	dhb			
CG2DC1	CG2D10	CG2O1	NG2S1	2.88	2	0.0	!	dhb			
CG2DC1	CG2D10	CG2O1	NG2S1	2.00	3	0.0	!	dhb			
HGA4	CG2DC1	CG2D10	CG2O1	3.2000	2	180.00	!	dhb			
CG331	CG2DC1	CG2D10	CG2O1	3.5000	2	180.00	!	dhb		c11c7c6c5	
CG331	CG2DC1	CG2D10	CG2O1	1.700	1	0.00					
CG331	CG2DC1	CG2D10	CG2O1	0.500	3	0.00					
CG2DC2	CG2D10	CG2O1	NG2S1	2.10	1	180.0	!	c7c6c5n10			
CG2DC2	CG2D10	CG2O1	NG2S1	2.88	2	180.0					
CG2DC2	CG2D10	CG2O1	NG2S1	2.00	3	180.0					
CG2D10	NG2S1	CG2O1	CG331	2.29	1	180.0	!	c2c4n8c6			
CG2D10	NG2S1	CG2O1	CG331	3.48	2	180.0					
CG2D10	NG2S1	CG2O1	CG331	0.63	3	0.0					
CG2O1	CG2D10	NG2S1	CG2O1	2.50	1	0.0					
CG2O1	CG2D10	NG2S1	CG2O1	1.50	2	180.0					

CG201	CG2D10	NG2S1	CG201	0.30	3	0.0
CG201	CG2D10	NG2S1	CG201	0.75	5	0.0
CG2DC3	CG2D10	NG2S1	CG201	0.50	1	180.0
CG2DC3	CG2D10	NG2S1	CG201	0.50	2	0.0
CG2DC3	CG2D10	NG2S1	CG201	0.20	3	180.0
CG2D10	CG201	NG2S1	CG331	2.37	1	0.0
CG2D10	CG201	NG2S1	CG331	0.50	2	0.0
CG2DC3	CG2D10	CG201	NG2S1	2.10	1	180.0 !c7c6c5n10
CG2DC3	CG2D10	CG201	NG2S1	2.88	2	0.0
CG2DC3	CG2D10	CG201	NG2S1	2.00	3	0.0
CG2DC3	CG2D10	CG201	OG2D1	0.57	1	0.0 !c7c6c509o9
CG2DC3	CG2D10	CG201	OG2D1	0.59	2	0.0
CG2DC3	CG2D10	CG201	OG2D1	2.96	3	0.0
NG2S1	CG2D10	CG201	NG2S1	1.53	1	180.0 !n8c6c5n10
NG2S1	CG2D10	CG201	NG2S1	3.63	2	180.0
NG2S1	CG2D10	CG201	NG2S1	0.10	3	180.0
NG2S1	CG2D10	CG201	OG2D1	0.79	1	180.0 !n8c6c5o9
NG2S1	CG2D10	CG201	OG2D1	2.85	2	180.0
NG2S1	CG2D10	CG201	OG2D1	1.49	3	0.0
CG2D10	NG2S1	CG201	OG2D1	2.45	1	180.0 !o3c4n8c6
CG2D10	NG2S1	CG201	OG2D1	0.69	2	0.0
CG2D10	NG2S1	CG201	OG2D1	1.09	3	0.0

! For joining protein and CGen sets

NH1	CT1	C	NG2S1	0.6000	1	0.00
CT1	C	NG2S1	HGP1	2.5000	2	180.00
CT1	C	NG2S1	CG2D10	1.6000	1	0.00
CT1	C	NG2S1	CG2D10	2.5000	2	180.00
HB1	CT1	C	NG2S1	0.0000	1	0.00
CT3	CT1	C	NG2S1	0.0000	1	0.00
C	NG2S1	CG2D10	CG2DC3	0.50	1	180.0
C	NG2S1	CG2D10	CG2DC3	0.50	2	0.0
C	NG2S1	CG2D10	CG2DC3	0.20	3	180.0
C	NG2S1	CG2D10	CG201	2.50	1	0.0
C	NG2S1	CG2D10	CG201	1.50	2	180.0
C	NG2S1	CG2D10	CG201	0.30	3	0.0
C	NG2S1	CG2D10	CG201	0.75	5	0.0
O	C	NG2S1	HGP1	2.5000	2	180.00
O	C	NG2S1	CG2D10	2.5000	2	180.00
NG2S1	CG2D10	CG201	NH1	0.6000	1	0.00
CG2D10	CG201	NH1	H	2.5000	2	180.00
CG2D10	CG201	NH1	CT1	1.6000	1	0.00
CG2D10	CG201	NH1	CT1	2.5000	2	180.00
CG2DC3	CG2D10	CG201	NH1	2.10	1	180.0
CG2DC3	CG2D10	CG201	NH1	2.88	2	0.0
CG2DC3	CG2D10	CG201	NH1	2.00	3	0.0
CG201	NH1	CT1	HB1	0.0000	1	0.0
CG201	NH1	CT1	CT3	1.8000	1	0.00
CG201	NH1	CT1	C	0.2000	1	180.00
OG2D1	CG201	NH1	H	2.5000	2	180.00
OG2D1	CG201	NH1	CT1	2.5000	2	180.00
C	NG2S1	CG2D10	CG2DC1	0.50	1	180.0
C	NG2S1	CG2D10	CG2DC1	0.50	2	0.0
C	NG2S1	CG2D10	CG2DC1	0.20	3	180.0
CG2DC1	CG2D10	CG201	NH1	2.10	1	180.0
CG2DC1	CG2D10	CG201	NH1	2.88	2	0.0
CG2DC1	CG2D10	CG201	NH1	2.00	3	0.0
CT1	CT1	C	NG2S1	0.0000	1	0.00
CG2D10	CG201	NH1	CTD1	1.6000	1	0.00
CG2D10	CG201	NH1	CTD1	2.5000	2	180.00
CG201	NH1	CTD1	HB1	0.0000	1	0.0

CG2O1	NH1	CTD1	CT3	1.8000	1	0.00
CG2O1	NH1	CTD1	C	0.2000	1	180.00
OG2D1	CG2O1	NH1	CTD1	2.5000	2	180.00
CG2O1	NH1	CT1	CT2	1.8000	1	0.00
NH3	CT1	C	NG2S1	0.6000	1	0.00
CG2O1	NH1	CT1	CC	0.2000	1	180.00
CG2O1	NH1	CTD1	CT2	1.8000	1	0.00

CTD1	CT2	S	CT2	0.2400	1	180.00	!	from CT3	CT2	S	CT3
CTD1	CT2	S	CT2	0.3700	3	0.00	!	from CT3	CT2	S	CT3
CT2	S	CT2	CT1	0.2400	1	180.00	!	from CT3	CT2	S	CT3
CT2	S	CT2	CT1	0.3700	3	0.00	!	from CT3	CT2	S	CT3
CT2	S	CT2	HA2	0.2800	3	0.00	!	from HA2	CT2	S	CT3
CT3	CT2	S	CT2	0.2400	1	180.00	!	from CT3	CT2	S	CT3
CT3	CT2	S	CT2	0.3700	3	0.00	!	from CT3	CT2	S	CT3

IMPROPERS

CG2D10	CG2DC3	CG2O1	NG2S1	72.0000	0	0.00	!	Molecule ,	from CG2O5	CG2O3
CG2R61	OG2D3									
CG2O1	CG2D10	NG2S1	OG2D1	120.0000	0	0.00	!	Molecule ,	from CG2O1	
CG2DC1	NG2S1	OG2D1								
CG2D10	CG2DC1	CG2O1	NG2S1	72.0000	0	0.00	!	Molecule ,	from CG2O5	CG2O3
CG2R61	OG2D3									
CG2O1	CG2D10	NH1	OG2D1	120.0000	0	0.00				

CMAF

!! CMAF terms to allow DHAR and DHAB to be included in the peptide chain. CMAF is not applied to the

!! non-standard residues, but definition of phi and psi is changed for neighborous due to different atom

!! type names in CGEN and protein parameter sets.

C	NH1	CT1	C	NH1	CT1	C	NG2S1	24
---	-----	-----	---	-----	-----	---	-------	----

! phi = -180.0

0.126790	0.768700	0.971260	1.250970	2.121010
2.720430	2.089440	1.789790	0.780870	-0.688474
1.001130	-2.200520	-4.827670	-4.821447	-4.913223
-3.591106	-2.766446	-2.784200	-2.454589	-2.346991
-2.335350	-1.522656	-0.951542	-0.036650	

! phi = -165.0

-0.127133	1.377090	1.577020	1.872290	2.398990
2.486630	2.436754	1.929070	1.086456	0.643400
0.258676	-2.800440	-4.009477	-4.135306	-3.420090
-2.602140	-2.299128	-1.501241	-1.101780	-0.861434
-0.640168	-0.207701	-1.076344	-1.122030	

! phi = -150.0

0.084069	1.420317	1.624350	2.047200	2.653910
2.716410	2.321416	1.985454	1.557466	2.463293
-0.225720	-1.815886	-2.583256	-3.006154	-2.551995
-1.890683	-1.354215	-0.727243	0.068512	-0.225016
-0.765479	-1.283444	-1.293226	-0.816303	

! phi = -135.0

0.927992	1.521370	2.242218	2.546305	3.111384
2.918410	2.460813	2.187970	2.058314	1.852278
0.115935	-1.183897	-1.995479	-2.278329	-1.959136
-1.340467	-0.932949	0.021790	0.313725	-0.517358
-1.152891	-0.983285	-0.566518	-0.442565	

! phi = -120.0				
1.357468	1.959160	2.698894	3.037857	3.698960
3.558453	2.639296	2.773853	2.719664	1.627997
0.705667	-0.785637	-2.118268	-2.628489	-1.803113
-0.425969	-0.062320	0.439040	0.910952	-0.546994
-0.968118	-0.856791	-0.250116	0.449309	
! phi = -105.0				
2.045006	2.544424	2.818030	3.088582	3.370620
3.551568	3.073520	2.903794	2.956634	2.124759
0.906487	-0.823628	-2.090819	-2.241579	-1.456524
0.206160	0.082195	0.771710	1.040241	-0.124647
-0.316550	-0.164333	0.314474	0.733747	
! phi = -90.0				
1.451735	2.748481	2.738185	3.156796	3.450028
3.344157	3.180200	3.898724	3.335030	2.440579
0.912671	-0.606502	-1.511772	-1.620864	-0.962798
-0.020653	0.415153	0.908250	0.459433	0.145910
-0.071054	0.017622	0.280839	0.748823	
! phi = -75.0				
1.378160	3.345958	2.352424	3.063543	3.814070
3.700796	3.580310	4.212293	3.536425	1.693809
0.095172	-0.682452	-0.123614	-0.427765	-0.598368
0.226352	0.423308	0.301999	0.551890	0.191719
-0.253585	-0.190548	-0.253412	0.468922	
! phi = -60.0				
0.237754	1.229980	1.716960	3.168570	4.208190
4.391860	4.276080	3.673107	2.272295	-0.482789
-0.406695	-0.038919	-0.357600	-0.823341	-0.173146
0.139806	0.267796	0.322420	0.309664	-0.666399
-0.948631	-1.534365	-1.479968	-0.204264	
! phi = -45.0				
-1.184837	0.078060	2.347410	4.211350	5.376000
5.389940	4.380200	2.461506	1.123713	0.107016
0.007574	-0.149443	-0.797230	-0.582210	0.082910
0.271580	-0.045570	0.379430	0.247770	-0.890956
-1.582430	-1.954532	-1.980965	-2.000433	
! phi = -30.0				
-1.174720	1.067030	4.180460	6.741610	6.070770
4.806470	2.783340	1.320806	0.765978	-0.008448
0.276860	-0.707140	1.314360	1.522590	1.915550
2.223490	0.194290	0.534000	0.331780	-1.595147
-2.849141	-3.550465	-3.277369	-2.655135	
! phi = -15.0				
0.293590	5.588070	3.732620	3.217620	3.272450
2.517320	1.588700	1.381760	0.856410	0.655170
1.616970	0.846920	0.511070	0.740760	1.021020
1.616580	-0.342400	0.181770	-0.613920	-2.558037
-3.786839	-3.807325	-3.155346	-1.749204	
! phi = 0.0				
2.832310	0.787990	0.323280	0.479230	0.628600
0.976330	1.238750	1.671950	1.645480	2.520340
1.606970	0.776350	0.119780	0.070390	0.121170

-1.569230	-1.213010	-1.846360	-2.744510	-3.792530
-3.934880	-3.615930	-2.675750	-0.924170	
! phi = 15.0				
-0.778340	-1.912680	-2.052140	-1.846280	-1.047430
0.183400	1.682950	2.223500	1.358370	2.448660
1.436920	0.678570	-0.237060	-0.535320	-0.790380
-2.182580	-3.251140	-4.195110	-4.269270	-3.908210
-3.455620	-2.773970	1.755370	0.313410	
! phi = 30.0				
-2.963810	-3.483730	-3.441809	-2.400349	-1.125083
0.336200	1.428450	1.394630	0.970370	2.462720
1.522430	0.553620	-0.407380	-1.482950	-3.613920
-4.159810	-4.709721	-4.496271	-3.764540	-2.959140
-1.963850	-1.071260	-1.599580	-2.445320	
! phi = 45.0				
-4.021496	-3.836549	-3.365327	-2.334377	-0.984725
0.362000	0.814380	0.754110	0.502370	1.903420
0.770220	-0.416420	-3.286310	-3.875270	-4.611550
-5.287977	-5.146239	-4.038627	-2.865450	-2.368170
-2.860490	-3.416560	-3.666490	-3.595217	
! phi = 60.0				
-3.353683	-2.984416	-2.317412	-1.240143	-0.257890
0.722610	0.668070	0.438130	2.395330	1.632470
-2.041450	-3.218100	-3.915080	-4.568574	-5.096776
-5.526955	-5.005312	-3.777879	-2.840678	-3.508820
-3.756430	-3.640810	-3.451845	-3.342810	
! phi = 75.0				
-2.248733	-1.641080	-1.010583	0.039656	0.636063
0.823710	0.517140	-0.013120	-0.370910	-1.192809
-2.305650	-3.420580	-4.484960	-5.597237	-5.601264
-5.727739	-4.740525	-3.819378	-3.685150	-4.151360
-4.170739	-3.725589	-3.736732	-2.620673	
! phi = 90.0				
-1.720840	-1.177830	-0.428430	0.277730	0.807900
0.803260	0.482510	-0.336900	-0.786270	-1.774070
-2.793220	-3.828560	-5.211800	-6.294328	-6.617221
-5.763953	-5.072995	-3.911450	-4.158306	-4.473413
-4.099325	-3.769822	-3.157300	-2.651694	
! phi = 105.0				
-1.850640	-1.092420	-0.445020	0.128490	1.005520
0.884820	0.485850	-0.218470	-0.857670	-1.682330
-3.014400	-4.481110	-6.053510	-6.865400	-6.871130
-5.728240	-3.912230	-4.802110	-5.034640	-4.715990
-4.600554	-4.086721	-3.274630	-2.410940	
! phi = 120.0				
-1.969230	-1.116650	-0.540250	-0.150330	0.763520
1.038890	0.758480	0.313530	-0.333050	-1.872770
-3.366270	-5.008260	-6.124810	-7.034830	-6.724320
-3.700200	-4.510620	-5.185650	-5.361620	-4.847490
-4.444320	-4.004260	-3.415720	-2.751230	
! phi = 135.0				

-2.111250	-1.168960	-0.322790	-0.006920	0.316660
1.086270	0.939170	0.625340	-0.166360	-1.830310
-3.469470	-4.946030	-6.112560	-1.915580	-4.047310
-4.996740	-4.996730	-4.842690	-4.886620	-4.300540
-4.494620	-4.442210	-4.163570	-3.183510	

! phi = 150.0

-1.757590	-0.403620	0.023920	0.362390	0.634520
1.264920	1.361360	0.948420	-0.073680	-1.483560
-3.152820	1.835120	-1.762860	-5.093660	-5.744830
-5.390070	-4.783930	-4.190630	-4.115420	-4.042280
-4.125570	-4.028550	-4.026100	-2.937910	

! phi = 165.0

-0.810590	-0.071500	0.378890	0.543310	1.277880
1.641310	1.698840	1.519950	0.631950	-1.088670
-2.736530	-0.735240	-4.563830	-6.408350	-5.889450
-5.141750	-4.194970	-3.666490	-3.843450	-3.555000
-3.548722	-3.246995	-2.751289	-1.814368	

CG201 NH1 CT1 C NH1 CT1 C NH1 24

! phi = -180.0

0.126790	0.768700	0.971260	1.250970	2.121010
2.720430	2.089440	1.789790	0.780870	-0.688474
1.001130	-2.200520	-4.827670	-4.821447	-4.913223
-3.591106	-2.766446	-2.784200	-2.454589	-2.346991
-2.335350	-1.522656	-0.951542	-0.036650	

! phi = -165.0

-0.127133	1.377090	1.577020	1.872290	2.398990
2.486630	2.436754	1.929070	1.086456	0.643400
0.258676	-2.800440	-4.009477	-4.135306	-3.420090
-2.602140	-2.299128	-1.501241	-1.101780	-0.861434
-0.640168	-0.207701	-1.076344	-1.122030	

! phi = -150.0

0.084069	1.420317	1.624350	2.047200	2.653910
2.716410	2.321416	1.985454	1.557466	2.463293
-0.225720	-1.815886	-2.583256	-3.006154	-2.551995
-1.890683	-1.354215	-0.727243	0.068512	-0.225016
-0.765479	-1.283444	-1.293226	-0.816303	

! phi = -135.0

0.927992	1.521370	2.242218	2.546305	3.111384
2.918410	2.460813	2.187970	2.058314	1.852278
0.115935	-1.183897	-1.995479	-2.278329	-1.959136
-1.340467	-0.932949	0.021790	0.313725	-0.517358
-1.152891	-0.983285	-0.566518	-0.442565	

! phi = -120.0

1.357468	1.959160	2.698894	3.037857	3.698960
3.558453	2.639296	2.773853	2.719664	1.627997
0.705667	-0.785637	-2.118268	-2.628489	-1.803113
-0.425969	-0.062320	0.439040	0.910952	-0.546994
-0.968118	-0.856791	-0.250116	0.449309	

! phi = -105.0

2.045006	2.544424	2.818030	3.088582	3.370620
3.551568	3.073520	2.903794	2.956634	2.124759

0.906487	-0.823628	-2.090819	-2.241579	-1.456524
0.206160	0.082195	0.771710	1.040241	-0.124647
-0.316550	-0.164333	0.314474	0.733747	
! phi = -90.0				
1.451735	2.748481	2.738185	3.156796	3.450028
3.344157	3.180200	3.898724	3.335030	2.440579
0.912671	-0.606502	-1.511772	-1.620864	-0.962798
-0.020653	0.415153	0.908250	0.459433	0.145910
-0.071054	0.017622	0.280839	0.748823	
! phi = -75.0				
1.378160	3.345958	2.352424	3.063543	3.814070
3.700796	3.580310	4.212293	3.536425	1.693809
0.095172	-0.682452	-0.123614	-0.427765	-0.598368
0.226352	0.423308	0.301999	0.551890	0.191719
-0.253585	-0.190548	-0.253412	0.468922	
! phi = -60.0				
0.237754	1.229980	1.716960	3.168570	4.208190
4.391860	4.276080	3.673107	2.272295	-0.482789
-0.406695	-0.038919	-0.357600	-0.823341	-0.173146
0.139806	0.267796	0.322420	0.309664	-0.666399
-0.948631	-1.534365	-1.479968	-0.204264	
! phi = -45.0				
-1.184837	0.078060	2.347410	4.211350	5.376000
5.389940	4.380200	2.461506	1.123713	0.107016
0.007574	-0.149443	-0.797230	-0.582210	0.082910
0.271580	-0.045570	0.379430	0.247770	-0.890956
-1.582430	-1.954532	-1.980965	-2.000433	
! phi = -30.0				
-1.174720	1.067030	4.180460	6.741610	6.070770
4.806470	2.783340	1.320806	0.765978	-0.008448
0.276860	-0.707140	1.314360	1.522590	1.915550
2.223490	0.194290	0.534000	0.331780	-1.595147
-2.849141	-3.550465	-3.277369	-2.655135	
! phi = -15.0				
0.293590	5.588070	3.732620	3.217620	3.272450
2.517320	1.588700	1.381760	0.856410	0.655170
1.616970	0.846920	0.511070	0.740760	1.021020
1.616580	-0.342400	0.181770	-0.613920	-2.558037
-3.786839	-3.807325	-3.155346	-1.749204	
! phi = 0.0				
2.832310	0.787990	0.323280	0.479230	0.628600
0.976330	1.238750	1.671950	1.645480	2.520340
1.606970	0.776350	0.119780	0.070390	0.121170
-1.569230	-1.213010	-1.846360	-2.744510	-3.792530
-3.934880	-3.615930	-2.675750	-0.924170	
! phi = 15.0				
-0.778340	-1.912680	-2.052140	-1.846280	-1.047430
0.183400	1.682950	2.223500	1.358370	2.448660
1.436920	0.678570	-0.237060	-0.535320	-0.790380
-2.182580	-3.251140	-4.195110	-4.269270	-3.908210
-3.455620	-2.773970	1.755370	0.313410	

! phi = 30.0				
-2.963810	-3.483730	-3.441809	-2.400349	-1.125083
0.336200	1.428450	1.394630	0.970370	2.462720
1.522430	0.553620	-0.407380	-1.482950	-3.613920
-4.159810	-4.709721	-4.496271	-3.764540	-2.959140
-1.963850	-1.071260	-1.599580	-2.445320	
! phi = 45.0				
-4.021496	-3.836549	-3.365327	-2.334377	-0.984725
0.362000	0.814380	0.754110	0.502370	1.903420
0.770220	-0.416420	-3.286310	-3.875270	-4.611550
-5.287977	-5.146239	-4.038627	-2.865450	-2.368170
-2.860490	-3.416560	-3.666490	-3.595217	
! phi = 60.0				
-3.353683	-2.984416	-2.317412	-1.240143	-0.257890
0.722610	0.668070	0.438130	2.395330	1.632470
-2.041450	-3.218100	-3.915080	-4.568574	-5.096776
-5.526955	-5.005312	-3.777879	-2.840678	-3.508820
-3.756430	-3.640810	-3.451845	-3.342810	
! phi = 75.0				
-2.248733	-1.641080	-1.010583	0.039656	0.636063
0.823710	0.517140	-0.013120	-0.370910	-1.192809
-2.305650	-3.420580	-4.484960	-5.597237	-5.601264
-5.727739	-4.740525	-3.819378	-3.685150	-4.151360
-4.170739	-3.725589	-3.736732	-2.620673	
! phi = 90.0				
-1.720840	-1.177830	-0.428430	0.277730	0.807900
0.803260	0.482510	-0.336900	-0.786270	-1.774070
-2.793220	-3.828560	-5.211800	-6.294328	-6.617221
-5.763953	-5.072995	-3.911450	-4.158306	-4.473413
-4.099325	-3.769822	-3.157300	-2.651694	
! phi = 105.0				
-1.850640	-1.092420	-0.445020	0.128490	1.005520
0.884820	0.485850	-0.218470	-0.857670	-1.682330
-3.014400	-4.481110	-6.053510	-6.865400	-6.871130
-5.728240	-3.912230	-4.802110	-5.034640	-4.715990
-4.600554	-4.086721	-3.274630	-2.410940	
! phi = 120.0				
-1.969230	-1.116650	-0.540250	-0.150330	0.763520
1.038890	0.758480	0.313530	-0.333050	-1.872770
-3.366270	-5.008260	-6.124810	-7.034830	-6.724320
-3.700200	-4.510620	-5.185650	-5.361620	-4.847490
-4.444320	-4.004260	-3.415720	-2.751230	
! phi = 135.0				
-2.111250	-1.168960	-0.322790	-0.006920	0.316660
1.086270	0.939170	0.625340	-0.166360	-1.830310
-3.469470	-4.946030	-6.112560	-1.915580	-4.047310
-4.996740	-4.996730	-4.842690	-4.886620	-4.300540
-4.494620	-4.442210	-4.163570	-3.183510	
! phi = 150.0				
-1.757590	-0.403620	0.023920	0.362390	0.634520
1.264920	1.361360	0.948420	-0.073680	-1.483560
-3.152820	1.835120	-1.762860	-5.093660	-5.744830

-5.390070	-4.783930	-4.190630	-4.115420	-4.042280
-4.125570	-4.028550	-4.026100	-2.937910	

! phi = 165.0

-0.810590	-0.071500	0.378890	0.543310	1.277880
1.641310	1.698840	1.519950	0.631950	-1.088670
-2.736530	-0.735240	-4.563830	-6.408350	-5.889450
-5.141750	-4.194970	-3.666490	-3.843450	-3.555000
-3.548722	-3.246995	-2.751289	-1.814368	

CG2O1 NH1 CT1 C NH1 CT1 C NG2S1 24

! phi = -180.0

0.126790	0.768700	0.971260	1.250970	2.121010
2.720430	2.089440	1.789790	0.780870	-0.688474
1.001130	-2.200520	-4.827670	-4.821447	-4.913223
-3.591106	-2.766446	-2.784200	-2.454589	-2.346991
-2.335350	-1.522656	-0.951542	-0.036650	

! phi = -165.0

-0.127133	1.377090	1.577020	1.872290	2.398990
2.486630	2.436754	1.929070	1.086456	0.643400
0.258676	-2.800440	-4.009477	-4.135306	-3.420090
-2.602140	-2.299128	-1.501241	-1.101780	-0.861434
-0.640168	-0.207701	-1.076344	-1.122030	

! phi = -150.0

0.084069	1.420317	1.624350	2.047200	2.653910
2.716410	2.321416	1.985454	1.557466	2.463293
-0.225720	-1.815886	-2.583256	-3.006154	-2.551995
-1.890683	-1.354215	-0.727243	0.068512	-0.225016
-0.765479	-1.283444	-1.293226	-0.816303	

! phi = -135.0

0.927992	1.521370	2.242218	2.546305	3.111384
2.918410	2.460813	2.187970	2.058314	1.852278
0.115935	-1.183897	-1.995479	-2.278329	-1.959136
-1.340467	-0.932949	0.021790	0.313725	-0.517358
-1.152891	-0.983285	-0.566518	-0.442565	

! phi = -120.0

1.357468	1.959160	2.698894	3.037857	3.698960
3.558453	2.639296	2.773853	2.719664	1.627997
0.705667	-0.785637	-2.118268	-2.628489	-1.803113
-0.425969	-0.062320	0.439040	0.910952	-0.546994
-0.968118	-0.856791	-0.250116	0.449309	

! phi = -105.0

2.045006	2.544424	2.818030	3.088582	3.370620
3.551568	3.073520	2.903794	2.956634	2.124759
0.906487	-0.823628	-2.090819	-2.241579	-1.456524
0.206160	0.082195	0.771710	1.040241	-0.124647
-0.316550	-0.164333	0.314474	0.733747	

! phi = -90.0

1.451735	2.748481	2.738185	3.156796	3.450028
3.344157	3.180200	3.898724	3.335030	2.440579
0.912671	-0.606502	-1.511772	-1.620864	-0.962798
-0.020653	0.415153	0.908250	0.459433	0.145910

	-0.071054	0.017622	0.280839	0.748823	
! phi = -75.0					
	1.378160	3.345958	2.352424	3.063543	3.814070
	3.700796	3.580310	4.212293	3.536425	1.693809
	0.095172	-0.682452	-0.123614	-0.427765	-0.598368
	0.226352	0.423308	0.301999	0.551890	0.191719
	-0.253585	-0.190548	-0.253412	0.468922	
! phi = -60.0					
	0.237754	1.229980	1.716960	3.168570	4.208190
	4.391860	4.276080	3.673107	2.272295	-0.482789
	-0.406695	-0.038919	-0.357600	-0.823341	-0.173146
	0.139806	0.267796	0.322420	0.309664	-0.666399
	-0.948631	-1.534365	-1.479968	-0.204264	
! phi = -45.0					
	-1.184837	0.078060	2.347410	4.211350	5.376000
	5.389940	4.380200	2.461506	1.123713	0.107016
	0.007574	-0.149443	-0.797230	-0.582210	0.082910
	0.271580	-0.045570	0.379430	0.247770	-0.890956
	-1.582430	-1.954532	-1.980965	-2.000433	
! phi = -30.0					
	-1.174720	1.067030	4.180460	6.741610	6.070770
	4.806470	2.783340	1.320806	0.765978	-0.008448
	0.276860	-0.707140	1.314360	1.522590	1.915550
	2.223490	0.194290	0.534000	0.331780	-1.595147
	-2.849141	-3.550465	-3.277369	-2.655135	
! phi = -15.0					
	0.293590	5.588070	3.732620	3.217620	3.272450
	2.517320	1.588700	1.381760	0.856410	0.655170
	1.616970	0.846920	0.511070	0.740760	1.021020
	1.616580	-0.342400	0.181770	-0.613920	-2.558037
	-3.786839	-3.807325	-3.155346	-1.749204	
! phi = 0.0					
	2.832310	0.787990	0.323280	0.479230	0.628600
	0.976330	1.238750	1.671950	1.645480	2.520340
	1.606970	0.776350	0.119780	0.070390	0.121170
	-1.569230	-1.213010	-1.846360	-2.744510	-3.792530
	-3.934880	-3.615930	-2.675750	-0.924170	
! phi = 15.0					
	-0.778340	-1.912680	-2.052140	-1.846280	-1.047430
	0.183400	1.682950	2.223500	1.358370	2.448660
	1.436920	0.678570	-0.237060	-0.535320	-0.790380
	-2.182580	-3.251140	-4.195110	-4.269270	-3.908210
	-3.455620	-2.773970	1.755370	0.313410	
! phi = 30.0					
	-2.963810	-3.483730	-3.441809	-2.400349	-1.125083
	0.336200	1.428450	1.394630	0.970370	2.462720
	1.522430	0.553620	-0.407380	-1.482950	-3.613920
	-4.159810	-4.709721	-4.496271	-3.764540	-2.959140
	-1.963850	-1.071260	-1.599580	-2.445320	
! phi = 45.0					
	-4.021496	-3.836549	-3.365327	-2.334377	-0.984725

0.362000	0.814380	0.754110	0.502370	1.903420
0.770220	-0.416420	-3.286310	-3.875270	-4.611550
-5.287977	-5.146239	-4.038627	-2.865450	-2.368170
-2.860490	-3.416560	-3.666490	-3.595217	
! phi = 60.0				
-3.353683	-2.984416	-2.317412	-1.240143	-0.257890
0.722610	0.668070	0.438130	2.395330	1.632470
-2.041450	-3.218100	-3.915080	-4.568574	-5.096776
-5.526955	-5.005312	-3.777879	-2.840678	-3.508820
-3.756430	-3.640810	-3.451845	-3.342810	
! phi = 75.0				
-2.248733	-1.641080	-1.010583	0.039656	0.636063
0.823710	0.517140	-0.013120	-0.370910	-1.192809
-2.305650	-3.420580	-4.484960	-5.597237	-5.601264
-5.727739	-4.740525	-3.819378	-3.685150	-4.151360
-4.170739	-3.725589	-3.736732	-2.620673	
! phi = 90.0				
-1.720840	-1.177830	-0.428430	0.277730	0.807900
0.803260	0.482510	-0.336900	-0.786270	-1.774070
-2.793220	-3.828560	-5.211800	-6.294328	-6.617221
-5.763953	-5.072995	-3.911450	-4.158306	-4.473413
-4.099325	-3.769822	-3.157300	-2.651694	
! phi = 105.0				
-1.850640	-1.092420	-0.445020	0.128490	1.005520
0.884820	0.485850	-0.218470	-0.857670	-1.682330
-3.014400	-4.481110	-6.053510	-6.865400	-6.871130
-5.728240	-3.912230	-4.802110	-5.034640	-4.715990
-4.600554	-4.086721	-3.274630	-2.410940	
! phi = 120.0				
-1.969230	-1.116650	-0.540250	-0.150330	0.763520
1.038890	0.758480	0.313530	-0.333050	-1.872770
-3.366270	-5.008260	-6.124810	-7.034830	-6.724320
-3.700200	-4.510620	-5.185650	-5.361620	-4.847490
-4.444320	-4.004260	-3.415720	-2.751230	
! phi = 135.0				
-2.111250	-1.168960	-0.322790	-0.006920	0.316660
1.086270	0.939170	0.625340	-0.166360	-1.830310
-3.469470	-4.946030	-6.112560	-1.915580	-4.047310
-4.996740	-4.996730	-4.842690	-4.886620	-4.300540
-4.494620	-4.442210	-4.163570	-3.183510	
! phi = 150.0				
-1.757590	-0.403620	0.023920	0.362390	0.634520
1.264920	1.361360	0.948420	-0.073680	-1.483560
-3.152820	1.835120	-1.762860	-5.093660	-5.744830
-5.390070	-4.783930	-4.190630	-4.115420	-4.042280
-4.125570	-4.028550	-4.026100	-2.937910	
! phi = 165.0				
-0.810590	-0.071500	0.378890	0.543310	1.277880
1.641310	1.698840	1.519950	0.631950	-1.088670
-2.736530	-0.735240	-4.563830	-6.408350	-5.889450
-5.141750	-4.194970	-3.666490	-3.843450	-3.555000
-3.548722	-3.246995	-2.751289	-1.814368	

CG201	NH1	CTD1	C	NH1	CTD1	C	NH1	24	
!-180									
	0.318000			0.161300			-0.741600	-1.303800	-2.114700
	-2.129330			-2.239660			-2.572520	-2.555440	-3.375000
	-4.686760			-4.591700			-4.627070	-2.004200	1.196740
	-0.505800			0.958820			1.968850	2.270310	2.902970
	2.303900			1.436500			1.159000	0.957800	
!-165									
	-0.602100			-1.593500			-2.518600	-3.010270	-3.315480
	-3.326870			-3.621140			-3.447370	-3.971900	-4.909480
	-5.645370			-6.183050			-4.382570	-0.544900	-2.544430
	-0.901520			0.815600			1.702920	1.882240	1.826490
	1.464090			0.732300			0.572900	0.128200	
!-150									
	-1.550010			-2.719240			-3.799900	-3.804440	-3.908390
	-3.834080			-3.912760			-3.989630	-4.580850	-5.180800
	-5.551653			-4.939713			-1.574530	2.019030	-2.977770
	-1.303570			0.104220			1.125620	1.539620	1.443750
	0.814930			0.545220			0.212300	-0.206550	
!-135									
	-1.919560			-2.986620			-3.966600	-4.249090	-4.309170
	-4.120940			-4.711580			-4.670431	-4.825664	-4.833039
	-3.895350			-1.748976			-5.944140	-4.773780	-3.285510
	-1.651960			0.008830			0.799790	1.114040	1.261370
	0.491610			0.169660			-0.143000	-0.983360	
!-120									
	-1.792360			-2.574640			-3.240070	-3.832430	-4.278530
	-4.687260			-5.205396			-5.031707	-4.359533	-3.545746
	-6.568035			-6.863508			-5.928660	-4.813000	-3.172860
	-1.681690			-0.146590			0.496930	0.939250	1.216890
	0.939030			0.024420			-0.364730	-0.940250	
!-105									
	-1.676510			-2.239220			-3.105060	-3.921610	-4.441700
	-4.561879			-4.882414			-4.649232	-3.754099	-5.566184
	-6.683430			-6.663330			-5.848020	-4.271050	-2.796960
	-1.461650			-0.643270			-0.013500	0.682650	1.073420
	1.188540			0.308530			-0.266340	-0.915370	
!-90									
	-1.545490			-2.479890			-2.989360	-3.607340	-3.943710
	-4.322090			-4.006360			-3.753650	-4.908200	-5.583350
	-6.423640			-6.093210			-5.004050	-3.607860	-2.557550
	-1.542900			-0.569000			-0.126800	0.685300	0.998100
	0.995970			0.462260			-0.246420	-0.998620	
!-75									
	-2.073750			-2.446160			-3.565280	-3.562650	-4.017330
	-4.003830			-3.535470			-3.663780	-4.577080	-5.554240
	-5.420920			-5.414150			-4.293180	-3.212010	-2.092400
	-0.995800			-0.189500			0.168400	0.701600	1.007800
	0.817400			0.219300			-0.831880	-1.463780	
!-60									
	-3.152770			-3.137590			-3.251010	-3.455590	-3.593703

-3.356621	-2.687230	-3.623970	-4.846670	-5.363020
-4.930860	-4.397530	-3.728840	-3.020230	-1.844300
1.819200	2.580400	0.625100	0.854200	0.907700
-0.073900	-1.054400	-2.127020	-2.788900	

!-45

-3.770150	-3.342460	-3.435857	-3.233680	-2.697704
-2.206907	-2.705960	-3.879900	-4.985030	-5.124630
-4.443270	-3.700260	-3.097500	-0.220130	0.969900
2.113150	0.716400	0.961900	1.015200	0.560500
-0.783400	-2.123570	-3.139530	-3.594750	

!-30

-2.695470	-2.217380	-1.439010	-0.914050	-1.800940
-2.792774	-3.600060	-4.332720	-4.547400	-3.999100
-3.448410	-1.305800	-0.219190	0.752670	1.727130
2.668630	1.173190	1.589820	1.620230	0.534230
-0.915690	-2.172410	-3.190240	-3.214490	

!-15

-0.577690	0.468040	1.911320	-2.603130	-3.261575
-3.724230	-4.092000	-4.025430	-3.089640	-2.017270
-0.620850	-0.355680	-0.052690	0.865190	1.624910
2.635730	1.539850	2.399590	1.862800	0.373900
-0.840940	-1.616660	-1.795490	-1.652460	

!0

2.983660	-0.731340	-2.449770	-3.374620	-3.714280
-3.587390	-2.552950	-1.668870	-1.037370	-1.389120
0.305970	0.254170	0.301930	0.955800	1.783820
2.694860	1.815380	1.838200	1.412000	1.158560
0.826180	0.701570	0.549430	0.944190	

!15

0.516980	-1.453141	-2.871540	-3.554290	-3.554230
-2.340490	-0.408410	0.382550	-0.135960	1.830730
1.229850	0.941560	0.702980	1.028110	1.797600
0.830350	1.023040	1.546780	1.757890	2.690890
3.459170	3.410046	3.899220	5.776320	

!30

-0.862960	-2.353690	-3.002680	-3.299920	-2.614530
-1.371160	0.552350	0.761870	0.431270	2.449210
2.135430	1.728890	1.507040	-0.517670	0.466670
0.169940	0.932780	1.487640	2.948260	4.980480
6.256220	6.939911	4.394500	1.306322	

!45

-0.888920	-1.727400	-1.736220	-1.725400	-1.359300
-0.668800	0.476000	0.617900	0.194000	0.496600
0.296100	-0.384200	-0.607670	0.044310	0.189700
0.275600	1.289210	2.626790	4.550970	5.572150
5.571590	4.423240	2.600280	0.373350	

!60

0.477650	0.015200	-1.274500	-1.332300	-0.746600
-0.459700	0.522600	0.536700	0.480700	0.347700
0.027200	-0.632100	-0.174500	0.136700	-0.239500
-0.322300	2.427630	3.838230	4.445790	4.572180
4.408980	3.392150	1.959630	1.483230	

!75

1.564200	0.652600	-0.071900	-0.009100	-0.071100
0.376500	0.736900	0.484900	0.605400	0.412600
-0.412200	-0.252200	0.044600	-0.518700	0.253000
1.845200	3.690420	4.370540	3.741090	3.869090
3.993580	3.251780	2.549500	3.542540	

!90

1.624000	0.922100	0.454500	0.192500	0.105500
0.324700	0.640500	1.090200	0.601400	0.169800
-0.777900	-1.448000	-1.345400	-0.443700	1.071200
2.597020	3.488740	4.051840	3.335460	3.503140
3.612780	3.323710	2.909250	2.919700	

!105

2.216200	0.905700	0.488100	0.010900	-0.138900
0.056000	1.225000	0.963200	0.276600	0.397500
-1.274200	-2.066100	-1.919700	-0.656900	1.070000
2.284170	3.112630	3.058460	3.229440	3.710040
3.531610	3.252290	2.985200	2.715100	

!120

1.530400	0.622100	-0.075800	-0.680200	-0.789200
-0.366900	1.095800	0.627100	0.126200	-0.240800
-1.624000	-2.452600	-1.945500	-0.616400	0.870830
1.789390	2.878530	2.931690	2.798480	3.719400
3.862340	3.203840	2.868200	2.130900	

!135

1.101400	-0.269000	-0.391000	-0.804800	-0.972800
-0.337200	0.496800	0.205700	-0.750400	-1.160500
-1.781500	-2.101700	-1.820130	-1.014040	0.280910
2.019040	2.221130	2.349690	2.623870	3.083140
3.277890	2.715500	2.414300	1.696300	

!150

0.255900	-0.642300	-1.115500	-1.103100	-0.583400
-0.041400	0.253100	-0.544200	-1.173200	-1.711300
-2.372180	-2.824240	-2.404170	-1.646520	-0.051970
2.636860	1.722010	2.149900	2.486900	2.883800
2.822900	2.218200	1.798300	1.594400	

!165

0.046900	-0.944200	-0.893100	-0.016800	-0.444100
-0.665900	-0.907900	-1.309920	-2.110050	-2.412550
-3.225790	-3.937160	-3.819750	-2.622840	0.443660
0.817160	1.255900	2.097480	2.606750	2.658300
2.572300	2.046800	1.753200	1.552400	

END
RETURN