

## 8.3. CONSTRAINTS AND RESTRAINTS IN REFINEMENT

Table 8.3.2.1. *Coordinates of atoms (in Å) in standard groups appearing in polypeptides and proteins; restraint relations may be determined from these coordinates using methods described by Hendrickson (1985)*

Main chain, links and terminal groups			
<b>Main</b>			
N	1.20134	0.84658	0.00000
C $\alpha$	0.00000	0.00000	0.00000
C	-1.25029	0.88107	0.00000
O	-2.18525	0.66029	-0.78409
<b>C terminal</b>			
N	1.20006	0.84799	0.00000
C $\alpha$	0.00000	0.00000	0.00000
C	-1.26095	0.86727	0.00000
O	-2.32397	0.27288	-0.29188
O <sub>i</sub>	-1.15186	2.04837	0.35987
<b>N amino terminal</b>			
N	1.20134	0.84658	0.00000
C $\alpha$	0.00000	0.00000	0.00000
C	-1.25029	0.88107	0.00000
O	-2.18525	0.66029	-0.78409
<b>N formyl terminal</b>			
N	1.19423	0.82137	0.00000
C $\alpha$	0.00000	0.00000	0.00000
C	-1.24896	0.88255	0.00000
O	-2.10649	0.78632	-0.90439
O <sub>i</sub>	2.46193	-0.77877	-0.93569
C <sub>i</sub>	2.33913	0.39064	-0.53355
<b>N acetyl terminal</b>			
N	1.19423	0.82137	0.00000
C $\alpha$	0.00000	0.00000	0.00000
C	-1.24896	0.88255	0.00000
O	-2.10649	0.78632	-0.90439
O <sub>i</sub>	2.46193	-0.77877	-0.93569
C <sub>1</sub>	2.33913	0.39064	-0.53355
C <sub>2</sub>	3.44659	1.39160	-0.63532
<b>trans peptide link</b>			
C $\alpha$	0.00000	0.00000	0.00000
C	0.57800	1.41700	0.00000
O	1.80400	1.60700	0.00001
N	-0.33500	2.37000	0.00000
C $\alpha$	0.00000	3.80100	0.00000
<b>cis peptide link</b>			
C $\alpha$	0.00000	0.00000	0.00000
C	1.30900	0.79200	0.00000
O	2.38500	0.17600	0.00000
N	1.23500	2.11000	0.00000
C $\alpha$	0.00000	2.90700	0.00000
<b>trans proline link</b>			
C $\alpha$	0.00000	0.00000	0.00000
C	0.57800	1.41700	0.00000
O	1.80400	1.60700	0.00001
N	-0.33500	2.37000	0.00000
C $\alpha$	0.00000	3.80100	0.00000
C $\delta$	-1.80000	2.19600	0.00000
<b>cis proline link</b>			
C $\alpha$	0.00000	0.00000	0.00000
C	1.30900	0.79200	0.00000
O	2.38500	0.17600	0.00000
N	1.23500	2.11000	0.00000
C $\alpha$	0.00000	2.90700	0.00000
C $\delta$	2.45500	2.93900	0.00000

Table 8.3.2.1 (cont.)

Side chains for amino acids			
<b>Ala A</b>			
C $\beta$	0.02022	-0.92681	1.20938
<b>Arg R</b>			
C $\beta$	-0.02207	-0.93780	1.20831
C $\gamma$	-0.09067	-0.23808	2.55932
C $\delta$	-0.79074	-1.07410	3.57563
N $\epsilon$	-0.76228	-0.46664	4.89930
C $\zeta$	-1.57539	-0.83569	5.89157
N $\eta$ 1	-2.60422	-1.65104	5.68019
N $\eta$ 2	-1.38328	-0.33329	7.11065
<b>Asn N</b>			
C $\beta$	0.04600	-1.02794	1.12104
C $\gamma$	-0.15292	-0.42844	2.50080
O $\delta$ 1	-0.39364	0.78048	2.63809
N $\delta$ 2	-0.06382	-1.27086	3.52863
<b>Asp D</b>			
C $\beta$	0.04600	-1.02794	1.12104
C $\gamma$	-0.15292	-0.42844	2.50080
O $\delta$ 1	-0.39364	0.78048	2.63809
O $\delta$ 2	-0.06930	-1.21904	3.46540
<b>Cys C</b>			
C $\beta$	0.01317	-0.95892	1.18266
S $\gamma$	-0.07941	-0.15367	2.80168
<b>Gln Q</b>			
C $\beta$	-0.01691	-0.98634	1.16423
C $\gamma$	-0.08291	-0.32584	2.52866
C $\delta$	-0.20841	-1.31760	3.65937
O $\epsilon$ 1	-0.48899	-2.49684	3.46331
N $\epsilon$ 2	-0.00450	-0.81846	4.87646
<b>Glu E</b>			
C $\beta$	-0.06551	-0.87677	1.25157
C $\gamma$	1.15947	-1.71468	1.59818
C $\delta$	1.40807	-2.90920	0.72611
O $\epsilon$ 1	0.92644	-3.06007	-0.38343
O $\epsilon$ 2	2.16269	-3.74330	1.27140
<b>Gly G (no nonhydrogen atoms)</b>			
<b>His H</b>			
C $\beta$	-0.06434	-0.96857	1.20324
C $\gamma$	-0.52019	-0.29684	2.46369
N $\delta$ 1	0.26457	0.53405	3.22184
C $\epsilon$ 1	-0.46699	1.05500	4.19371
N $\epsilon$ 2	-1.69370	0.59727	4.09040
C $\delta$ 2	-1.75570	-0.25685	3.02097
<b>Ile I</b>			
C $\beta$	0.03196	-0.97649	1.23019
C $\gamma$ 1	-0.83268	-2.22363	0.92046
C $\gamma$ 2	-0.39832	-0.28853	2.54980
C $\delta$ 1	-0.77555	-3.32741	2.01167
<b>Leu L</b>			
C $\beta$	0.09835	-0.94411	1.20341
C $\gamma$	-0.96072	-2.02814	1.32143
C $\delta$ 1	-0.89548	-2.98661	0.13861
C $\delta$ 2	-0.73340	-2.79002	2.62540
<b>Lys K</b>			
C $\beta$	-0.03606	-0.92129	1.21541
C $\gamma$	1.19773	-1.81387	1.35938
C $\delta$	1.05466	-2.77178	2.53242
C $\epsilon$	2.34215	-3.51295	2.82637
N $\zeta$	2.16781	-4.42240	3.98733

## 8. REFINEMENT OF STRUCTURAL PARAMETERS

Table 8.3.2.1 (*cont.*)

Met M			
C $\beta$	0.02044	-0.96506	1.17716
C $\gamma$	-1.00916	-2.05384	1.00286
S $\delta$	-0.77961	-3.24454	2.37236
C $\epsilon$	-2.08622	-4.42220	1.97795
Phe F			
C $\beta$	0.00662	-1.03603	1.11081
C $\gamma$	0.03254	-0.49711	2.50951
C $\delta$ 1	-1.15813	-0.12084	3.13467
C $\epsilon$ 1	-1.15720	0.38038	4.42732
C $\zeta$	0.05385	0.51332	5.11032
C $\epsilon$ 2	1.26137	0.11613	4.50975
C $\delta$ 2	1.23668	-0.38351	3.20288
Pro P			
C $\beta$	0.12372	-0.78264	1.31393
C $\gamma$	0.89489	0.13845	2.22063
C $\delta$	1.87411	0.86170	1.30572
Ser S			
C $\beta$	-0.00255	-0.96014	1.17670
O $\gamma$	-0.19791	-0.28358	2.40542
Thr T			
C $\beta$	-0.00660	-0.98712	1.23470
O $\gamma$ 1	0.04119	-0.14519	2.43011
C $\gamma$ 2	1.12889	-2.01366	1.21493
Trp W			
C $\beta$	0.02501	-0.98461	1.16268
C $\gamma$	0.03297	-0.36560	2.51660
C $\delta$ 1	-1.03107	0.15011	3.20411
N $\epsilon$ 1	-0.62445	0.62417	4.42903
C $\epsilon$ 2	0.72100	0.41985	4.55667
C $\zeta$ 2	1.57452	0.72329	5.60758
C $\eta$ 2	2.91029	0.38415	5.45120
C $\eta$ 3	3.37037	-0.23008	4.28944
C $\epsilon$ 3	2.51952	-0.53303	3.24549
C $\delta$ 2	1.17472	-0.20516	3.37412
Tyr Y			
C $\beta$	0.00470	-0.95328	1.20778
C $\gamma$	-0.18427	-0.27254	2.54372
C $\delta$ 1	0.89731	0.26132	3.25049
C $\epsilon$ 1	0.72371	0.85064	4.50059
C $\zeta$	-0.54776	0.88971	5.06861
C $\epsilon$ 2	-1.63905	0.38287	4.37622
C $\delta$ 2	-1.44975	-0.19374	3.12415
O $\eta$	-0.76405	1.40409	6.31652
Val V			
C $\beta$	0.05260	-0.99339	1.17429
C $\gamma$ 1	-0.13288	-0.31545	2.52668
C $\gamma$ 2	-0.94265	-2.12930	0.99811

Table 8.3.2.2. *Ideal values for distances (Å), torsion angles (°), etc. for a glycine-alanine dipeptide with a trans peptide bond; distance type 1 is a bond, type 2 a next-nearest-neighbour distance involving a bond angle*

Interatomic distances						
Number				Distance	Type	
1	N(1)	to	C(1) $\alpha$	1.470	1	
2	C $\alpha$ (1)	to	C(1)	1.530	1	
3	C(1)	to	O(1)	1.240	1	
4	N(1)	to	C(1)	2.452	2	
5	C(1) $\alpha$	to	O(1)	2.414	2	
6	N(2)	to	C(2) $\alpha$	1.469	1	
7	C(2) $\alpha$	to	C(2)	1.530	1	
8	C(2)	to	O(2)	1.252	1	
9	N(2)	to	C(2)	2.461	2	
10	C(2) $\alpha$	to	O(2)	2.358	2	
11	C(2) $\beta$	to	C(2) $\alpha$	1.524	1	
12	C(2) $\beta$	to	C(2)	2.515	2	
13	C(2) $\beta$	to	N(2)	2.450	2	
14	C(2)	to	O(2) <sub>t</sub>	1.240	1	
15	O(2)	to	O(2) <sub>t</sub>	2.225	2	
16	C(2) $\alpha$	to	O(2) <sub>t</sub>	2.377	2	
17	N(2)	to	C(1)	1.320	1	
18	N(2)	to	O(1)	2.271	2	
19	N(2)	to	C(1) $\alpha$	2.394	2	
20	C(2) $\alpha$	to	C(1)	2.453	2	
Planar groups						
1	CTRM	C(2) $\alpha$	C(2)	O(2)	O(2)	
2	LINK	C(1) $\alpha$	C(1)	O(1)	N(2)	C(2) $\alpha$
Chiral centres						
		Central atom				Chiral volume (Å <sup>3</sup> )
1	Ala	C(2) $\alpha$	N(2)	C(2)	C(2) $\beta$	2.492
Possible nonbonded contacts						
Number				Distance		
1	N(1)	to	O(1)	3.050		
2	N(2)	to	O(2)	3.050		
3	O(2)	to	C(2) $\beta$	3.350		
4	N(2)	to	O(2) <sub>t</sub>	3.050		
5	O(2) <sub>t</sub>	to	C(2) $\beta$	3.350		
Torsion angles						
N(1)	C(1) $\alpha$	C(1)	N(2)	0.0		
C(1) $\alpha$	C(1)	N(2)	C(2) $\alpha$	180.0		
C(1)	N(2)	C(2) $\alpha$	C(2)	0.0		
N(2)	C(2) $\alpha$	C(2)	O(2) <sub>t</sub>	0.0		

where  $\chi_{\text{ideal}}$  and  $\chi_{\text{model}}$  are dihedral angles between planar groups at opposite ends of the bond.

Interatomic distances are independent of the handedness of an enantiomorphous group. If  $\mathbf{r}_c$  is the position vector of a central atom and  $\mathbf{r}_1$ ,  $\mathbf{r}_2$ , and  $\mathbf{r}_3$  are the positions of three atoms bonded to it, such that the four atoms are not coplanar, the *chiral volume* is defined by

$$V_c = (\mathbf{r}_1 - \mathbf{r}_c) \cdot [(\mathbf{r}_2 - \mathbf{r}_c) \times (\mathbf{r}_3 - \mathbf{r}_c)], \quad (8.3.2.8)$$

where  $\times$  indicates the vector product. The chiral volume may be either positive or negative, depending on the handedness of the group. It may be restrained by including terms of the form

$$\Delta_c = (V_{\text{ideal}} - V_{\text{model}})^2 / \sigma_c^2. \quad (8.3.2.9)$$

Table 8.3.2.1 gives ideal coordinates, in an orthonormal coordinate system measured in Å, of various groups that are

$$\Delta_n = (d_{\text{min}} - d_{\text{model}})^4 / \sigma_n^4, \quad (8.3.2.6)$$

which are included only when  $d_{\text{model}} < d_{\text{min}}$ . Macromolecules usually gain flexibility by relatively unrestricted rotation about single bonds. There are, nevertheless, significant restrictions on these torsion angles, which may, therefore, be restrained by terms of the form

$$\Delta_t = (\chi_{\text{ideal}} - \chi_{\text{model}})^2 / \sigma_t^2, \quad (8.3.2.7)$$